

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: April 7, 2005, 00:34:03 ; Search time 176 Seconds
(without alignments)
966.901 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 440

Sequence: 1 MKFGPLACLLALLCLGSGE.....KLGFINWDINKDQRRSRIP 440

Scoring table:

Gapop 60.0 , Gapext 60.0

2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1

ID AAY9354 standard; protein; 440 AA.

DE Human PRO1411 (UNQ729) amino acid sequence SEQ ID NO:52.

PN WO200012708-A2.

PD 09-MAR-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 3; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 2

ID AAB66103 standard; protein; 440 AA.

DE Protein of the invention #15.

PN WO200078961-A1.

PD 28-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 3

ID AAB31205 standard; protein; 440 AA.

DE Amino acid sequence of human polypeptide PRO1411.

PN WO200077037-A2.

PD 21-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 4

ID AAU29124 standard; protein; 440 AA.

DE Human PRO polypeptide sequence #101.

PN WO200168848-A2.

PD 20-SEP-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 5

ID AAB87551 standard; protein; 440 AA.

DE Human PRO1411.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 4; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 6

ID AAU83669 standard; protein; 440 AA.

DE Human PRO protein, Seq ID No 156.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 5; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 7

ID ABG95876 standard; protein; 440 AA.

DE Human secreted/transmembrane protein PRO1411.

PN US2002119130-A1.

PD 29-AUG-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 5; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 8

ID ABB84891 standard; protein; 440 AA.

DE Human PRO1411 protein sequence SEQ ID NO:150.

PN WO200200690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 5; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

ID ABB95497 standard; protein; 440 AA.

DE Human angiogenesis related protein PRO1411 SEQ ID NO: 150.

PN WO200208284-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

PA (BAKE//) BAKER K P.

PA (FERR//) FERRARA N.

PA (GERB//) GERBER H.

PA (GERB//) GERBETSEN M E.

PA (GODD//) GODDARD A. A.

PA (GODO//) GODOWSKI P J.

PA (GURN//) GURNEY A L.

PA (HILL//) HILLAN K J.

PA (MARS//) MARSTERS S A.

PA (PANJ//) PAN J.

PA (PAON//) PAONI N F.

PA (STEP//) STEPHAN J F.

PA (WATA//) WATANABE C K.

PA (WILL//) WILLIAMS P M.

PA (WOOD//) WOOD W I.

Query Match 100.0%; Score 440; DB 5; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 10

ID ABU58500 standard; protein; 440 AA.

DE Human PRO polypeptide #101.

PN US2003027272-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 11

ID ABU88048 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.

PN US2003032127-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 12

ID ABU84363 standard; protein; 440 AA.

DE Human secreted/transmembrane protein (PRO) #101.

PN US2003032112-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 13

ID ABR66237 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003027278-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 14

ID ABR65627 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

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PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABR94705 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO25176 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO141.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO33782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO85678 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO98838 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO98053 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO91759 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO89452 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO86293 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
ID ABO67506 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036162-A1.
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PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 35
ID ABU80534 standard; protein; 440 AA.
DE Human secreted/transmembrane protein #101.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 36
ID ABU90901 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 37
ID ABO33960 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO411.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 38
ID ABR99452 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 39
ID ABR9842 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 40
ID ABO16365 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 41
ID ABR92265 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 42
ID ABO18906 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 43
ID ABR78327 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 44
ID ABU71977 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 45
ID ABU85063 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 46
ID ABO00202 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 47
ID ABO11534 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 48
ID ABO02179 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 49
ID ABU8753 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 50
ID ABU67294 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 51
ID ABU83448 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 52
ID ABO06249 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 53
ID ABR59285 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 54
ID ABO09347 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.

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PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ABO19211 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ABO11229 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ABR66847 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ABO16060 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ABO13766 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ABU71531 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ABU65669 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 202.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ABO07517 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ABO03704 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ABR67152 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ABO15755 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ABU56036 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO1411.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ABU72312 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ABU65364 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ABU95309 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ABU71212 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ABO07822 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ABR70063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ABR69396 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ABO01537 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003008353-A1.
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PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 75
ID ABU81339 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 76
ID ABR60136 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 77
ID ABU0985 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 78
ID ABR67871 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 79
ID ABR65259 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 80
ID ABR68481 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 81
ID ABR71893 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 82
ID ABU85373 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 83
ID ABU89063 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 84
ID ABU83143 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032105-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 85
ID ABU94999 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 86
ID ABU90547 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 87
ID ABU84058 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 88
ID ABU93709 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 89
ID ABR64954 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 90
ID ABR68786 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 91
ID ABO06602 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 92
ID ABR99147 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 93
ID ABU57031 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 94
ID ABU72062 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ABR5983 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ABR2270 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ABR7281 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ABR7163 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ABR3753 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ABO8127 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ABR2501 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ABR1838 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ABR66002 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ABR1171 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ABR59831 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ABR4019 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ABR9872 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ABR2125 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ABR6542 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ABR90960 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ABO53286 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ABR4387 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ABR79269 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ABR6598 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032129-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 115
ID ABU86903 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 116
ID ABU94692 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 117
ID AB004619 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 118
ID ABR70368 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 119
ID ABU98533 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 120
ID ABR65932 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 121
ID ABR64649 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 122
ID ABU79574 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 123
ID ABU92965 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 124
ID ABU95924 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 125
ID ABU91144 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 126
ID ABU90237 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 127
ID AB009652 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 128
ID AB010924 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 129
ID ABR70978 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 130
ID ABU98288 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 131
ID ABU87586 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 132
ID ABU91454 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 133
ID ABU89293 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 134
ID ABU84668 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 135

Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 125
ID ABU91144 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 126
ID ABU90237 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 127
ID AB009652 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 128
ID AB010924 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 129
ID ABR70978 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 130
ID ABU98288 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 131
ID ABU87586 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 132
ID ABU91454 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 133
ID ABU89293 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 134
ID ABU84668 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 135

ID ABR69758 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ABR80135 standard; protein; 440 AA.
DE Human PRO protein #101.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ABR82500 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ABR93404 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ABO09957 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ABO09042 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ABR96464 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ABR10610 standard; protein; 440 AA.
DE Human secreted/transmembrane protein #101.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ABR72134 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ABR95619 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 145
ID ABR79805 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ABR96828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ABR70673 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ABO05024 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ABO08432 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ABO05639 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ABR74028 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ABR95620 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ABR80917 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ABR81222 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049743-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ABM00918 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ABR88520 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ABM77341 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ABO28825 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ABO31570 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ABR07987 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ABO40467 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ABO35892 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ABO44031 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADA77954 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ABM24826 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ABO03094 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ABR90350 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ABM17264 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ABR95010 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ABR95315 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ABR72305 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADB17109 standard; protein; 440 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ABO21553 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.

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PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ABR97817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ABR87605 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ABR77646 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ABR27876 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ABR06157 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ABR03663 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ABR35114 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ABR26351 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ABO48133 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ABR92875 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ABO24636 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003085159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ABM11647 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ABM02748 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ABM16044 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003084463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ABO27605 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ABM29096 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ABM07072 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003086899-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ABM21166 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ABO09512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ABO41382 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ABO36197 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ABO43726 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ABO76426 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ABO76122 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ABO25741 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ABO26046 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ABO03399 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ABO02484 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ABO4264 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 1411.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ABR90655 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ABR73723 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ABO16975 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ABR94400 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ABR75907 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ABR71283 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ABR93180 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ABR93485 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 211
ID ABO39552 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ABO33596 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ABO27910 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ABO30045 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ABO33254 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ABO4942 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ASM08902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ABO36502 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ABO35587 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ABR86995 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

ID ABO39552 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ABO10427 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ABO11952 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ABO52098 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ABO52403 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ADA19914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ABO23721 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ADB17297 standard; protein; 440 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ABR97207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ABR86995 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

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PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 230
ID ABM11037 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 231
ID ABM28181 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 232
ID ABO32180 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 233
ID ABM15307 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 234
ID ABO06462 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 235
ID ABO04273 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 236
ID ABM22386 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 237
ID ABO07682 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 238
ID ABO40772 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068684-A1.

PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 239
ID ABM35419 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 240
ID ABM33182 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 241
ID ABO52708 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 242
ID ABO50268 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 243
ID ABO99262 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 244
ID ABO04314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 245
ID ABO05944 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 246
ID ABM18484 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 247
ID ABR97512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 6; Length 440;
RESULT 248
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ID ABR80612 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 249
ID ABM01223 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 250
ID ABR88825 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 251
ID ABM13477 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 252
ID ABM20861 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 253
ID ABO41992 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 254
ID ABO42602 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 255
ID ABM10122 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 256
ID ABO38637 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 257
ID ABM32877 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 258
ID ABM22691 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 259
ID ABM74902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 260
ID ADA79746 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 261
ID ABR96292 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 262
ID ABM02443 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 263
ID ABR86385 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 264
ID ABR86690 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 265
ID ABM16654 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 266
ID ABM29706 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003084456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;

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RESULT 267
ID ABO29130 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ABM23911 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ABM23301 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 270
ID ADA4728 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 271
ID ABM22081 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 272
ID ABO37722 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 273
ID ABM28486 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 274
ID ABM28791 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 275
ID ABM66435 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 276
ID ABM75817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 277
ID ABM34097 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 278
ID ABM34402 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 279
ID ABO20333 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 280
ID ABO21248 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 281
ID ABO22163 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 282
ID ADA20086 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 283
ID ABR9597 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ABR85775 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ABR99757 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ABO0613 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 287
ID ABO0308 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ABO29740 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ABO23606 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ABO29401 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ABO38332 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ABO4532 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ABO20556 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ABO41473 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ABO16670 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ABO18296 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ABO22723 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ABO23028 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ABR92570 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ABR81527 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ABM77951 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ABR89740 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ABM26656 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ABM13782 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 440; DB 6; Length 440;
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ABO28520 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ABO30350 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ABO07377 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ABO03968 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ABO37112 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ABO41687 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ABO35282 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ABO25131 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ABO47523 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ABO47828 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ABO48438 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ABO51488 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ABO51793 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ABO50573 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ABR79697 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ABM16959 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ABO17991 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 322
ID ABO20943 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 323
ID ABR96902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054462-A1.
PD 20-MAR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 324
ID ABM12257 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064445-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 03-APR-2003.
ID ABM16349 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 03-APR-2003.
ID ABM24216 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 03-APR-2003.
ID ABM14697 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 10-APR-2003.
ID ABM04578 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 10-APR-2003.
ID ABM06767 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 10-APR-2003.
ID ABM09207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 10-APR-2003.
ID ABO39247 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 10-APR-2003.
ID ABM75512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 27-FEB-2003.
ID ABM25436 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 05-JUN-2003.
ID ABM19946 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 13-MAR-2003.
ID ABO46852 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 13-MAR-2003.
ID ABO47157 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 13-MAR-2003.
ID ADA83271 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 13-FEB-2003.
ID ABR71588 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 13-FEB-2003.
ID ABR72198 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 20-FEB-2003.
ID ABR98537 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US20030356129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 27-FEB-2003.
ID ABO06907 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
PD 27-FEB-2003.
ID ABR84860 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 6; Length 440;
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ABR73418 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID ABR76512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ABR73113 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ABJ72433 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ABM18179 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ABO20638 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ABO25381 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ABO25686 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ABR94095 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ABR80002 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ABM1342 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ABO32949 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ABO30655 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ABO30960 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 357
ID AEM27266 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ABM30011 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ABM05547 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ABM15612 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ABM08597 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ABO42297 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ABO38027 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ABO45937 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ABM66740 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366
ID ADB20314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ABM19641 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ABO49353 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ABO49658 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ADA78566 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ABO34328 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 1411.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ABR88215 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ADA00383 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 411.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ABM26961 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ABM03358 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID ABO39857 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003086889-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID ABO49963 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ABO50878 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ABO5334 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ABR74538 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 381
ID ABO44449 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 382
ID ABR77117 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 383
ID ABR17874 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 384
ID ABR95925 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 385
ID ABO21858 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 386
ID ABO20028 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 387
ID ABO24331 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 388
ID ABR86080 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 389
ID ABR10732 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 390
ID ABR76731 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 391
ID ABR89435 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 392
ID ABR12562 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 393
ID ABR05852 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 394
ID ABO34977 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 395
ID ABR03053 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 396
ID ABR19031 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 397
ID ABR19336 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 398
ID ABO46547 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 399
ID ABR05852 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 399
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ID ABO49048 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049757-A1.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 400
ID ABR69091 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 401
ID ABR89130 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 402
ID ABR72503 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 403
ID ABR74333 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 404
ID ABO18601 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 405
ID ABR80307 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 406
ID ABO01528 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 407
ID ABO02138 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 408
ID ABR87300 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 409
ID ABM12867 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 410
ID ABM30621 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003084443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 411
ID ABM24521 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003084444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 412
ID ABO29435 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 413
ID ABO31265 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 414
ID ABM14392 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 415
ID ABM09817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 416
ID ABO38942 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 417
ID ABM34707 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104538-A1.
PD 05-JUN-2003.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 418
ID ABO51183 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 419
ID ABO04009 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 420
ID ABO10479 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 421
ID ABR7722 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 422
ID ABR78932 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 423
ID ABO24026 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 424
ID ABR93790 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 425
ID ABO1833 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 426
ID ABR78256 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 427
ID ABO33473 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 428
ID ABR90045 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 429
ID ABR27571 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 430
ID ABR13172 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 431
ID ABO31875 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 432
ID ABR14087 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 433
ID ABR08292 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 434
ID ABO40162 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 435
ID ABR74597 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 436
ID ABR33792 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 437
ID ABR20251 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104556-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 438
ID ABO48743 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 439
ID ABR72808 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 440
ID ABO15450 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 441
ID ABR85165 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 442
ID ABO15145 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 443
ID ABO17280 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 444
ID ABO19863 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 445
ID ABR17569 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 446
ID ABR72135 standard; protein; 440 AA.
DE Human membrane bound receptor/protein PRO1411 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 447
ID ABR85470 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 448
ID ABR77036 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 449
ID ABO28215 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 450
ID ABR22996 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 451
ID ABR30316 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 452
ID ABR21776 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 453
ID ABR21471 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 454
ID ABR15002 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 455
ID ABO41077 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 456
ID ABO36807 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 457
ID ABO37417 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 458
ID ABO75207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 459
ID ABO33487 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 460
ID ABO46242 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 461
ID ADA82637 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 462
ID ADB85625 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 463
ID ADB83646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 464
ID ADB80752 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 465
ID ADB73293 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 466
ID ABO31841 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 467
ID ABO78375 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 468
ID ABO31231 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 469
ID ADB85023 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 470
ID ABO78129 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 471
ID ADB85945 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 472
ID ABO32146 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 473
ID ABO32451 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 474
ID ADB87195 standard; protein; 440 AA.

DE Human PRO polypeptide #78.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 475
ID ADB84777 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 476
ID ADB68304 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 477
ID ADB68111 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 478
ID ADB31536 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 479
ID ADB30926 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:203.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 480
ID ADB83892 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 481
ID ADB73047 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 482
ID ADB90928 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 483
ID ADC07008 standard; protein; 440 AA.
DE Human PRO1411 protein.

PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 484
ID ADC17921 standard; protein; 440 AA.
DE Human PRO polypeptide #15.
PN US2003084925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 485
ID ADC17187 standard; protein; 440 AA.
DE Mammalian PRO polypeptide (SeqID 52).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 486
ID ADC14885 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 487
ID ADC36885 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003088085-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 488
ID ADC52380 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 489
ID ADC21875 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 490
ID ADC49906 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 491
ID ADC49105 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 492
ID ADC49622 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088071-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 493
ID ADC47483 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 494
ID ADC47228 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 495
ID ADC78103 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 496
ID ADD06338 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 497
ID ADD05675 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 498
ID ADD10439 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 499
ID ADC77857 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 500
ID ADD11399 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 501
ID ADD50820 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 502
ID ADD51066 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 503
ID ADD70567 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 504
ID ADD39644 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 505
ID ADD70090 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 506
ID ADD37192 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 507
ID ADD36056 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 508
ID ADD38211 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 509
ID ADD39167 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 510
ID ADD50547 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 511
ID ADD50301 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 512
ID ADD38690 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 513
ID ADD40121 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 514
ID ADD51312 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 515
ID ADE50342 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 516
ID ADE19954 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 517
ID ADE49865 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 518
ID ADE21423 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 519
ID ADF29848 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US20031204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 520
ID ADF55741 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 521
ID ADG01057 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 522
ID ADG08610 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 523
ID ADG02670 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 524
ID ADG01377 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 525
ID ADF95552 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 526
ID ADF95231 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 527
ID ADG12367 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 528
ID ADH24084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 7; Length 440;
RESULT 529
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ID ADH34110 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 530
ID ADH29943 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 531
ID ADH23914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 532
ID ADH09027 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
FN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 533
ID ADG85318 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 534
ID ADH24594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 535
ID ADH37450 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO411.
FN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 536
ID ADH02039 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
FN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 537
ID ADH37620 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO411.
FN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 538
ID ADG85658 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 539
ID ADH24254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 540
ID ADH38548 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 541
ID ADG63787 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
FN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 542
ID ADG83669 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
FN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 543
ID ADH29477 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 544
ID ADH27593 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
FN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 545
ID ADH37790 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO1411.
FN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 546
ID ADH37967 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO411.
FN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 547
ID ADH57387 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.

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PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 548
ID ADH53529 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 549
ID ADH53699 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 550
ID ADH52035 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 551
ID ADH49890 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 552
ID ADI25400 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 553
ID ADH90193 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 554
ID ADI25570 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 555
ID ADH97744 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 556
ID ADH99245 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003065142-A1.

PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 557
ID ADI03592 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 558
ID ADI11949 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 559
ID ADH90023 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 560
ID ADH98424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 561
ID ADI11099 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 562
ID ADI11609 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 563
ID ADH98254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 564
ID ADH98594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 440; DB 7; Length 440;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 565
ID ADH98084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181673-A1.
PD 25-SEP-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 566
ID ADI05072 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 567
ID ADI03422 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO411.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 568
ID ADI04817 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 569
ID ADH78271 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 570
ID ADI19615 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 571
ID ADH90363 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 572
ID ADI03082 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 573
ID ADH77931 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 574
ID ADH97914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 575
ID ADI01299 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 576
ID ADI01994 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 577
ID ADI03252 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 578
ID ADI11439 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 579
ID ADI02341 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 580
ID ADI11779 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 581
ID ADI05416 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 582
ID ADH79488 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 583
ID ADI19445 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 584
ID ADH97914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 584
ID ADI05246 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 585
ID ADH79658 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 586
ID ADI01484 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 587
ID ADI01654 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 588
ID ADI01824 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 589
ID ADH79828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 590
ID ADI04646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 591
ID ADI02782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 592
ID ADH78101 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 593
ID ADI25740 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 594
ID ADI25910 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 595
ID ADK65422 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 596
ID ADH98764 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 597
ID ADH80005 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 598
ID ADM30342 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 599
ID ADL93736 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 600
ID ADC48859 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 601
ID ADC52190 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 602
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ADE21030 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 603
ID ADE05874 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 604
ID ADD75103 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 605
ID ADD75849 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 606
ID ADD85081 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 607
ID ADD86907 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 608
ID ADE20784 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 609
ID ADE39081 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 610
ID ADE05628 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 611
ID ADD73613 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 612
ID ADD78453 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 613
ID ADE41400 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 614
ID ADE74339 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 615
ID ADE21276 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 616
ID ADD77391 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 617
ID ADE20538 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 618
ID ADD75603 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 619
ID ADD74119 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 620
ID ADD74365 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100709-A1.
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PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 630
ID ADD77637 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 631
ID ADD77883 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 632
ID ADD85341 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 633
ID ADD73873 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 634
ID ADD74611 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 635
ID ADD77139 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 636
ID ADD85833 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 637
ID ADE05382 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 638
ID ADD74857 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 639
ID ADE74951 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211574-A1.
PD 13-NOV-2003.

PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 621
ID ADD76095 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 622
ID ADD85587 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 623
ID ADE05136 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 624
ID ADD75349 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 625
ID ADD76893 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 626
ID ADD86661 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 627
ID ADE41201 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 628
ID ADD78129 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 629
ID ADE74951 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211574-A1.
PD 13-NOV-2003.
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DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 658
ID ADH33736 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 659
ID ADG82851 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 660
ID ADH02940 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 661
ID ADH02379 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 662
ID ADH07986 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 663
ID ADG69383 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 664
ID ADH39204 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 665
ID ADH03894 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 666
ID ADH03417 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003068768-A1.

PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 667
ID ADH26132 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 668
ID ADG83944 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 669
ID ADH39062 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 670
ID ADG8548 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 671
ID ADG63636 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 672
ID ADH06282 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 673
ID ADH30112 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 674
ID ADH24424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 675
ID ADH33101 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068768-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 676
ID ADG6953 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 677
ID ADH07816 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 678
ID ADG85828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 679
ID ADH39374 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 680
ID ADH33566 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 681
ID ADH33906 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 682
ID ADH01116 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 683
ID ADG69723 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 684
ID ADH02209 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 685
ID ADG69213 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 686
ID ADG85998 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 687
ID ADH24934 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 688
ID ADH39551 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 689
ID ADH02549 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 690
ID ADG69043 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 691
ID ADH07646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 692
ID ADG86168 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 440; DB 8; Length 440;
RESULT 693
ID ADH24764 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.


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RESULT 712
ID ADJ98578 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 713
ID ADJ98748 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 714
ID ADH78907 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 715
ID ADJ99141 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 716
ID ADJ99311 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 717
ID ADJ98929 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 718
ID ADH79077 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 719
ID ADK00937 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 720
ID ADK14458 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 721
ID ADN37967 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 722
ID ADK82928 standard; protein; 440 AA.
DE Human PRO polypeptide #75.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 723
ID ADJ64611 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 724
ID ADK66632 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 725
ID ADM31507 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 726
ID ADM36554 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 727
ID ADM40359 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 728
ID ADM80907 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 729
ID ADL94571 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 730
ID ADN37967 standard; protein; 440 AA.
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DE Novel human secreted and transmembrane protein PRO1411.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 440; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 731
ID ABL32808 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 78.4%; Score 345; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 6.5e-291;
RESULT 732
ID ABO27306 standard; protein; 372 AA.
DE Human secreted/transmembrane polypeptide PRO411.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 77.3%; Score 340; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.2e-286;
RESULT 733
ID ABO34192 standard; protein; 372 AA.
DE Human secreted/transmembrane polypeptide PRO 1411.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 77.3%; Score 340; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.2e-286;
RESULT 734
ID AAB38324 standard; protein; 387 AA.
DE Human secreted protein encoded by gene 4 clone HKAJK47.
PN WO2000061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.5%; Score 178; DB 3; Length 387;
Best Local Similarity 99.6%; Pred. No. 7.1e-146;
RESULT 735
ID AAY50939 standard; protein; 358 AA.
DE Human adult skin cDNA clone vd3_1 derived protein #1.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 31.8%; Score 140; DB 3; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.9e-113;
RESULT 736
ID AAY50940 standard; protein; 369 AA.
DE Human adult skin cDNA clone vd3_1 derived protein #2.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 31.8%; Score 140; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 7.1e-113;
RESULT 737
ID AAY50941 standard; protein; 479 AA.
DE Human adult skin cDNA clone vd4_1 derived protein.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 31.8%; Score 140; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.9e-113;
RESULT 738
ID ADP07783 standard; protein; 186 AA.
DE Human secreted protein, seq id 266.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 20.5%; Score 90; DB 8; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
RESULT 739
ID AAY60056 standard; protein; 230 AA.
DE Human endometrium tumour EST encoded protein 116.

PN DE19817948-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 19.5%; Score 86; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-66;
RESULT 740
ID AAM94219 standard; protein; 116 AA.
DE Human reproductive system related antigen SEQ ID NO: 2877.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.5%; Score 55; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
RESULT 741
ID ADE28209 standard; protein; 203 AA.
DE Human MDDT protein - SEQ ID 59.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.1%; Score 40; DB 7; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.2e-26;
RESULT 742
ID AAY12417 standard; protein; 76 AA.
DE Human 5' EST secreted protein SEQ ID NO:448.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.0%; Score 35; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
RESULT 743
ID AAG01482 standard; protein; 72 AA.
DE Human secreted protein, SEQ ID NO: 5563.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 5.7%; Score 25; DB 3; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
RESULT 744
ID AAG01483 standard; protein; 72 AA.
DE Human secreted protein, SEQ ID NO: 5564.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 5.7%; Score 25; DB 3; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
RESULT 745
ID AAB73503 standard; protein; 123 AA.
DE Human transferase HTFS-10, SEQ ID NO:10.
PN WO200132888-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.7%; Score 25; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
RESULT 746
ID ABU25709 standard; protein; 1751 AA.
DE Protein encoded by Prokaryotic essential gene #11236.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.4%; Score 15; DB 6; Length 1751;
Best Local Similarity 100.0%; Pred. No. 0.0011;
RESULT 747
ID AAE35982 standard; peptide; 16 AA.
DE Linker peptide #2 used in the exemplification of the invention.
PN WO2002101079-A2.
PD 19-DEC-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 3.0%; Score 13; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00098;
RESULT 748
ID ADQ66425 standard; protein; 120 AA.
DE Novel human protein sequence #1398.
PN EP1440981-A2.

PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 3.0%; Score 13; DB 8; Length 120;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 RESULT 749
 ID AA317241 standard; protein; 476 AA.
 DE Heterodera glycines cellulase HG-engl.
 PN WO9801569-A1.
 PD 15-JAN-1998.
 PA (RIJK-) RIJSLANDBOUWHOGESCHOOL.
 Query Match 3.0%; Score 13; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 RESULT 750
 ID AA43910 standard; protein; 484 AA.
 DE Heterodera glycines svp encoded cellulase.
 PN EP818538-A1.
 PD 14-JAN-1998.
 PA (RIJK-) RIJSLANDBOUWHOGESCHOOL.
 Query Match 3.0%; Score 13; DB 2; Length 484;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 RESULT 751
 ID ABB68240 standard; protein; 828 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 31512.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.7%; Score 12; DB 4; Length 828;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 RESULT 752
 ID ADA20331 standard; protein; 214 AA.
 DE Mutant human CITED2 protein amino acids 1-214.
 PN WO2003038441-A2.
 PD 08-MAY-2003.
 PA (ISIS-) ISIS INNOVATION LTD.
 Query Match 2.5%; Score 11; DB 6; Length 214;
 Best Local Similarity 100.0%; Pred. No. 0.52;
 RESULT 753
 ID ABB69351 standard; protein; 252 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 34845.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.5%; Score 11; DB 4; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.6;
 RESULT 754
 ID AAB60461 standard; protein; 270 AA.
 DE Human cell cycle and proliferation protein CCYPR-9, SEQ ID NO:9.
 PN WO200107471-A2.
 PD 01-FEB-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.5%; Score 11; DB 4; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 755
 ID ADA20318 standard; protein; 270 AA.
 DE Human CITED2 protein.
 PN WO2003038441-A2.
 PD 08-MAY-2003.
 PA (ISIS-) ISIS INNOVATION LTD.
 Query Match 2.5%; Score 11; DB 6; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 756
 ID ADD18604 standard; protein; 270 AA.
 DE Human disease related protein SeqID35.
 PN WO2003018621-A2.
 PD 06-MAR-2003.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 2.5%; Score 11; DB 7; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 757
 ID ABE60370 standard; protein; 270 AA.
 DE Human Protein Q99967, SEQ ID NO 6278.
 PN WO2003018475-A2.
 PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 2.5%; Score 11; DB 7; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 758
 ID ADE60373 standard; protein; 270 AA.
 DE Human Protein Q99967, SEQ ID NO 6282.
 PN WO2003018475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 2.5%; Score 11; DB 7; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 759
 ID ADD45931 standard; protein; 270 AA.
 DE Human Protein Q99967, SEQ ID NO 11603.
 PN WO2003018475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 2.5%; Score 11; DB 7; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 760
 ID ADN95881 standard; protein; 270 AA.
 DE Human BEC/LEC-related protein sequence SeqID805.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 2.5%; Score 11; DB 7; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 761
 ID ADO19714 standard; protein; 270 AA.
 DE Human PRO polypeptide #320.
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 2.5%; Score 11; DB 8; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 762
 ID ADO19616 standard; protein; 270 AA.
 DE Human PRO polypeptide #273.
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 2.5%; Score 11; DB 8; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 763
 ID ADR14659 standard; protein; 270 AA.
 DE Human NF-kappaB pathway-associated protein SeqID660.
 PN WO2004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 2.5%; Score 11; DB 8; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 764
 ID ADP54707 standard; protein; 270 AA.
 DE Human PRO protein sequence SEQ ID NO:683.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 2.5%; Score 11; DB 8; Length 270;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 RESULT 765
 ID ADJ35152 standard; protein; 445 AA.
 DE Xylanase from an environmental sample seq id 368.
 PN WO20030186654-A2.
 PD 24-DEC-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 2.5%; Score 11; DB 8; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0.98;
 RESULT 766
 ID ABR55544 standard; protein; 452 AA.

DE Amino acid sequence of mature murine mucinase AMCase.
PN W02003038079-A2.
PD 08-MAY-2003.
PA (MACR-) MACROZYME BV. 2.5%; Score 11; DB 7; Length 452;
Query Match 100.0%; Pred. No. 1;
Best Local Similarity 100.0%; Pred. No. 1;
RESULT 767
ID ABR55543 standard; protein; 473 AA.
DE Amino acid sequence of murine mucinase AMCase.
PN W02003038079-A2.
PD 08-MAY-2003.
PA (MACR-) MACROZYME BV. 2.5%; Score 11; DB 7; Length 473;
Query Match 100.0%; Pred. No. 1;
Best Local Similarity 100.0%; Pred. No. 1;
RESULT 768
ID ADC51464 standard; protein; 473 AA.
DE Chitotriase 52.03 protein SEQ ID NO:2.
PN CN1382800-A.
PD 04-DEC-2002.
PA (BIOW-) BIONDOWN GENE DEV INC SHANGHAI. 2.5%; Score 11; DB 7; Length 473;
Query Match 100.0%; Pred. No. 1;
Best Local Similarity 100.0%; Pred. No. 1;
RESULT 769
ID ABU09914 standard; protein; 520 AA.
DE Partial mouse acidic mammalian chitinase (AMCase) precursor.
PN W02003031582-A2.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
PA (CURA-) CURAGEN CORP.
PA (STEW) STEWART T A.
PA (KELL) KELLY K M.
Query Match 2.5%; Score 11; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.1;
RESULT 770
ID ABB70436 standard; protein; 644 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38100.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.5%; Score 11; DB 4; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.4;
RESULT 771
ID ADH48368 standard; protein; 718 AA.
DE Human KPP protein SEQ ID NO:26.
PN W02004001008-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.5%; Score 11; DB 8; Length 718;
Best Local Similarity 100.0%; Pred. No. 1.5;
RESULT 772
ID ADB09224 standard; protein; 844 AA.
DE Allostococcus otitis antigenic protein SEQ ID NO:3164.
PN W02003048304-A2.
PD 12-JUN-2003.
PA (AWHP) WYETH HOLDINGS CORP.
Query Match 2.5%; Score 11; DB 6; Length 844;
Best Local Similarity 100.0%; Pred. No. 1.7;
RESULT 773
ID ADB09226 standard; protein; 871 AA.
DE Allostococcus otitis antigenic protein SEQ ID NO:3166.
PN W02003048304-A2.
PD 12-JUN-2003.
PA (AWHP) WYETH HOLDINGS CORP.
Query Match 2.5%; Score 11; DB 6; Length 871;
Best Local Similarity 100.0%; Pred. No. 1.8;
RESULT 774
ID ADB85183 standard; protein; 923 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5432.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.5%; Score 11; DB 8; Length 923;
Best Local Similarity 100.0%; Pred. No. 1.9;
RESULT 775
ID ABP70836 standard; protein; 953 AA.
DE Human serine/threonine kinase-related protein.
PN W02003018786-A2.
PD 06-MAR-2003.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 11; DB 6; Length 953;
Best Local Similarity 100.0%; Pred. No. 1.9;
RESULT 776
ID ADC77693 standard; protein; 953 AA.
DE Human 16314 protein SEQ ID NO:56.
PN W02003073983-A2.
PD 12-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.5%; Score 11; DB 7; Length 953;
Best Local Similarity 100.0%; Pred. No. 1.9;
RESULT 777
ID ADO01049 standard; protein; 954 AA.
DE Human homologue of Fruit fly AD-related protein CG8789 #3.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 2.5%; Score 11; DB 8; Length 954;
Best Local Similarity 100.0%; Pred. No. 1.9;
RESULT 778
ID RAG94132 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 326.
PN W0200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 2.3%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.26;
RESULT 779
ID ADO43232 standard; peptide; 10 AA.
DE Bioactivation peptide extension used to solubilise quantum dot.
PN W02004039830-A2.
PD 13-MAY-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.3%; Score 10; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.26;
RESULT 780
ID ADO57970 standard; peptide; 15 AA.
DE MHC multimer linker peptide SEQ ID 5.
PN DE10247014-A1.
PD 22-APR-2004.
PA (ERFL) ERFL V.
Query Match 2.3%; Score 10; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.37;
RESULT 781
ID ADO43228 standard; peptide; 20 AA.
DE Bioactivation peptide used to solubilise quantum dot.
PN W02004039830-A2.
PD 13-MAY-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.3%; Score 10; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.48;
RESULT 782
ID AAU77733 standard; protein; 119 AA.
DE Novel human secreted protein #5.
PN W0200214341-A1.
PD 21-FEB-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 10; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.3;
RESULT 783
ID AAM92862 standard; protein; 203 AA.
DE Human digestive system antigen SEQ ID NO: 2211.
PN W0200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 10; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.7;
RESULT 784

ID ADQ97309 standard; protein; 214 AA.
DE Human cancer associated sequence HP08-029, SEQ ID 286.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 10; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.8;
RESULT 785
ID ABG08358 standard; protein; 324 AA.
DE Novel human diagnostic protein #8349.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 10; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 5.5;
RESULT 786
ID ABB97580 standard; protein; 368 AA.
DE Novel human protein SEQ ID NO: 848.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 10; DB 5; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 787
ID ABU09916 standard; protein; 368 AA.
DE Human eosinophil chemotactic-like cytokine.
PN WO2003031582-A2.
PD 17-APR-2003.
PA (GETH-) GENENTECH INC.
PA (CURA-) CURAGEN CORP.
PA (STEW/) STEWART T A.
PA (KELL/) KELLY K M.
Query Match 2.3%; Score 10; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 788
ID ADP69059 standard; protein; 368 AA.
DE Human NOV6f protein SEQ ID NO:54.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 2.3%; Score 10; DB 8; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 789
ID ADP69057 standard; protein; 368 AA.
DE Human NOV6e protein SEQ ID NO:52.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 2.3%; Score 10; DB 8; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 790
ID ADP69061 standard; protein; 368 AA.
DE Human NOV6g protein SEQ ID NO:56.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 2.3%; Score 10; DB 8; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 791
ID ADP69053 standard; protein; 368 AA.
DE Human NOV6c protein SEQ ID NO:48.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 2.3%; Score 10; DB 8; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 792
ID ADP69055 standard; protein; 368 AA.
DE Human NOV6d protein SEQ ID NO:50.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 2.3%; Score 10; DB 8; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 793
ID ADP69049 standard; protein; 368 AA.
DE Human NOV6a protein SEQ ID NO:44.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 2.3%; Score 10; DB 8; Length 368;
Best Local Similarity 100.0%; Pred. No. 6.1;
RESULT 794
ID ABU56729 standard; protein; 441 AA.
DE Lung cancer-associated polypeptide #322.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.3%; Score 10; DB 6; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2;
RESULT 795
ID ADD45205 standard; protein; 441 AA.
DE Human Protein S34118, SEQ ID NO 10638.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 10; DB 7; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2;
RESULT 796
ID ADE55546 standard; protein; 441 AA.
DE Human Protein S34118, SEQ ID NO 1363.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 10; DB 7; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2;
RESULT 797
ID ADN39194 standard; protein; 441 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:512.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 2.3%; Score 10; DB 7; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2;
RESULT 798
ID ADQ21597 standard; protein; 441 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4417.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.3%; Score 10; DB 8; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2;
RESULT 799
ID AAG62541 standard; protein; 455 AA.
DE Disease treatment related protein SEQ ID NO: 1.
PN WO200136633-A1.
PD 25-MAY-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.3%; Score 10; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 7.4;
RESULT 800
ID AAG62543 standard; protein; 476 AA.
DE Disease treatment related protein SEQ ID NO: 5.
PN WO200136633-A1.
PD 25-MAY-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.3%; Score 10; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.7;
RESULT 801
ID ABU09915 standard; protein; 476 AA.
DE Human acidic mammalian chitinase (AMCase) precursor.
PN WO2003031582-A2.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

PA (CURA-) CURAGEN CORP.
PA (STEW/) STEWART T A.
PA (KELL/) KELLY K M.
Query Match 2.3%; Score 10; DB 6; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.7;
RESULT 802
ID ABR55542 standard; protein; 476 AA.
DE Amino acid sequence of human mucinase AMCase.
PN WO2003038079-A2.
PD 08-MAY-2003.
PA (MACR-) MACROZYME BV.
Query Match 2.3%; Score 10; DB 7; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.7;
RESULT 803
ID ADP69051 standard; protein; 476 AA.
DE Human NOV6b protein SEQ ID NO:46.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 2.3%; Score 10; DB 8; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.7;
RESULT 804
ID AAB68273 standard; protein; 501 AA.
DE Amino acid sequence of an Arabidopsis thaliana PMR6 gene.
PN WO200129230-A2.
PD 26-APR-2001.
PA (CARN-) CARNEGIE INST WASHINGTON.
Query Match 2.3%; Score 10; DB 4; Length 501;
Best Local Similarity 100.0%; Pred. No. 8.1;
RESULT 805
ID ADN74843 standard; protein; 501 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 2738.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDISEIGN NV.
Query Match 2.3%; Score 10; DB 8; Length 501;
Best Local Similarity 100.0%; Pred. No. 8.1;
RESULT 806
ID AAE19445 standard; protein; 537 AA.
DE Hansenula polymorpha GPI cell wall anchor protein, HpgAalp.
PN WO200212509-A1.
PD 14-FEB-2002.
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
Query Match 2.3%; Score 10; DB 5; Length 537;
Best Local Similarity 100.0%; Pred. No. 8.6;
RESULT 807
ID ABB92667 standard; protein; 542 AA.
DE Herbicidally active polypeptide SEQ ID NO 1878.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB-) BAYER AG.
Query Match 2.3%; Score 10; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 8.6;
RESULT 808
ID AAU12046 standard; protein; 626 AA.
DE Clostridium difficile S-layer protein cell wall binding portion (ORFG).
PN WO200194599-A1.
PD 13-DEC-2001.
PA (SMIT-) SMITTSKYDSINSTITUTET.
Query Match 2.3%; Score 10; DB 5; Length 626;
Best Local Similarity 100.0%; Pred. No. 9.8;
RESULT 809
ID ABU25345 standard; protein; 628 AA.
DE Protein encoded by Prokaryotic essential gene #10872.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 10; DB 6; Length 628;
Best Local Similarity 100.0%; Pred. No. 9.8;
RESULT 810
ID ABU03140 standard; protein; 866 AA.
DE Alpha amylase polypeptide #101.
PN WO200268589-A2.

PD 06-SEP-2002.
PA (DIVE-) DIVERSA CORP.
Query Match 2.3%; Score 10; DB 6; Length 866;
Best Local Similarity 100.0%; Pred. No. 13;
RESULT 811
ID ABB69760 standard; protein; 952 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36072.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 2.3%; Score 10; DB 4; Length 952;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 812
ID ABB59829 standard; protein; 1893 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6279.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 2.3%; Score 10; DB 4; Length 1893;
Best Local Similarity 100.0%; Pred. No. 26;
RESULT 813
ID ABB64682 standard; protein; 2090 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20838.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 2.3%; Score 10; DB 4; Length 2090;
Best Local Similarity 100.0%; Pred. No. 28;
RESULT 814
ID AAG94130 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 324.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 2.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9;
RESULT 815
ID ABW00721 standard; peptide; 10 AA.
DE Peptide spacer #1 used in the invention.
PN US2002168375-A1.
PD 14-NOV-2002.
PA (CHIR-) CHIRON CORP.
Query Match 2.0%; Score 9; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9;
RESULT 816
ID ADH88625 standard; protein; 60 AA.
DE Enterococcus faecalis polypeptide #3105.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 2.0%; Score 9; DB 7; Length 60;
Best Local Similarity 100.0%; Pred. No. 9.3;
RESULT 817
ID ADC32840 standard; protein; 96 AA.
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2922.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.0%; Score 9; DB 7; Length 96;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 818
ID ABJ39196 standard; protein; 111 AA.
DE Fragment d, glycine rich sticky domain 1 of the human S protein.
PN WO2003050311-A2.
PD 19-JUN-2003.
PA (WELA-) WELIA AG.
Query Match 2.0%; Score 9; DB 7; Length 111;
Best Local Similarity 100.0%; Pred. No. 16;
RESULT 819
ID ABJ39195 standard; protein; 146 AA.
DE Fragment c, cleavage product of human s (corneodesmosin skin) protein.
PN WO2003050311-A2.

PD 19-JUN-2003.
PA (WELA) WELLA AG.
Query Match 2.0%; Score 9; DB 7; Length 146;
Best Local Similarity 100.0%; Pred. No. 20;
RESULT 820
ID ADJ92311 standard; protein; 167 AA.
DE Mouse hair keratin-associated-protein SEQ ID NO:170.
PN WO2003042387-A1.
PD 22-MAY-2003.
PA (UYKE-) UNIV KEIO.
PA (NIPR-) JAPAN SOC PROMOTION SCI.
Query Match 2.0%; Score 9; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No. 23;
RESULT 821
ID AAB54279 standard; protein; 175 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:731.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.0%; Score 9; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 24;
RESULT 822
ID ADC96370 standard; protein; 184 AA.
DE E. faecium protein sequence SEQ ID 5997.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.0%; Score 9; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 25;
RESULT 823
ID AAU16338 standard; protein; 199 AA.
DE Human novel secreted protein, Seq ID 1291.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.0%; Score 9; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 824
ID ABU55407 standard; protein; 199 AA.
DE Human novel polypeptide #494.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.0%; Score 9; DB 6; Length 199;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 825
ID AAU15883 standard; protein; 201 AA.
DE Human novel secreted protein, Seq ID 836.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.0%; Score 9; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 826
ID ABU54952 standard; protein; 201 AA.
DE Human novel polypeptide #39.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.0%; Score 9; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 27;
RESULT 827
ID ABO60412 standard; protein; 219 AA.
DE Human genome derived single exon protein #6646.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

Query Match 2.0%; Score 9; DB 8; Length 219;
Best Local Similarity 100.0%; Pred. No. 29;
RESULT 828
ID ABB70402 standard; protein; 253 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37998.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 33;
RESULT 829
ID ABB70259 standard; protein; 280 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37569.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 7; Length 280;
Best Local Similarity 100.0%; Pred. No. 36;
RESULT 830
ID ADE55544 standard; protein; 396 AA.
DE Rat Protein AJ004858, SEQ ID NO 1361.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.0%; Score 9; DB 7; Length 396;
Best Local Similarity 100.0%; Pred. No. 48;
RESULT 831
ID ADD45203 standard; protein; 396 AA.
DE Rat Protein AJ004858, SEQ ID NO 10636.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.0%; Score 9; DB 7; Length 396;
Best Local Similarity 100.0%; Pred. No. 48;
RESULT 832
ID ADQ97306 standard; protein; 464 AA.
DE Mouse cancer associated sequence MP08-029, SEQ ID 283.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.0%; Score 9; DB 8; Length 464;
Best Local Similarity 100.0%; Pred. No. 56;
RESULT 833
ID AAB57004 standard; protein; 476 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1582.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 2.0%; Score 9; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 57;
RESULT 834
ID AAB95574 standard; protein; 480 AA.
DE Human protein sequence SEQ ID NO:18225.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.0%; Score 9; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 57;
RESULT 835
ID ABJ39147 standard; protein; 486 AA.
DE Human S protein encoded by the skin corneodesmosin (CDSN) gene (S-gene).
PN WO2003050311-A2.
PD 19-JUN-2003.
PA (WELA) WELLA AG.
Query Match 2.0%; Score 9; DB 7; Length 486;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 836
ID ADQ21504 standard; protein; 486 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4324.
PN WO2004048938-A2.

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PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.0%; Score 9; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 837
ID ADR51219 standard; protein; 504 AA.
DE Anti-biofilm polypeptide #5.
PN WO2004066945-A2.
PD 12-AUG-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 2.0%; Score 9; DB 8; Length 504;
Best Local Similarity 100.0%; Pred. No. 60;
RESULT 838
ID AAW80498 standard; protein; 529 AA.
DE A protein designated corneodesmosin.
PN FR2761362-A1.
PD 02-OCT-1998.
PA (OREA ) L'OREAL SA.
Query Match 2.0%; Score 9; DB 2; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 839
ID AAW85055 standard; protein; 529 AA.
DE Human protein designated corneodesmosin.
PN FR2761363-A1.
PD 02-OCT-1998.
PA (OREA ) L'OREAL SA.
Query Match 2.0%; Score 9; DB 2; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 840
ID AAY44989 standard; protein; 529 AA.
DE Human epidermal protein-6.
PN WO200006727-A2.
PD 10-FEB-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.0%; Score 9; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 841
ID AAG64152 standard; protein; 529 AA.
DE Polypeptide #1 for vulgar psoriasis diagnosis.
PN WO200142458-A1.
PD 14-JUN-2001.
PA (INOK/) INOKO H.
Query Match 2.0%; Score 9; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 842
ID AAU27550 standard; protein; 529 AA.
DE Corneodesmosin.
PN WO200162788-A2.
PD 30-AUG-2001.
PA (OXAG-) OXAGEN LTD.
Query Match 2.0%; Score 9; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 843
ID ABJ39148 standard; protein; 529 AA.
DE Human corneodesmosin (CDSN) protein.
PN WO2003050311-A2.
PD 19-JUN-2003.
PA (WELA ) WELLA AG.
Query Match 2.0%; Score 9; DB 7; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 844
ID ADN04226 standard; protein; 529 AA.
DE Antiporiatic protein sequence #308.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 2.0%; Score 9; DB 8; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 845
ID ADP12525 standard; protein; 529 AA.
DE Protein encoded by mRNA of the invention #135.
PN WO2004042346-A2.
PD 21-MAY-2004.

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.0%; Score 9; DB 8; Length 529;
Best Local Similarity 100.0%; Pred. No. 62;
RESULT 846
ID ABB69163 standard; protein; 596 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34281.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 596;
Best Local Similarity 100.0%; Pred. No. 69;
RESULT 847
ID ADA35429 standard; protein; 607 AA.
DE Acinetobacter baumannii protein #2590.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.0%; Score 9; DB 6; Length 607;
Best Local Similarity 100.0%; Pred. No. 70;
RESULT 848
ID AAB92857 standard; protein; 624 AA.
DE Human protein sequence SEQ ID NO:11428.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.0%; Score 9; DB 4; Length 624;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 849
ID ADM04489 standard; protein; 634 AA.
DE Human protein of the invention SEQ ID NO:3174.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.0%; Score 9; DB 7; Length 634;
Best Local Similarity 100.0%; Pred. No. 73;
RESULT 850
ID AAW55483 standard; protein; 668 AA.
DE H. pylori ORF 14ap10815_20585777_ci_13 cell envelope OMP.
PN WO9737044-A1.
PD 09-OCT-1997.
PA (ASTR ) ASTRA AB.
Query Match 2.0%; Score 9; DB 2; Length 668;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 851
ID AAB46377 standard; protein; 668 AA.
DE H. pylori HPN137 protein.
PN WO200073502-A2.
PD 07-DEC-2000.
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (CREA-) CREATOGEN GMBH.
Query Match 2.0%; Score 9; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 852
ID ADJ49662 standard; protein; 675 AA.
DE Oil-associated gene related protein #1162.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 2.0%; Score 9; DB 8; Length 675;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 853
ID AAW55328 standard; protein; 677 AA.
DE H. pylori ORF hp3el0349orf27 protein.
PN WO9737044-A1.
PD 09-OCT-1997.
PA (ASTR ) ASTRA AB.
Query Match 2.0%; Score 9; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 78;
RESULT 854
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ID ABB60904 standard; protein; 688 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9504.
PN WO200171042-A2.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 79;
RESULT 855
ID ABB68902 standard; protein; 729 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33498.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 83;
RESULT 856
ID ADR10276 standard; protein; 972 AA.
DE Human protein useful for treating neurological disease Seq 3782.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.0%; Score 9; DB 8; Length 972;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 857
ID ABB67028 standard; protein; 1046 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27876.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 1046;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 858
ID ABB59068 standard; protein; 1064 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3996.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 1064;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
RESULT 859
ID ABB62237 standard; protein; 1097 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13503.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 1097;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
RESULT 860
ID ABB64387 standard; protein; 1171 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19953.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 1171;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
RESULT 861
ID ABB70775 standard; protein; 1357 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39117.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 1357;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RESULT 862
ID ABB59325 standard; protein; 1486 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 4767.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.0%; Score 9; DB 4; Length 1486;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 863
ID AAE36104 standard; protein; 1709 AA.
DE Human chromodomain helicase DNA binding protein (CHD) #2.
PN WO200298899-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 2.0%; Score 9; DB 6; Length 1709;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
RESULT 864
ID ABO07199 standard; protein; 1709 AA.
DE Human p53 modifying protein, SEQ ID 159.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 2.0%; Score 9; DB 6; Length 1709;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
RESULT 865
ID ADP23690 standard; protein; 1709 AA.
DE PRO polypeptide SEQ ID NO:868.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 2.0%; Score 9; DB 8; Length 1738;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 866
ID ABB83985 standard; protein; 1738 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4134.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.0%; Score 9; DB 8; Length 1738;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 867
ID ADB80349 standard; protein; 1839 AA.
DE Human MDT protein SEQ ID NO:36.
PN WO2003016497-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.0%; Score 9; DB 7; Length 1839;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 868
ID AAG94122 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 316.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 869
ID AAG97122 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3316.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 870
ID AAG97134 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3328.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 871
ID AAG93958 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 152.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 872
ID AAG87504 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2453.

PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 873
ID AAG87505 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2454.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 874
ID AAG87506 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2455.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 875
ID AAG85279 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 228.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 876
ID AAG85067 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 16.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 877
ID AAG85633 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 582.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 878
ID AAG85099 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 48.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 879
ID AAG87507 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2456.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.8%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 880
ID AAE38484 standard; peptide; 10 AA.
DE Peptide linker #3.
PN WO2003068802-A2.
PD 21-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.8%; Score 8; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
RESULT 881
ID AAE38483 standard; peptide; 16 AA.
DE Peptide linker #2.
PN WO2003068802-A2.

PD 21-AUG-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 1.8%; Score 8; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 22;
RESULT 882
ID AAB37493 standard; peptide; 17 AA.
DE Peptide linker #2 used as a control peptide.
PN WO200066182-A1.
PD 09-NOV-2000.
PA (UYVA-) UNIV VANDERBILT.
Query Match 1.8%; Score 8; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 23;
RESULT 883
ID ADT91223 standard; peptide; 17 AA.
DE Radiation-inducible alpha2bbeta3 integrin binding control peptide #4.
PN US2004191249-A1.
PD 30-SEP-2004.
PA (UYVA-) UNIV VANDERBILT.
Query Match 1.8%; Score 8; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 23;
RESULT 884
ID ADT91222 standard; peptide; 22 AA.
DE Radiation-inducible alpha2bbeta3 integrin binding control peptide #3.
PN US2004191249-A1.
PD 30-SEP-2004.
PA (UYVA-) UNIV VANDERBILT.
Query Match 1.8%; Score 8; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 28;
RESULT 885
ID AAY59113 standard; peptide; 28 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 1.8%; Score 8; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 35;
RESULT 886
ID ADB83483 standard; peptide; 28 AA.
DE Selected BLIP Mask peptide sequence, HB501-2.
PN WO2003069312-A2.
PD 21-AUG-2003.
PA (KALO-) KALOBIOS INC.
Query Match 1.8%; Score 8; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 35;
RESULT 887
ID AAY59121 standard; peptide; 30 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 1.8%; Score 8; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 37;
RESULT 888
ID ADB83489 standard; peptide; 30 AA.
DE Selected BLIP Mask peptide sequence, HB501-8.
PN WO2003069312-A2.
PD 21-AUG-2003.
PA (KALO-) KALOBIOS INC.
Query Match 1.8%; Score 8; DB 7; Length 30;
Best Local Similarity 100.0%; Pred. No. 37;
RESULT 889
ID RAY59109 standard; peptide; 31 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 1.8%; Score 8; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 38;
RESULT 890
ID ADB83485 standard; peptide; 32 AA.
DE Selected BLIP Mask peptide sequence, HB501-4.
PN WO2003069312-A2.
PD 21-AUG-2003.

PA (KALO-) KALOBIOUS INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 891
 ID ADB83490 standard; peptide; 32 AA.
 DE Selected BLIP Mask peptide sequence, HB501-9.
 PN W02003069312-A2.
 PD 21-AUG-2003.
 PA (KALO-) KALOBIOUS INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 892
 ID ADB83488 standard; peptide; 32 AA.
 DE Selected BLIP Mask peptide sequence, HB501-7.
 PN W02003069312-A2.
 PD 21-AUG-2003.
 PA (KALO-) KALOBIOUS INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 893
 ID ADB83486 standard; peptide; 32 AA.
 DE Selected BLIP Mask peptide sequence, HB501-5.
 PN W02003069312-A2.
 PD 21-AUG-2003.
 PA (KALO-) KALOBIOUS INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 894
 ID ADB83484 standard; peptide; 32 AA.
 DE Selected BLIP Mask peptide sequence, HB501-3.
 PN W02003069312-A2.
 PD 21-AUG-2003.
 PA (KALO-) KALOBIOUS INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 895
 ID ADB83482 standard; peptide; 32 AA.
 DE Selected BLIP Mask peptide sequence, HB501-1.
 PN W02003069312-A2.
 PD 21-AUG-2003.
 PA (KALO-) KALOBIOUS INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 896
 ID ADB83487 standard; peptide; 32 AA.
 DE Selected BLIP Mask peptide sequence, HB501-6.
 PN W02003069312-A2.
 PD 21-AUG-2003.
 PA (KALO-) KALOBIOUS INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 897
 ID ADM08430 standard; peptide; 32 AA.
 DE Canine immunoglobulin group 3 VL species framework 3 peptide 15.
 PN W02003060080-A2.
 PD 24-JUL-2003.
 PA (IDEX-) IDEXX LAB INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 898
 ID ADM08336 standard; peptide; 32 AA.
 DE Canine immunoglobulin group 3 VL subgenus framework 3 peptide 6.
 PN W02003060080-A2.
 PD 24-JUL-2003.
 PA (IDEX-) IDEXX LAB INC.
 Query Match 1.8%; Score 8; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 40;
 RESULT 899
 ID ADL27343 standard; peptide; 33 AA.
 DE Eitope used to test prethrombin adzymes.
 PN W02004018878-A2.
 PD 11-MAR-2004.
 PA (COMP-) COMPOUND THERAPEUTICS INC.

PA (AFXY/) AFEYAN N B.
 Query Match 1.8%; Score 8; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 41;
 RESULT 900
 ID AAU48534 standard; protein; 58 AA.
 DE Protonibacterium acnes immunogenic protein #9430.
 PN W0200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 1.8%; Score 8; DB 4; Length 58;
 Best Local Similarity 100.0%; Pred. No. 67;
 RESULT 901
 ID AEM45053 standard; protein; 58 AA.
 DE Protonibacterium acnes predicted ORF-encoded polypeptide #9729.
 PN W02003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 1.8%; Score 8; DB 6; Length 58;
 Best Local Similarity 100.0%; Pred. No. 67;
 RESULT 902
 ID AAY59696 standard; protein; 62 AA.
 DE Secreted protein 57-19-2-G8-CL1_3.
 PN W0940185-A2.
 PD 12-AUG-1999.
 PA (GEST-) GENSET.
 Query Match 1.8%; Score 8; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 71;
 RESULT 903
 ID ADM77846 standard; protein; 62 AA.
 DE Human protein #43.
 PN US2003162176-A1.
 PD 28-AUG-2003.
 PA (EDWA/) EDWARDS J D M.
 PA (DUC/) DUCLETS A.
 PA (BOUG/) BOUCLELERET L.
 Query Match 1.8%; Score 8; DB 7; Length 62;
 Best Local Similarity 100.0%; Pred. No. 71;
 RESULT 904
 ID ADP19527 standard; protein; 62 AA.
 DE Human secreted polypeptide #378.
 PN US2004110939-A1.
 PD 10-JUN-2004.
 PA (GEST-) GENSET SA.
 Query Match 1.8%; Score 8; DB 8; Length 62;
 Best Local Similarity 100.0%; Pred. No. 71;
 RESULT 905
 ID AAM21759 standard; protein; 63 AA.
 DE Peptide #8193 encoded by probe for measuring cervical gene expression.
 PN W0200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 1.8%; Score 8; DB 4; Length 63;
 Best Local Similarity 100.0%; Pred. No. 72;
 RESULT 906
 ID ABB44131 standard; peptide; 63 AA.
 DE Peptide #11637 encoded by human foetal liver single exon probe.
 PN W0200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 1.8%; Score 8; DB 4; Length 63;
 Best Local Similarity 100.0%; Pred. No. 72;
 RESULT 907
 ID AAM38081 standard; protein; 63 AA.
 DE Peptide #12118 encoded by probe for measuring placental gene expression.
 PN W0200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 1.8%; Score 8; DB 4; Length 63;
 Best Local Similarity 100.0%; Pred. No. 72;
 RESULT 908
 ID ABB27013 standard; protein; 63 AA.
 DE Protein #9012 encoded by probe for measuring heart cell gene expression.
 PN W0200157274-A2.

PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 909
ID AAM77859 standard; protein; 63 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38165.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 910
ID AAM65154 standard; protein; 63 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 37259.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 911
ID ABG59511 standard; peptide; 63 AA.
DE Human liver peptide, SEQ ID No 38159.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 912
ID ABG4687 standard; peptide; 63 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36552.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 5; Length 63;
Best Local Similarity 100.0%; Pred. No. 72;
RESULT 913
ID AAU37867 standard; protein; 67 AA.
DE Streptococcus pneumoniae cellular proliferation protein #296.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 76;
RESULT 914
ID ASU02289 standard; protein; 67 AA.
DE S. pneumoniae type 4 strain protein from coding region #1857.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 1.8%; Score 8; DB 6; Length 67;
Best Local Similarity 100.0%; Pred. No. 76;
RESULT 915
ID ASU46220 standard; protein; 67 AA.
DE Protein encoded by Prokaryotic essential gene #31747.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 67;
Best Local Similarity 100.0%; Pred. No. 76;
RESULT 916
ID ADK46533 standard; protein; 67 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3048.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.8%; Score 8; DB 8; Length 67;
Best Local Similarity 100.0%; Pred. No. 76;
RESULT 917
ID AAU38017 standard; protein; 68 AA.
DE Streptococcus pneumoniae cellular proliferation protein #446.
PN WO200170955-A2.

PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 77;
RESULT 918
ID ADR94888 standard; protein; 77 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3523.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.8%; Score 8; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 85;
RESULT 919
ID AAM86130 standard; protein; 82 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:13723.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.8%; Score 8; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 90;
RESULT 920
ID ADB09048 standard; protein; 91 AA.
DE Alloicoccus otitis antigenic protein SEQ ID NO:2988.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 1.8%; Score 8; DB 6; Length 91;
Best Local Similarity 100.0%; Pred. No. 99;
RESULT 921
ID AAG03015 standard; protein; 95 AA.
DE Human secreted protein, SEQ ID NO: 7096.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 1.8%; Score 8; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 922
ID RAU47045 standard; protein; 95 AA.
DE Propionibacterium acnes immunogenic protein #7941.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.8%; Score 8; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 923
ID ABM43564 standard; protein; 95 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8240.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.8%; Score 8; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e+02;
RESULT 924
ID AAG03558 standard; protein; 103 AA.
DE Human secreted protein, SEQ ID NO: 7639.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 1.8%; Score 8; DB 3; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 925
ID ABA41967 standard; peptide; 103 AA.
DE Peptide #9473 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 926
ID AAM35768 standard; protein; 103 AA.
DE Peptide #9805 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 927
ID AAM75658 standard; protein; 103 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35964.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 928
ID AAM62844 standard; protein; 103 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34949.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 929
ID AAG57399 standard; peptide; 103 AA.
DE Human liver peptide, SEQ ID NO 36047.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 930
ID AAG45161 standard; peptide; 103 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34826.
PN W0200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.8%; Score 8; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 931
ID AAW11848 standard; protein; 104 AA.
DE Saccharomyces cerevisiae acetamidase internal consensus fragment.
PN EP758020-A2.
PD 12-FEB-1997.
PA (KONN) GIST-BROCADES BV.
Query Match 1.8%; Score 8; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 932
ID AAM50034 standard; protein; 104 AA.
DE N. clavipes epidroin synthetic homologue SBI protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 942
ID AAG54787 standard; protein; 152 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69975.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 943
ID AAB63563 standard; protein; 154 AA.
DE Human gastric cancer associated antigen protein sequence SEQ ID NO: 925.
PN W0200073801-A2.
PD 07-DEC-2000.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 1.8%; Score 8; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
RESULT 944
ID AAW82486 standard; protein; 159 AA.
DE Ehrlichia sp. E74.1 protein.
PN W09849312-A2.
PD 05-NOV-1998.
PA (AQUI-) AQUILA BIOPHARMACEUTICALS INC.
Query Match 1.8%; Score 8; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
RESULT 945
ID AAG26487 standard; protein; 161 AA.

Query Match 1.8%; Score 8; DB 8; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
RESULT 936
ID ABB62125 standard; protein; 125 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13167.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
RESULT 937
ID AAG92718 standard; protein; 137 AA.
DE C. glutamicum protein fragment SEQ ID NO: 6472.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 1.8%; Score 8; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RESULT 938
ID AAM50036 standard; protein; 137 AA.
DE N. clavipes epidroin synthetic homologue SD1 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RESULT 939
ID ABB70412 standard; protein; 139 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38028.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RESULT 940
ID AAG26489 standard; protein; 142 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 30963.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 941
ID AAG26488 standard; protein; 146 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 30962.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 942
ID AAG54787 standard; protein; 152 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69975.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
RESULT 943
ID AAB63563 standard; protein; 154 AA.
DE Human gastric cancer associated antigen protein sequence SEQ ID NO: 925.
PN W0200073801-A2.
PD 07-DEC-2000.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 1.8%; Score 8; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
RESULT 944
ID AAW82486 standard; protein; 159 AA.
DE Ehrlichia sp. E74.1 protein.
PN W09849312-A2.
PD 05-NOV-1998.
PA (AQUI-) AQUILA BIOPHARMACEUTICALS INC.
Query Match 1.8%; Score 8; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
RESULT 945
ID AAG26487 standard; protein; 161 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 30961.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
RESULT 946
ID ABU1844 standard; protein; 178 AA.
DE Human MDT polypeptide SEQ ID 791.
PN W0200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.8%; Score 8; DB 6; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 947
ID ADN99741 standard; protein; 178 AA.
DE Novel human protein sequence #557.
PN W02004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 1.8%; Score 8; DB 8; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 948
ID AAM93486 standard; protein; 180 AA.
DE Human polypeptide, SEQ ID NO: 3175.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 1.8%; Score 8; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 949
ID ADL31142 standard; protein; 180 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3175.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 8; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 950
ID AAG07583 standard; protein; 182 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4792.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
RESULT 951
ID ADN74835 standard; protein; 190 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 2730.
PN W02004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPEDESIGN NV.
Query Match 1.8%; Score 8; DB 8; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 952
ID AAG07582 standard; protein; 194 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4791.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 953
ID AAY95937 standard; protein; 202 AA.
DE Porcine adenovirus 3 E1B-202R protein.
PN W0200050076-A1.
PD 31-AUG-2000.
PA (PURD) PURDUE RES FOUND.
Query Match 1.8%; Score 8; DB 3; Length 202;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 954
ID AAB64527 standard; protein; 215 AA.
DE Gene 32 human secreted protein homologous amino acid sequence #165.
PN W0200077255-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.8%; Score 8; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
RESULT 955
ID AAM50040 standard; protein; 219 AA.
DE N. clavipes spidroin synthetic homologue PA2 protein.
PN DB10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
RESULT 956
ID AAM50035 standard; protein; 230 AA.
DE N. clavipes spidroin synthetic homologue SE1 protein.
PN DB10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 957
ID ABJ26668 standard; protein; 232 AA.
DE Human protein modification + maintenance molecule protein SEQ ID NO 22.
PN W0200300844-A2.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.8%; Score 8; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 958
ID ADC39240 standard; protein; 232 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 184.
PN W02003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 959
ID ADC31414 standard; protein; 232 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1496.
PN W02003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSE INC.
Query Match 1.8%; Score 8; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 960
ID ADQ65777 standard; protein; 232 AA.
DE Novel human protein sequence #1750.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 8; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 961
ID ADQ66668 standard; protein; 232 AA.
DE Novel human protein sequence #1641.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 8; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 962
ID ADC87119 standard; protein; 235 AA.
DE Human GPCR protein SEQ ID NO:1572.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 1.8%; Score 8; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
RESULT 963
ID ABP45001 standard; protein; 255 AA.
DE Human Blys binding scrv SEQ ID 1012.
PN W0200202641-A1.
PD 10-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 Query Match 1.8%; Score 8; DB 5; Length 255;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 RESULT 964
 ID AUC95828 standard; protein; 255 AA.
 DE Single chain antibody that immunospecifically binds Blys SeqID 1012.
 PN WO2003055979-A2.
 PD 10-JUL-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.8%; Score 8; DB 7; Length 255;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 RESULT 965
 ID AAM50048 standard; protein; 264 AA.
 DE N. clavipes epididymal synthetic homologue FA2 protein #2.
 PN DE10113781-A1.
 PD 13-DEC-2001.
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
 Query Match 1.8%; Score 8; DB 5; Length 264;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 966
 ID AAU17599 standard; protein; 267 AA.
 DE Novel signal transduction pathway protein, Seq ID 1164.
 PN WO200154733-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.8%; Score 8; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 967
 ID AAM95431 standard; protein; 267 AA.
 DE Human reproductive system related antigen SEQ ID NO: 4089.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.8%; Score 8; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 968
 ID ABB96121 standard; protein; 267 AA.
 DE Human testicular antigen SEQ ID NO: 1505.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.8%; Score 8; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 969
 ID ADB94307 standard; protein; 267 AA.
 DE Human novel protein #541.
 PN US2002168711-A1.
 PD 14-NOV-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 1.8%; Score 8; DB 7; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 RESULT 970
 ID AAM50044 standard; protein; 271 AA.
 DE N. clavipes epididymal synthetic homologue SFI protein.
 PN DE10113781-A1.
 PD 13-DEC-2001.
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
 Query Match 1.8%; Score 8; DB 5; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 RESULT 971
 ID ABB68131 standard; protein; 273 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 31185.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.8%; Score 8; DB 4; Length 273;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 RESULT 972
 ID ABB69618 standard; protein; 276 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 35646.
 PN WO200171042-A2.

PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.8%; Score 8; DB 4; Length 276;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 RESULT 973
 ID AAY81909 standard; protein; 278 AA.
 DE Pseudomonas fluorescens xylanase protein sequence.
 PN JP11318474-A.
 PD 24-NOV-1999.
 PA (BIOT-) DEV CENT BIOTECHNOLOGY.
 Query Match 1.8%; Score 8; DB 3; Length 278;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 RESULT 974
 ID ABB70296 standard; protein; 288 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 37680.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.8%; Score 8; DB 4; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 RESULT 975
 ID AAM20066 standard; protein; 297 AA.
 DE Thielavia terrestris NRRL 8126 xylanase.
 PN WO9727293-A1.
 PD 31-JUL-1997.
 PA (NOVO) NOVO-NORDISK AS.
 Query Match 1.8%; Score 8; DB 2; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 976
 ID ADJ34998 standard; protein; 303 AA.
 DE Xylanase from an environmental sample seq id 214.
 PN WO2003106654-A2.
 PD 24-DEC-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 1.8%; Score 8; DB 8; Length 303;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 977
 ID ABO52944 standard; protein; 305 AA.
 DE Human spliceosome associated protein (SAP) #49.
 PN US2003068803-A1.
 PD 10-APR-2003.
 PA (REED/) REED R.
 PA (ZHOU/) ZHOU Z.
 Query Match 1.8%; Score 8; DB 6; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 978
 ID AEM81703 standard; protein; 305 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO82532, SEQ:4393.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.8%; Score 8; DB 8; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 979
 ID AEM80558 standard; protein; 305 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO81124, SEQ:1411.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.8%; Score 8; DB 8; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 980
 ID AEM81704 standard; protein; 305 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO82533, SEQ:4395.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.8%; Score 8; DB 8; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 RESULT 981
 ID AAG72184 standard; protein; 311 AA.
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1865.
 PN WO200127158-A2.

PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 1.8%; Score 8; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 982
ID AAG72566 standard; protein; 311 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2247.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 1.8%; Score 8; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 983
ID AAU24692 standard; protein; 311 AA.
DE Human olfactory receptor AOLF191.
PN WO200168805-A2.
PD 20-SEP-2001.
PA (SENO-) SENOMYX INC.
Query Match 1.8%; Score 8; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 984
ID ABG76795 standard; protein; 311 AA.
DE Human G-protein coupled receptor (GPCR) protein #29.
PN WO200259313-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 985
ID ABP51596 standard; protein; 311 AA.
DE Human G-protein coupled receptor SEQ ID NO:74.
PN WO200250276-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 986
ID ABP95818 standard; protein; 311 AA.
DE Human GPCR polypeptide SEQ ID NO 446.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 1.8%; Score 8; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 987
ID AAU95661 standard; protein; 311 AA.
DE Human olfactory and pheromone G protein-coupled receptor #148.
PN WO200224726-A2.
PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.
Query Match 1.8%; Score 8; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 988
ID AAU85312 standard; protein; 311 AA.
DE G-coupled olfactory receptor #173.
PN WO200198526-A2.
PD 27-DEC-2001.
PA (SENO-) SENOMYX INC.
Query Match 1.8%; Score 8; DB 5; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 989
ID ADC85819 standard; protein; 311 AA.
DE Human GPCR protein SEQ ID NO:272.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 1.8%; Score 8; DB 7; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 990
ID ADI04317 standard; protein; 311 AA.

DE Human G-protein coupled receptor #37.
PN US2003198955-A1.
PD 23-OCT-2003.
PA (LILL-) LI L.
PA (PADI-) PADIGARU M.
PA (BALL-) BALLINGER R A.
PA (KEKU-) KEKUDA R.
PA (COLM-) COLMAN S D.
PA (SPYT-) SPYTEK K A.
PA (CASW-) CASHMAN S J.
PA (EDIN-) EDINGER S R.
PA (GERL-) GERLACH V.
PA (SCIO-) SCIORE P.
PA (SMIT-) SMITHSON G.
PA (PEYN-) PEYMAN J A.
PA (MACD-) MACDOUGALL J R.
PA (STON-) STONE D J.
PA (VERN-) VERNET C A M.
PA (SHEN-) SHENOY S G.
PA (GUNT-) GUNTHER E.
PA (MILL-) MILLET I.
PA (TCHE-) TCHERNEV V T.
PA (ANDE-) ANDERSON D W.
PA (GUSE-) GUSEV V Y.
PA (MALY-) MALYANKAR U M.
PA (ZHON-) ZHONG H.
PA (ELLE-) ELLERMAN K.
PA (WOLE-) WOLENC A R.
Query Match 1.8%; Score 8; DB 7; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 991
ID ADG83404 standard; protein; 311 AA.
DE Human Olfactory and pheromone GPCR #59.
PN US2003221205-A1.
PD 27-NOV-2003.
PA (VEIT-) VEITHEN A.
Query Match 1.8%; Score 8; DB 8; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 992
ID ABB80187 standard; protein; 313 AA.
DE A. fumigatus AfXYL3.
PN WO2003012071-A2.
PD 13-FEB-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 993
ID AAG70693 standard; protein; 315 AA.
DE S cerevisiae apoptosis associated protein YCR073WA.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC-) JANSSEN PHARM NV.
Query Match 1.8%; Score 8; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 994
ID ABR01623 standard; protein; 315 AA.
DE Human G-protein coupled receptor SEQ ID 106.
PN WO2003000735-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 1.8%; Score 8; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 995
ID ADQ19957 standard; protein; 316 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2777.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.8%; Score 8; DB 8; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
RESULT 996
ID ABB69613 standard; protein; 319 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35631.

PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.8%; Score 8; DB 4; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 RESULT 997
 ID ADQ19814 standard; protein; 332 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2633.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 1.8%; Score 8; DB 8; Length 332;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 RESULT 998
 ID ADR99168 standard; protein; 333 AA.
 DE ANMECR1, SEQ ID 174.
 PN WO2004078035-A2.
 PD 16-SEP-2004.
 PA (FARB) BAYER PHARM CORP.
 Query Match 1.8%; Score 8; DB 8; Length 333;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 RESULT 999
 ID AAY29904 standard; protein; 334 AA.
 DE Human MDC and human scfV fusion protein.
 PN WO9946392-A1.
 PD 16-SEP-1999.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 1.8%; Score 8; DB 2; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 RESULT 1000
 ID ADM03842 standard; protein; 334 AA.
 DE Human protein of the invention SEQ ID NO:2527.
 PN EPI347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 1.8%; Score 8; DB 7; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 RESULT 1001
 ID AAY29905 standard; protein; 339 AA.
 DE Human SDF-1 and human scfV fusion protein.
 PN WO9946392-A1.
 PD 16-SEP-1999.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 1.8%; Score 8; DB 2; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 RESULT 1002
 ID ABB62884 standard; protein; 346 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15444.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.8%; Score 8; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 RESULT 1003
 ID AAY29903 standard; protein; 348 AA.
 DE Human MCP-3 and human scfV fusion protein.
 PN WO9946392-A1.
 PD 16-SEP-1999.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 1.8%; Score 8; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 RESULT 1004
 ID ADJ35000 standard; protein; 354 AA.
 DE Xylanase from an environmental sample seq id 216.
 PN WO2003106654-A2.
 PD 24-DEC-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 1.8%; Score 8; DB 8; Length 354;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 RESULT 1005
 ID ABB68677 standard; protein; 355 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 32823.
 PN WO200171042-A2.

PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.8%; Score 8; DB 4; Length 355;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 RESULT 1006
 ID ADO65824 standard; protein; 359 AA.
 DE Novel human protein sequence #797.
 PN EPI440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 1.8%; Score 8; DB 8; Length 359;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 RESULT 1007
 ID AAW30267 standard; protein; 360 AA.
 DE Amino acid sequence of an enzyme with xylanase activity.
 PN WO9736995-A2.
 PD 09-OCT-1997.
 PA (PACI-) PACIFIC ENZYMES LTD.
 Query Match 1.8%; Score 8; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 RESULT 1008
 ID ABG25391 standard; protein; 361 AA.
 DE Novel human diagnostic protein #25382.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.8%; Score 8; DB 4; Length 361;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 RESULT 1009
 ID ABG22687 standard; protein; 363 AA.
 DE Novel human diagnostic protein #22678.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.8%; Score 8; DB 4; Length 363;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 RESULT 1010
 ID ADN9674 standard; protein; 363 AA.
 DE Novel human protein sequence #490.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.8%; Score 8; DB 8; Length 363;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 RESULT 1011
 ID AAM50043 standard; protein; 364 AA.
 DE N. clavipes epidroin synthetic homologue SM12 protein.
 PN DE10113781-A1.
 PD 13-DEC-2001.
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
 Query Match 1.8%; Score 8; DB 5; Length 364;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 RESULT 1012
 ID AAR87012 standard; protein; 368 AA.
 DE Xylanase D.
 PN WO9534662-A1.
 PD 21-DEC-1995.
 PA (KONN) GIST-BROCADES BV.
 Query Match 1.8%; Score 8; DB 2; Length 368;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 RESULT 1013
 ID AAU54062 standard; protein; 372 AA.
 DE Propionibacterium acnes immunogenic protein #14958.
 PN WO200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 1.8%; Score 8; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 RESULT 1014
 ID ASM65617 standard; protein; 372 AA.
 DE Propionibacterium acnes immunogenic polypeptide #30293.
 PN WO2003033515-A1.
 PD 24-APR-2003.

PA (CORI-) CORIXA CORP.
Query Match 1.8%; Score 8; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 1015
ID ABM50581 standard; protein; 372 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15257.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.8%; Score 8; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 1016
ID ABB67616 standard; protein; 380 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29640.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 1017
ID ABB67616 standard; protein; 380 AA.
DE Protein encoded by Prokaryotic essential gene #18794.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 1018
ID ADS29129 standard; protein; 380 AA.
DE Bacterial polypeptide #18162.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.8%; Score 8; DB 8; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 1019
ID ADN39342 standard; protein; 381 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:B36.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.8%; Score 8; DB 7; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 1020
ID ABP62776 standard; protein; 391 AA.
DE Protein fragment #13 of S. roseosporus biosynthetic gene cluster.
PN W0200259322-A2.
PD 01-AUG-2002.
PA (MIAO/) MIAO V P W.
PA (BRIA/) BRIAN P.
PA (BALT/) BALTZ R H.
PA (SILV/) SILVA C J.
Query Match 1.8%; Score 8; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 1021
ID ADJ72187 standard; protein; 391 AA.
DE S. roseosporus daptomycin biosynthesis gene cluster protein #13.
PN W02003014297-A2.
PD 20-FEB-2003.
PA (CUBI-) CUBIST PHARM INC.
Query Match 1.8%; Score 8; DB 7; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
RESULT 1022
ID AAG31490 standard; protein; 392 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37825.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 1023
ID ADN04966 standard; protein; 392 AA.
DE Antipsoriatic protein sequence #663.
PN W02004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.8%; Score 8; DB 8; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 1024
ID ADQ20013 standard; protein; 392 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2833.
PN W02004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.8%; Score 8; DB 8; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 1025
ID AAB70913 standard; protein; 396 AA.
DE Polyoma virus coat protein VP1 variant PyVP1-RGD148 protein.
PN W0200132851-A2.
PD 10-MAY-2001.
PA (ACGT-) ACGT PROGENOMICS AG.
Query Match 1.8%; Score 8; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 1026
ID ABR63546 standard; protein; 396 AA.
DE Danio rerio foxd3 homologue chicken CWH3.
PN W02003048196-A2.
PD 12-JUN-2003.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
Query Match 1.8%; Score 8; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 1027
ID AAG45048 standard; protein; 397 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56505.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 1028
ID ABB67545 standard; protein; 397 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29427.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
RESULT 1029
ID AAE37147 standard; protein; 405 AA.
DE Drosophila melanogaster salvador mutant protein #3.
PN W02003035845-A2.
PD 01-MAY-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 1.8%; Score 8; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1030
ID ADB65137 standard; protein; 406 AA.
DE Human protein encoded by clone SPLEN20063250.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 7; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1031
ID ADR09419 standard; protein; 406 AA.
DE Human protein useful for treating neurological disease Seq 2925.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 8; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1032

ID ABB64734 standard; protein; 410 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20994.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1033
ID AAW94998 standard; protein; 412 AA.
DE Serine/threonine protein kinase-HTLAR33 (EST derived sequence).
PN EP894863-A1.
PD 03-FEB-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 1.8%; Score 8; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1034
ID AAG31489 standard; protein; 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37824.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 415;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1035
ID ABB59727 standard; protein; 415 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5973.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1036
ID AAG45047 standard; protein; 420 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56504.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 1037
ID AAG41764 standard; protein; 422 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52003.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 422;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 1038
ID AAR14186 standard; protein; 427 AA.
DE 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase.
PN WO9113978-A.
PD 19-SEP-1991.
PA (TRIN-) TRINITY COLLEGE DUB.
Query Match 1.8%; Score 8; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 1039
ID AAU93074 standard; protein; 430 AA.
DE Arabidopsis transcription factor #112.
PN WO200215575-A1.
PD 28-FEB-2002.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (PILG/) PILGRIM M.
PA (CREE/) CREELMAN R.
PA (DUBE/) DUBELL A J.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (KEDD/) KEDDIE J.
PA (ADAM/) ADAM L.
PA (RATC/) RATCLIFF O.
PA (REUB/) REUBER J L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (PINE/) PINEDA O.
Query Match 1.8%; Score 8; DB 5; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1040
ID ABR39479 standard; protein; 430 AA.
DE A. thaliana phytochrome interacting protein PIF4.
PN WO2003018777-A1.
PD 06-MAR-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 1.8%; Score 8; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1041
ID ADD30128 standard; protein; 430 AA.
DE Plant yield-related protein from clone G1494.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 1.8%; Score 8; DB 7; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1042
ID ADI41829 standard; protein; 430 AA.
DE Plant transcription factor #146.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAR/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 1.8%; Score 8; DB 8; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1043
ID ADO3453 standard; protein; 430 AA.
DE Thalecress transcription factor protein #558.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 1.8%; Score 8; DB 8; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1044
ID ABO81890 standard; protein; 436 AA.
DE Pseudomonas aeruginosa polypeptide #14065.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.8%; Score 8; DB 7; Length 436;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1045
ID ABB92544 standard; protein; 441 AA.
DE Herbicidally active polypeptide SEQ ID NO 1755.

PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 1.8%; Score 8; DB 5; Length 441;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1046
ID AAW46790 standard; protein; 442 AA.
DE Arabidopsis thaliana UFO gene product.
PD 12-FEB-1998.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 1.8%; Score 8; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1047
ID ABR42684 standard; protein; 442 AA.
DE Arabidopsis unusual floral organs (UFO) protein.
PD 24-APR-2003.
PA (TECH-) TECHNOLOGIESTICHTING STW.
Query Match 1.8%; Score 8; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1048
ID AAG29728 standard; protein; 447 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35420.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 1049
ID ABR54251 standard; protein; 450 AA.
DE Human NOV39b protein SEQ ID NO:170.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 6; Length 450;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 1050
ID ABB68662 standard; protein; 452 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32778.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 1051
ID ABO77072 standard; protein; 452 AA.
DE Pseudomonas aeruginosa polypeptide #9247.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 1.8%; Score 8; DB 7; Length 452;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 1052
ID ADP04829 standard; protein; 453 AA.
DE Sea squirt protein with tissue specific expression in development. Seq424.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 1.8%; Score 8; DB 8; Length 453;
Best Local Similarity 100.0%; Pred. No. 4e+02;
RESULT 1053
ID AAG29727 standard; protein; 468 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35419.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
RESULT 1054
ID AAG31488 standard; protein; 471 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37823.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 471;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1055
ID ADOS7237 standard; protein; 472 AA.
DE Kidney development associated protein seqid 4.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 1.8%; Score 8; DB 8; Length 472;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1056
ID AAG45045 standard; protein; 476 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56503.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1057
ID ABU48976 standard; protein; 477 AA.
DE Protein encoded by Prokaryotic essential gene #34503.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 477;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1058
ID ADR39740 standard; protein; 482 AA.
DE Human kinase and phosphatase KPP-13 protein SEQ ID NO:13.
PN WO2004074453-A2.
PD 02-SEP-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.8%; Score 8; DB 8; Length 482;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1059
ID ABU3313 standard; protein; 483 AA.
DE Protein encoded by Prokaryotic essential gene #18840.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 483;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1060
ID ABM15873 standard; protein; 484 AA.
DE Mycobacterium tuberculosis mycobacterial antigen protein SEQ ID NO:111.
PN WO2003033530-A2.
PD 24-APR-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 1.8%; Score 8; DB 6; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1061
ID ABU36943 standard; protein; 484 AA.
DE Protein encoded by Prokaryotic essential gene #22470.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1062
ID ABO23518 standard; protein; 484 AA.
DE Mycobacterium tuberculosis outlier protein #2.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match 1.8%; Score 8; DB 7; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1063
ID ADR08508 standard; protein; 488 AA.
DE Human protein useful for treating neurological disease Seq 2014.

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PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match 1.8%; Score 8; DB 8; Length 488;
  Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1064
ID AAM39373 standard; protein; 492 AA.
DE Human polypeptide SEQ ID NO 2518.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 1.8%; Score 8; DB 4; Length 492;
  Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1065
ID AAB94544 standard; protein; 492 AA.
DE Human protein sequence SEQ ID NO15293.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
  Query Match 1.8%; Score 8; DB 4; Length 492;
  Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1066
ID ABU52781 standard; protein; 492 AA.
DE Human transmembrane protein from DKFZphfbr2_82c20.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
  Query Match 1.8%; Score 8; DB 4; Length 492;
  Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1067
ID ABB90033 standard; protein; 492 AA.
DE Human polypeptide SEQ ID NO 2409.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 1.8%; Score 8; DB 5; Length 492;
  Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1068
ID ADQ96096 standard; protein; 492 AA.
DE T cell activation associated protein #137.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
  Query Match 1.8%; Score 8; DB 8; Length 492;
  Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1069
ID ABU19616 standard; protein; 496 AA.
DE Protein encoded by Prokaryotic essential gene #5143.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 1.8%; Score 8; DB 6; Length 496;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 1070
ID ABU22338 standard; protein; 496 AA.
DE Protein encoded by Prokaryotic essential gene #7865.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 1.8%; Score 8; DB 6; Length 496;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 1071
ID ABU48740 standard; protein; 506 AA.
DE Protein encoded by Prokaryotic essential gene #34267.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 1.8%; Score 8; DB 6; Length 506;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 1072
ID ABU17181 standard; protein; 506 AA.
DE Protein encoded by Prokaryotic essential gene #2708.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 1.8%; Score 8; DB 6; Length 506;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
RESULT 1073
ID AEM68647 standard; protein; 512 AA.
DE Photorhabdus luminescens protein sequence #1744.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
  Query Match 1.8%; Score 8; DB 6; Length 512;
  Best Local Similarity 100.0%; Pred. No. 4.5e+02;
RESULT 1074
ID AAB82611 standard; protein; 528 AA.
DE Spider recombinant silk protein PETNCDs.
PN WO200153333-A1.
PD 28-JUL-2001.
PA (MELL/) MELLO C M.
PA (ARCI/) ARCIDIACONO S.
PA (BUTL/) BUTLER M M.
PA (USSA) US SEC OF ARMY.
  Query Match 1.8%; Score 8; DB 4; Length 528;
  Best Local Similarity 100.0%; Pred. No. 4.6e+02;
RESULT 1075
ID AEM68676 standard; protein; 532 AA.
DE Photorhabdus luminescens protein sequence #1773.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
  Query Match 1.8%; Score 8; DB 6; Length 532;
  Best Local Similarity 100.0%; Pred. No. 4.6e+02;
RESULT 1076
ID ADA35942 standard; protein; 532 AA.
DE Acinetobacter baumannii protein #3103.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match 1.8%; Score 8; DB 6; Length 532;
  Best Local Similarity 100.0%; Pred. No. 4.6e+02;
RESULT 1077
ID AAY00865 standard; protein; 536 AA.
DE Cellobiohydrolase CBH B protein sequence.
PN WO9906574-A1.
PD 11-FEB-1999.
PA (KONN) GIST-BROCADES BV.
  Query Match 1.8%; Score 8; DB 2; Length 536;
  Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 1078
ID ABB68621 standard; protein; 541 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32655.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
  Query Match 1.8%; Score 8; DB 4; Length 541;
  Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 1079
ID AAW07702 standard; protein; 543 AA.
DE Mouse ETS2 repressor factor (ERF).
PN WO9639517-A1.
PD 12-DEC-1996.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
  Query Match 1.8%; Score 8; DB 2; Length 543;
  Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 1080
ID AAW07700 standard; protein; 548 AA.
DE Human ETS2 repressor factor (ERF).
PN WO9639517-A1.
PD 12-DEC-1996.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
  Query Match 1.8%; Score 8; DB 2; Length 548;
  Best Local Similarity 100.0%; Pred. No. 4.8e+02;

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RESULT 1081
ID ADD14028 standard; protein; 548 AA.
DE Human src biomarker polypeptide SEQ ID NO:217.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 1.8%; Score 8; DB 7; Length 548;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
RESULT 1082
ID ADD18620 standard; protein; 548 AA.
DE Human disease related protein SeqID51.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 1.8%; Score 8; DB 7; Length 548;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
RESULT 1083
ID ARM82121 standard; protein; 548 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO12892, SEQ:5477.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.8%; Score 8; DB 8; Length 548;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
RESULT 1084
ID ARM84614 standard; protein; 566 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4863.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.8%; Score 8; DB 8; Length 566;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 1085
ID AAG41763 standard; protein; 568 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52002.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 568;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 1086
ID ADG74258 standard; protein; 570 AA.
DE Fruit fly frizzled protein, SEQ ID No 43.
PN WO200292635-A2.
PD 21-NOV-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 1.8%; Score 8; DB 7; Length 570;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 1087
ID ABB71745 standard; protein; 582 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42027.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 1088
ID ADB85519 standard; protein; 584 AA.
DE Human MNB modulator of the SREBP pathway protein sequence.
PN WO2003066811-A2.
PD 14-AUG-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 1.8%; Score 8; DB 7; Length 584;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 1089
ID ADQ96272 standard; protein; 584 AA.
DE T cell activation associated protein #225.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAHI-) ASAHI KASEI PHARMA CORP.
Query Match 1.8%; Score 8; DB 8; Length 584;
Best Local Similarity 100.0%; Pred. No. 5e+02;
RESULT 1090
ID AAG41762 standard; protein; 590 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 52001.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.8%; Score 8; DB 3; Length 590;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1091
ID AAO20499 standard; protein; 593 AA.
DE Protein of APP related human homologue hCP41313 #1.
PN WO200226820-A2.
PD 04-APR-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 1.8%; Score 8; DB 5; Length 593;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1092
ID AAE37144 standard; protein; 608 AA.
DE Drosophila melanogaster salvador protein.
PN WO2003035845-A2.
PD 01-MAY-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 1.8%; Score 8; DB 6; Length 608;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1093
ID AAY35161 standard; protein; 609 AA.
DE Chlamydia pneumoniae surface exposed polypeptide.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 1.8%; Score 8; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1094
ID ADJ70515 standard; protein; 609 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2321.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.8%; Score 8; DB 7; Length 609;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 1095
ID AAM93441 standard; protein; 629 AA.
DE Human polypeptide, SEQ ID NO: 3082.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 1.8%; Score 8; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1096
ID ADL31049 standard; protein; 629 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3082.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 8; Length 629;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1097
ID ARM82107 standard; protein; 629 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO51771, SEQ:5435.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.8%; Score 8; DB 8; Length 629;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1098
ID AAM50042 standard; protein; 630 AA.
DE N. clavipes spidroin synthetic homologue SO1 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPRP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 630;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1099
ID AAB74207 standard; protein; 633 AA.

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DE Protein encoded by Arabidopsis gene #2.
PN WO200114563-A1.
PD 01-MAR-2001.
PA (GORI/) GORING D.
PA (STLV/) SILVA N.
Query Match 1.8%; Score 8; DB 4; Length 633;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1100
ID ABR91790 standard; protein; 633 AA.
DE Herbicidally active polypeptide SEQ ID NO 1001.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 1.8%; Score 8; DB 5; Length 633;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1101
ID ABU44612 standard; protein; 633 AA.
DE Protein encoded by Prokaryotic essential gene #30139.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 633;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1102
ID ABR82940 standard; protein; 633 AA.
DE Arabidopsis PERK1 receptor related protein.
PN WO2003072763-A1.
PD 04-SEP-2003.
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
Query Match 1.8%; Score 8; DB 7; Length 633;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1103
ID AAW79262 standard; protein; 635 AA.
DE Human protein SEQ ID NO 1924.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 635;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1104
ID AAO20500 standard; protein; 645 AA.
DE Protein of APP related human homologue hCP41313 #2.
PN WO200226820-A2.
PD 04-APR-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 1.8%; Score 8; DB 5; Length 645;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1105
ID ADJ49033 standard; protein; 645 AA.
DE O11-associated gene related protein #533.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 1.8%; Score 8; DB 8; Length 645;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1106
ID AAW27178 standard; protein; 646 AA.
DE Nephila clavipes spider silk protein.
PN WO9708315-A1.
PD 06-MAR-1997.
PA (BASE/) BASEL R M.
PA (ELIO/) ELION G R.
Query Match 1.8%; Score 8; DB 2; Length 646;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1107
ID AAO20518 standard; protein; 646 AA.
DE Protein of APP related human homologue hCP41313 #3.
PN WO200226820-A2.
PD 04-APR-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 1.8%; Score 8; DB 5; Length 646;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1108
ID ADB61321 standard; protein; 646 AA.
DE Spider silk related MasPI protein.
PN WO2003060099-A2.
PD 24-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
PA (ALWA/) ALWATTARI A.
Query Match 1.8%; Score 8; DB 7; Length 646;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1109
ID AUC35240 standard; protein; 646 AA.
DE MasPI silk protein, SEQ ID 1.
PN WO2003057727-A1.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 1.8%; Score 8; DB 7; Length 646;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1110
ID ADM46149 standard; protein; 646 AA.
DE Nephila clavipes spidroin 1 (MasPI) protein.
PN WO2003057720-A2.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 1.8%; Score 8; DB 7; Length 646;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1111
ID AAW81977 standard; protein; 649 AA.
DE Ehrlichia sp. B3 protein.
PN WO9849312-A2.
PD 05-NOV-1998.
PA (AQUI-) AQUILA BIOPHARMACEUTICALS INC.
Query Match 1.8%; Score 8; DB 2; Length 649;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1112
ID AAY40097 standard; protein; 651 AA.
DE Spider silk protein spidroine major 1.
PN FR2774588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 1.8%; Score 8; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1113
ID AAU11781 standard; protein; 651 AA.
DE Spider natural silk protein spidroin 1.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.8%; Score 8; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1114
ID ARG74687 standard; protein; 651 AA.
DE Human CGPD protein 914113CD1 SEQ ID 13.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.8%; Score 8; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
RESULT 1115
ID ABU62608 standard; protein; 663 AA.
DE Human P-TEFB protein, Cyclin T2A.
PN US2003039658-A1.
PD 27-FEB-2003.
PA (ESTA/) ESTABLE M.
PA (ROED/) ROEDER R A.
Query Match 1.8%; Score 8; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;

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RESULT 1116
ID AAM80246 standard; protein; 676 AA.
DE Human protein SEQ ID NO 3892.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSS-) HYSSQ INC.
Query Match 1.8%; Score 8; DB 4; Length 676;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1117
ID AAM50047 standard; protein; 676 AA.
DE N. clavipes spidroin synthetic homologue S01 protein #2.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKF-) IPK INST PFLANZENGENTIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 676;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1118
ID ADR09462 standard; protein; 676 AA.
DE Human protein useful for treating neurological disease Seq 2968.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 8; Length 676;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1119
ID ABB61419 standard; protein; 677 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 677;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1120
ID ADI40843 standard; protein; 677 AA.
DE Human kinase and phosphatase KPP-9 protein SEQ ID NO:9.
PN WO2004009778-A2.
PD 29-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.8%; Score 8; DB 8; Length 677;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1121
ID AAO16797 standard; protein; 682 AA.
DE Human secreted protein related to the EGF subfamily.
PN WO2003006483-A2.
PD 23-JAN-2003.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 6; Length 682;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1122
ID ADS10604 standard; protein; 691 AA.
DE Human therapeutic protein - SEQ ID 841.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 1.8%; Score 8; DB 8; Length 691;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1123
ID AAB65619 standard; protein; 692 AA.
DE Novel protein kinase, SEQ ID NO: 145.
PN WO200073469-A2.
PD 07-DEC-2000.
PA (SUGE-) SUGEN INC.
Query Match 1.8%; Score 8; DB 4; Length 692;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1124
ID ADN38946 standard; protein; 692 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:264.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.8%; Score 8; DB 7; Length 692;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1125
ID ADI29225 standard; protein; 692 AA.
DE Human MARK3-associated protein #19.
PN US2003232771-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 1.8%; Score 8; DB 8; Length 692;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
RESULT 1126
ID AAW31267 standard; protein; 694 AA.
DE Drosophila frizzled-2 protein (wnt receptor).
PN WO9739357-A1.
PD 23-OCT-1997.
PA (STRD-) UNIV LELAND STANFORD JUNIOR.
PA (UYJO-) UNIV JOHNS HOPKINS.
Query Match 1.8%; Score 8; DB 2; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1127
ID ABB71797 standard; protein; 694 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42183.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1128
ID ABR58650 standard; protein; 695 AA.
DE Human cancer related protein SEQ ID NO:307.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.8%; Score 8; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1129
ID AAR14308 standard; protein; 718 AA.
DE N. clavipes dragline silk protein-1.
PN EP452925-A.
PD 23-OCT-1991.
PA (UYWY-) UNIV OF WYOMING.
Query Match 1.8%; Score 8; DB 2; Length 718;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1130
ID AAW53346 standard; protein; 718 AA.
DE Nephila clavipes spider silk protein.
PN US5728810-A.
PD 17-MAR-1998.
PA (UYWY-) UNIV WYOMING.
Query Match 1.8%; Score 8; DB 2; Length 718;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1131
ID AAY59070 standard; protein; 718 AA.
DE N. clavipes spider silk protein 1.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 1.8%; Score 8; DB 3; Length 718;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1132
ID ABB65778 standard; protein; 724 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24126.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
RESULT 1133
ID ADM04578 standard; protein; 724 AA.
DE Human protein of the invention SEQ ID NO:3263.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 7; Length 724;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
RESULT 1134
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ID ABU62609 standard; protein; 730 AA.
DE Human P-TEFB protein, Cyclin T2B.
PN US2003039658-A1.
PD 27-FEB-2003.
PA (ESTA/) ESTABLE M.
PA (ROED/) ROEDER R A.
Query Match 1.8%; Score 8; DB 6; Length 730;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
RESULT 1135
ID ADJ69158 standard; protein; 730 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID564.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.8%; Score 8; DB 7; Length 730;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
RESULT 1136
ID ABB60124 standard; protein; 752 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7164.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 752;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 1137
ID AA41734 standard; protein; 763 AA.
DE Human TRAP-2 kinase.
PN WO9801541-A1.
PD 15-JAN-1998.
PA (TULA-) TULARIK INC.
Query Match 1.8%; Score 8; DB 2; Length 763;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1138
ID AAU02222 standard; protein; 763 AA.
DE Rat Dyrrk, a homologue of Drosophila minibrain mnb.
PN US6251664-B1.
PD 26-JUN-2001.
PA (PALL/) ESTIVILL PALLEVA X.
Query Match 1.8%; Score 8; DB 4; Length 763;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1139
ID AAU02221 standard; protein; 763 AA.
DE Human MNB, homologue of Drosophila minibrain mnb.
PN US6251664-B1.
PD 26-JUN-2001.
PA (PALL/) ESTIVILL PALLEVA X.
Query Match 1.8%; Score 8; DB 4; Length 763;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1140
ID ABB57155 standard; protein; 763 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:377.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 1.8%; Score 8; DB 5; Length 763;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1141
ID ABR54250 standard; protein; 763 AA.
DE Human NOV39a protein SEQ ID NO:168.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 6; Length 763;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1142
ID AAU99562 standard; protein; 765 AA.
DE Novel human protein (NHP), kinase #2.
PN WO200231129-A2.
PD 18-APR-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 1.8%; Score 8; DB 5; Length 765;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;

RESULT 1143
ID ADJ96623 standard; protein; 765 AA.
DE Human calcium/calmodulin-dependent protein kinase DCAMKL2 protein Seq 80.
PN WO2004006838-A2.
PD 22-JAN-2004.
PA (SUGE-) SUGEN INC.
Query Match 1.8%; Score 8; DB 8; Length 765;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1144
ID AAG66161 standard; protein; 766 AA.
DE Human serine/threonine protein kinase, 15985.
PN WO200216588-A2.
PD 28-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.8%; Score 8; DB 5; Length 766;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1145
ID AAE21719 standard; protein; 766 AA.
DE Human PKIN-14 protein.
PN WO200218557-A2.
PD 07-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.8%; Score 8; DB 5; Length 766;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1146
ID AAU99561 standard; protein; 766 AA.
DE Novel human protein (NHP), kinase #1.
PN WO200231129-A2.
PD 18-APR-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 1.8%; Score 8; DB 5; Length 766;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1147
ID ADC77671 standard; protein; 766 AA.
DE Human 15985 protein SEQ ID NO:34.
PN WO2003073983-A2.
PD 12-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.8%; Score 8; DB 7; Length 766;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1148
ID ADQ9118 standard; protein; 766 AA.
DE Human urological disorder related protein 15985 SEQ:70.
PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.8%; Score 8; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1149
ID ADN23352 standard; protein; 772 AA.
DE Bacterial polypeptide #6005.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.8%; Score 8; DB 8; Length 772;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1150
ID AAM50045 standard; protein; 773 AA.
DE N. clavipes spidroin homologue SM12-70xELP for plant expression.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 773;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1151
ID ADN23353 standard; protein; 775 AA.
DE Bacterial polypeptide #6006.
PN US2003233675-A1.
PD 18-DEC-2003.

PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.8%; Score 8; DB 8; Length 775;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
RESULT 1152
ID AAM50046 standard; protein; 777 AA.
DE N. clavipes spidroin homologue SM12-70xELP for E. coli expression.
PN DB10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 777;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 1153
ID ABU36827 standard; protein; 778 AA.
DE Protein encoded by Prokaryotic essential gene #22354.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 778;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 1154
ID ADI40872 standard; protein; 783 AA.
DE Human kinase and phosphatase KPP-38 protein SEQ ID NO:38.
PN WO2004009778-A2.
PD 29-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.8%; Score 8; DB 8; Length 783;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 1155
ID ABB62304 standard; protein; 805 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13704.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 805;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1156
ID ABB60866 standard; protein; 806 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 806;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1157
ID AAW37501 standard; protein; 816 AA.
DE Human nel-related protein type 2.
PN EP796913-A2.
PD 24-SEP-1997.
PA (SAKA) OTSUKA PHARM CO LTD.
Query Match 1.8%; Score 8; DB 2; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1158
ID ABR56522 standard; protein; 816 AA.
DE Human nel-related protein type 2 SEQ ID:37.
PN EP1295944-A2.
PD 26-MAR-2003.
PA (SAKA) OTSUKA PHARM CO LTD.
Query Match 1.8%; Score 8; DB 6; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1159
ID ADQ18201 standard; protein; 816 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1018.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 1.8%; Score 8; DB 8; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1160
ID ADQ76516 standard; protein; 816 AA.

DE Amino acid sequence of human NRP2.
PN EP1439230-A2.
PD 21-JUL-2004.
PA (SAKA) OTSUKA PHARM CO LTD.
PA (PROT-) PROTEIN DESIGN LAB INC.
Query Match 1.8%; Score 8; DB 8; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1161
ID ADP56112 standard; protein; 816 AA.
DE Human PRO protein sequence SEQ ID NO:2088.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 1.8%; Score 8; DB 8; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1162
ID ADR32029 standard; protein; 816 AA.
DE Human NELL2, SEQ ID 8.
PN WO2004072100-A2.
PD 26-AUG-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 1.8%; Score 8; DB 8; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1163
ID ABB64699 standard; protein; 821 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20889.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 821;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1164
ID ABP97380 standard; protein; 825 AA.
DE Human DCAMKL1-like serine/threonine kinase, SEQ ID NO:2.
PN WO2003018816-A1.
PD 06-MAR-2003.
PA (FARB) BAYER AG.
Query Match 1.8%; Score 8; DB 6; Length 825;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1165
ID ADA54824 standard; protein; 846 AA.
DE Human protein, SEQ ID 2392.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 1.8%; Score 8; DB 6; Length 846;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1166
ID ADG39856 standard; protein; 847 AA.
DE Protein similar to human NOV12 #2.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADL/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALV/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 1.8%; Score 8; DB 7; Length 847;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1167
ID ABB60212 standard; protein; 869 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7428.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PRKB-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 869;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1168
ID ADJ69388 standard; protein; 877 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1194.
FN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.8%; Score 8; DB 7; Length 877;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
RESULT 1169
ID ADM29420 standard; protein; 917 AA.
DE Mouse macrophage colony stimulating factor 1 receptor.
FN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 7; Length 917;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1170
ID ADM29419 standard; protein; 917 AA.
DE Rat macrophage colony stimulating factor 1 receptor.
FN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 7; Length 917;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1171
ID ABR61376 standard; protein; 928 AA.
DE Human GlcNAC-phosphotransferase alpha-subunit.
FN US6537785-B1.
PD 25-MAR-2003.
PA (GENZ-) GENZYME GLYCOBIOLOGY RES INST INC.
Query Match 1.8%; Score 8; DB 4; Length 928;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1172
ID ADD27812 standard; protein; 928 AA.
DE Human GlcNAC-phosphotransferase alpha subunit.
FN US2003119088-A1.
PD 26-JUN-2003.
PA (NOVA-) NOVAZYME PHARM INC.
Query Match 1.8%; Score 8; DB 7; Length 928;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1173
ID ABRW01488 standard; protein; 928 AA.
DE Human GlcNAC-phosphotransferase alpha subunit precursor protein.
FN US2003124652-A1.
PD 03-JUL-2003.
PA (NOVA-) NOVAZYME PHARM INC.
Query Match 1.8%; Score 8; DB 7; Length 928;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1174
ID ABRW01537 standard; protein; 928 AA.
DE Human GlcNAC-phosphotransferase alpha subunit precursor protein.
FN US2003124653-A1.
PD 03-JUL-2003.
PA (NOVA-) NOVAZYME PHARM INC.
Query Match 1.8%; Score 8; DB 7; Length 928;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
RESULT 1175
ID AD001020 standard; protein; 968 AA.
DE Fruit fly AD-related protein CG14918.
FN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 1.8%; Score 8; DB 8; Length 968;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1176
ID AAM50038 standard; protein; 989 AA.
DE N. clavipes spideroin synthetic homologue S01SM12 protein.
FN DE10113781-A1.

PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 989;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1177
ID ABG14604 standard; protein; 994 AA.
DE Novel human diagnostic protein #14595.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 994;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1178
ID ABG07468 standard; protein; 994 AA.
DE Novel human diagnostic protein #7459.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 994;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1179
ID ABG19901 standard; protein; 994 AA.
DE Novel human diagnostic protein #19892.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 994;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1180
ID ABG14924 standard; protein; 994 AA.
DE Novel human diagnostic protein #14915.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 994;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1181
ID ADJ69375 standard; protein; 1027 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1181.
FN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.8%; Score 8; DB 7; Length 1027;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
RESULT 1182
ID ABB63413 standard; protein; 1108 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17031.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 1108;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
RESULT 1183
ID ADN21459 standard; protein; 1133 AA.
DE Bacterial polypeptide #4112.
FN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 1.8%; Score 8; DB 8; Length 1133;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1184
ID AAY68784 standard; protein; 1135 AA.
DE Amino acid sequence of a human phosphorylation effector PHSP-16.
FN WO200006728-A2.
PD 10-FEB-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 1.8%; Score 8; DB 3; Length 1135;
Best Local Similarity 100.0%; Pred. No. 9e+02;

RESULT 1185
ID AAR6391 standard; protein; 1141 AA.
DE Human SREBP-2.
PN WO9426922-A2.
PD 24-NOV-1994.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 1.8%; Score 8; DB 2; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1186
ID AAY50700 standard; protein; 1141 AA.
DE Human SREBP-2 protein.
PN DE19816902-A1.
PD 28-OCT-1999.
PA (KRON/) KRONE W.
PA (MUEL/) MUELLER-WIELAND D.
Query Match 1.8%; Score 8; DB 2; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1187
ID ADK60415 standard; protein; 1141 AA.
DE Angiogenesis differentially expressed protein #55.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 1.8%; Score 8; DB 8; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1188
ID ADK60716 standard; protein; 1141 AA.
DE Angiogenesis differentially expressed protein #55.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 1.8%; Score 8; DB 8; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1189
ID ADP73339 standard; protein; 1141 AA.
DE Human mitogen-activated protein kinase kinase kinase 4 (MAP4K4).
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 1.8%; Score 8; DB 8; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1190
ID AEM82371 standard; protein; 1141 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO83293, SEQ:6086.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.8%; Score 8; DB 8; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1191
ID ADQ39979 standard; protein; 1141 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1642.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 8; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1192
ID ADQ39980 standard; protein; 1141 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1643.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 8; Length 1141;
Best Local Similarity 100.0%; Pred. No. 9e+02;
RESULT 1193
ID AAB43016 standard; protein; 1165 AA.
DE Human ORFX ORF2780 polypeptide sequence SEQ ID NO:5560.
PN WO200058473-A2.
PD 05-OCT-2000.

PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 3; Length 1165;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 1194
ID ABG17470 standard; protein; 1165 AA.
DE Novel human diagnostic protein #17461.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 1195
ID AAO18509 standard; protein; 1165 AA.
DE Human insulin receptor signaling modifier SEQ ID NO: 40.
PN WO200255664-A2.
PD 18-JUL-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 1.8%; Score 8; DB 5; Length 1165;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 1196
ID ABU03499 standard; protein; 1165 AA.
DE Angiogenesis-associated human protein sequence #44.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 1.8%; Score 8; DB 6; Length 1165;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 1197
ID ADO85778 standard; protein; 1165 AA.
DE Rac/axin/beta-catenin pathway modulating MAPK-associated protein #2.
PN WO2004048542-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 1.8%; Score 8; DB 8; Length 1166;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
RESULT 1198
ID ABG17468 standard; protein; 1175 AA.
DE Novel human diagnostic protein #17459.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 1175;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 1199
ID AAU76512 standard; protein; 1175 AA.
DE Human HSP/GCK-like kinase.
PN US6346416-B1.
PD 12-FEB-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 1.8%; Score 8; DB 5; Length 1175;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 1200
ID ADK60186 standard; protein; 1175 AA.
DE Angiogenesis differentially expressed protein GS-P9.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 1.8%; Score 8; DB 8; Length 1175;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 1201
ID ADK60487 standard; protein; 1175 AA.
DE Angiogenesis differentially expressed protein GS-P9.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 1.8%; Score 8; DB 8; Length 1175;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
RESULT 1202
ID ADP73110 standard; protein; 1175 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P9.
PN FR2843753-A1.

PD 27-FEB-2004.
 PA (GENE/)/ GENE S.
 PA (ALMS/)/ AL M S.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1175;
 RESULT 1203
 ID ADR40445 standard; protein; 1192 AA.
 DE Mouse inositol 1,4,5-triphosphate 3-kinase (IP3KB) enzyme.
 PN W02004066926-A2.
 PD 12-AUG-2004.
 PA (IRMI-) IRM LLC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1192;
 RESULT 1204
 ID ADR39772 standard; protein; 1194 AA.
 DE Human kinase and phosphatase KPP-45 protein SEQ ID NO:45.
 PN W02004074453-A2.
 PD 02-SEP-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1194;
 RESULT 1205
 ID ADD27810 standard; protein; 1199 AA.
 DE Soluble human GlnAc-phosphotransferase.
 PN US2003119088-A1.
 PD 26-JUN-2003.
 PA (NOVA-) NOVAZYME PHARM INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1199;
 RESULT 1206
 ID ABW01487 standard; protein; 1199 AA.
 DE N-acetylglucosamine-1(GlcNAc)-phosphotransferase.
 PN US2003124652-A1.
 PD 03-JUL-2003.
 PA (NOVA-) NOVAZYME PHARM INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1199;
 RESULT 1207
 ID ABW01536 standard; protein; 1199 AA.
 DE N-acetylglucosamine-1(GlcNAc)-phosphotransferase protein.
 PN US2003124653-A1.
 PD 03-JUL-2003.
 PA (NOVA-) NOVAZYME PHARM INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1199;
 RESULT 1208
 ID ABE04368 standard; protein; 1212 AA.
 DE Human kinase (PKIN)-9.
 PN W0200146397-A2.
 PD 28-JUN-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 4; Length 1212;
 RESULT 1209
 ID ADE25753 standard; protein; 1212 AA.
 DE Human protein differentially expressed in foam cells #30.
 PN US2003194721-A1.
 PD 16-OCT-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 7; Length 1212;
 RESULT 1210
 ID ABG17469 standard; protein; 1219 AA.
 DE Novel human diagnostic protein #17460.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 4; Length 1219;
 RESULT 1211
 ID ADR39771 standard; protein; 1222 AA.
 DE Human kinase and phosphatase KPP-44 protein SEQ ID NO:44.
 PN W02004074453-A2.
 PD 23-APR-1998.
 PD 02-SEP-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1222;
 RESULT 1212
 ID AA48895 standard; protein; 1230 AA.
 DE Candida albicans CST20 protein.
 PN W09818927-A1.
 PD 07-MAY-1998.
 PA (CANA) NAT RES COUNCIL CANADA.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 2; Length 1230;
 RESULT 1213
 ID ADN61483 standard; protein; 1230 AA.
 DE Human KPP-49 protein SEQ ID NO:49.
 PN W02004042022-A2.
 PD 21-MAY-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 8; Length 1233;
 RESULT 1214
 ID AAY55954 standard; protein; 1233 AA.
 DE Mouse STE20-related protein kinase NIK_m.
 PN W09953036-A2.
 PD 21-OCT-1999.
 PA (SUGS-) SUGEN INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 2; Length 1233;
 RESULT 1215
 ID AAY55931 standard; protein; 1239 AA.
 DE Human ZC1 protein.
 PN W09953036-A2.
 PD 21-OCT-1999.
 PA (SUGS-) SUGEN INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 2; Length 1239;
 RESULT 1216
 ID AAM50037 standard; protein; 1255 AA.
 DE N. clavipes spidroin synthetic homologue SO1S01 protein.
 PN DE10113781-A1.
 PD 13-DEC-2001.
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 5; Length 1255;
 RESULT 1217
 ID AAE25290 standard; protein; 1256 AA.
 DE Human nucleic acid-associated protein (NAAP-9).
 PN W0200250279-A2.
 PD 27-JUN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 5; Length 1256;
 RESULT 1218
 ID ABB78296 standard; protein; 1294 AA.
 DE Amino acid sequence of lipid-associated molecule (LIPAM)-7.
 PN W0200263005-A2.
 PD 15-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 5; Length 1294;
 RESULT 1219
 ID ABB71827 standard; protein; 1333 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 42273.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match
 Best Local Similarity 1.8%; Score 8; DB 4; Length 1333;
 RESULT 1220
 ID AAW59359 standard; protein; 1349 AA.
 DE Human retinal degeneration B3 polypeptide (hrdgB3).
 PN W09816639-A1.
 PD 23-APR-1998.

PA (SUGS-) SUGEN INC.
PA (UTNY-) UNIV NEW YORK MEDICAL CENT.
Query Match 1.8%; Score 8; DB 2; Length 1349;
Best Local Similarity 100.0%; Pred. No. 1e+03;
RESULT 1221
ID ADN00366 standard; protein; 1359 AA.
DE Novel human protein #7.
PN JP2004073126-A.
PD 11-MAR-2004.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 1.8%; Score 8; DB 8; Length 1359;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1222
ID ADN61482 standard; protein; 1384 AA.
DE Human KPP-48 protein SEQ ID NO:48.
PN WO2004042022-A2.
PD 21-MAY-2004.
PA (INCY-) INCYTE CORP.
Query Match 1.8%; Score 8; DB 8; Length 1384;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1223
ID ADJ96675 standard; protein; 1392 AA.
DE Human protein kinase ZC1 protein SeqID 132.
PN WO2004006838-A2.
PD 22-JAN-2004.
PA (SUGS-) SUGEN INC.
Query Match 1.8%; Score 8; DB 8; Length 1392;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1224
ID AAM78991 standard; protein; 1393 AA.
DE Human protein SEQ ID NO 1653.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 1393;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1225
ID ADH29597 standard; protein; 1431 AA.
DE Human CrkRS-related Gene variant protein.
PN US2003190621-A1.
PD 09-OCT-2003.
PA (DAIK/) DAI K.
Query Match 1.8%; Score 8; DB 8; Length 1431;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1226
ID ABU07381 standard; protein; 1459 AA.
DE Human protein NOV12.
PN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 1459;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1227
ID ADG39794 standard; protein; 1459 AA.
DE Human novel protein NOV12.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENNA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (WALY/) WALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 1.8%; Score 8; DB 7; Length 1459;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1228
ID AAB5644 standard; protein; 1490 AA.
DE Novel protein Kinase, SEQ ID NO: 171.
PN WO200073469-A2.
PD 07-DEC-2000.
PA (SUGS-) SUGEN INC.
Query Match 1.8%; Score 8; DB 4; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1229
ID ABR47427 standard; protein; 1490 AA.
DE Breast cancer associated protein sequence SEQ ID NO:86.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1230
ID ABO53039 standard; protein; 1490 AA.
DE Human spliceosome associated protein (SAP) #80.
PN US2003088803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 1.8%; Score 8; DB 6; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1231
ID ADD89963 standard; protein; 1490 AA.
DE Human cancer-associated protein kinase CRK7.
PN WO2003083096-A2.
PD 09-OCT-2003.
PA (KINE-) KINETEK PHARM INC.
Query Match 1.8%; Score 8; DB 7; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1232
ID ADJ69106 standard; protein; 1490 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID912.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.8%; Score 8; DB 7; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1233
ID ADH13182 standard; protein; 1490 AA.
DE Human malignant neoplasia-related protein SeqID31.
PN EP1365034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
Query Match 1.8%; Score 8; DB 8; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1234
ID ADH09507 standard; protein; 1490 AA.
DE Human host factor protein, SEQ ID No 35.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match 1.8%; Score 8; DB 8; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1235
ID ADH09508 standard; protein; 1490 AA.
DE Human host factor protein, SEQ ID No 36.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match 1.8%; Score 8; DB 8; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1236
ID ADH09506 standard; protein; 1490 AA.
DE Human host factor protein, SEQ ID No 34.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.

Query Match 1.8%; Score 8; DB 8; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1237
ID AD129251 standard; protein; 1490 AA.
DE Human MARK3-associated protein #38.
PN US2003232771-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 1.8%; Score 8; DB 8; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
RESULT 1238
ID ABB64829 standard; protein; 1518 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21279.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 1518;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
RESULT 1239
ID ABG17466 standard; protein; 1655 AA.
DE Novel human diagnostic protein #17457.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 1655;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1240
ID ABB94266 standard; protein; 1723 AA.
DE Chlamydia pneumoniae protein sequence SEQ ID NO:394.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.8%; Score 8; DB 5; Length 1723;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1241
ID ABB94267 standard; protein; 1723 AA.
DE Chlamydia pneumoniae protein sequence SEQ ID NO:395.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 1.8%; Score 8; DB 5; Length 1723;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1242
ID ABB90585 standard; protein; 1723 AA.
DE Chlamydia pneumoniae cp6830 protein, SEQ ID NO:119.
PN WO200202606-A2.
PD 10-JAN-2002.
PA (CHIR-) CHIRON SPA.
Query Match 1.8%; Score 8; DB 5; Length 1723;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1243
ID ABU26843 standard; protein; 1732 AA.
DE Protein encoded by Prokaryotic essential gene #12370.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.8%; Score 8; DB 6; Length 1732;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1244
ID ADN17774 standard; protein; 1797 AA.
DE Bacterial polypeptide #427.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 1.8%; Score 8; DB 8; Length 1797;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
RESULT 1245
ID ABB39949 standard; protein; 1823 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1612.

PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 8; Length 1823;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1246
ID AAR44504 standard; protein; 1830 AA.
DE Urea amide lyase.
PN JP05304965-A.
PD 19-NOV-1993.
PA (TOYM) TOYOCO KK.
Query Match 1.8%; Score 8; DB 2; Length 1830;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1247
ID ADJ68314 standard; protein; 1870 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID120.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.8%; Score 8; DB 7; Length 1870;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1248
ID AAM50039 standard; protein; 1880 AA.
DE N. clavipes spidroin synthetic homologue SO1SO1SO1 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 1.8%; Score 8; DB 5; Length 1880;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
RESULT 1249
ID ABU54584 standard; protein; 2017 AA.
DE Human NOVX polypeptide #43.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 1.8%; Score 8; DB 6; Length 2017;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1250
ID ADJ69868 standard; protein; 2060 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1674.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 1.8%; Score 8; DB 7; Length 2060;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1251
ID AAB31516 standard; protein; 2087 AA.
DE Amino acid sequence of the rat Shankla polypeptide.
PN WO200078921-A2.
PD 28-DEC-2000.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 1.8%; Score 8; DB 4; Length 2087;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1252
ID AAB12000 standard; protein; 2091 AA.
DE Rat p3103 protein.
PN JP2000184884-A.
PD 04-JUL-2000.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 1.8%; Score 8; DB 3; Length 2091;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1253
ID ADO39951 standard; protein; 2102 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1614.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 8; Length 2102;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1254

ID ADQ39950 standard; protein; 2108 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1613.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 8; Length 2108;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
RESULT 1255
ID ABB80768 standard; protein; 2145 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81398, SEQ:1980.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.8%; Score 8; DB 8; Length 2145;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1256
ID AAU33195 standard; protein; 2153 AA.
DE Novel human secreted protein #3686.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 1.8%; Score 8; DB 4; Length 2153;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1257
ID ABB80769 standard; protein; 2157 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81399, SEQ:1982.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.8%; Score 8; DB 8; Length 2157;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1258
ID ADQ39952 standard; protein; 2157 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1615.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 1.8%; Score 8; DB 8; Length 2157;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1259
ID ADQ89666 standard; protein; 2228 AA.
DE Antagonist of cell cycle progression polypeptide #48.
PN WO2004063362-A2.
PD 23-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 1.8%; Score 8; DB 8; Length 2228;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1260
ID ABB58139 standard; protein; 2230 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1209.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 2230;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1261
ID ABB63947 standard; protein; 3726 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18633.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.8%; Score 8; DB 4; Length 3726;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
RESULT 1262
ID ADQ57969 standard; peptide; 8 AA.
DE MHC multimer linker peptide SEQ ID 4.
PN DE10247014-A1.
PD 22-APR-2004.
PA (ERFL/) ERFLE V.
Query Match 1.6%; Score 7; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1263
ID AAY81276 standard; peptide; 10 AA.

DE Gly/Ser-rich linker peptide, SEQ ID NO:78.
PN WO200006717-A2.
PD 10-FEB-2000.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1264
ID RAG93434 standard; peptide; 10 AA.
DE Disconnected protein complementary peptide 105.
PN GB2356401-A.
PD 23-MAY-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1265
ID AAG97098 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3292.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1266
ID RAG97100 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3294.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1267
ID RAG95246 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 1440.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1268
ID AAG97132 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3326.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1269
ID RAG97096 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3290.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1270
ID RAG96428 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 2622.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1271
ID AAG97078 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3272.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1272
ID AAG94120 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 314.

PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1273
ID AAG95016 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 1210.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1274
ID AAG97102 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3296.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1275
ID AAG97136 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3330.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1276
ID AAG96426 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 2620.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1277
ID AAG97076 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3270.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1278
ID AAG97118 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 3312.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1279
ID AAG93850 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 44.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1280
ID AAG94062 standard; peptide; 10 AA.
DE Human complementary peptide, SEQ ID NO: 256.
PN WO200142277-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1281
ID AAG95129 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 78.
PN WO200142276-A1.

PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1282
ID AAG95127 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 76.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1283
ID AAG95329 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 278.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1284
ID AAG95131 standard; peptide; 10 AA.
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 80.
PN WO200142276-A1.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1285
ID AAM43046 standard; peptide; 10 AA.
DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 355.
PN WO200142278-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1286
ID AAM43044 standard; peptide; 10 AA.
DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 353.
PN WO200142278-A2.
PD 14-JUN-2001.
PA (PROT-) PROTEOM LTD.
Query Match 1.6%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1287
ID ADC34710 standard; peptide; 10 AA.
DE (Ser4Gly)2 protease substrate, PFPS11.
PN US603886-B1.
PD 07-JAN-2003.
PA (SELE-) SELECTIVE GENETICS INC.
Query Match 1.6%; Score 7; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
RESULT 1288
ID ADA38153 standard; peptide; 12 AA.
DE Peptide amphiphile composition 8 containing an RGD cell adhesion motif.
PN WO2003054146-A2.
PD 03-JUL-2003.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 1.6%; Score 7; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
RESULT 1289
ID ADR39905 standard; peptide; 12 AA.
DE Surgical implant-related peptide amphiphile 9.
PN WO2004072104-A2.
PD 26-AUG-2004.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 1.6%; Score 7; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
RESULT 1290
ID AAR27243 standard; peptide; 13 AA.
DE Sequence of serine-rich peptide linker.
PN WO9215682-A1.
PD 17-SEP-1992.

PA (CREA-) CREATIVE BIOMOLECULES INC.
 Query Match 1.6%; Score 7; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 RESULT 1291
 ID AAR92865 standard; peptide; 13 AA.
 DE Cell adhesion modulatory peptide Aps.
 PN DB4430601-A1.
 PD 23-FEB-1996.
 PA (BEIE-) BEIERSDORF AG.
 Query Match 1.6%; Score 7; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 RESULT 1292
 ID AAY59102 standard; peptide; 13 AA.
 DE N. clavipes spider silk protein 1 repeat fragment.
 PN US598984-A.
 PD 23-NOV-1999.
 PA (UYWY-) UNIV WYOMING.
 Query Match 1.6%; Score 7; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 RESULT 1293
 ID AAM98057 standard; peptide; 13 AA.
 DE Human peptide #1332 encoded by a SNP oligonucleotide.
 PN WO200147944-A2.
 PD 05-JUL-2001.
 PA (CURA-) CURAGEN CORP.
 Query Match 1.6%; Score 7; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 RESULT 1294
 ID AAM98358 standard; peptide; 14 AA.
 DE Human peptide #1633 encoded by a SNP oligonucleotide.
 PN WO200147944-A2.
 PD 05-JUL-2001.
 PA (CURA-) CURAGEN CORP.
 Query Match 1.6%; Score 7; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 RESULT 1295
 ID AAR39572 standard; protein; 15 AA.
 DE Sequence of a new linker.
 PN WO9316185-A2.
 PD 19-AUG-1993.
 PA (CREA-) CREATIVE BIOMOLECULES INC.
 PA (CETU-) CETUS ONCOLOGY CORP.
 Query Match 1.6%; Score 7; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1296
 ID AAW53355 standard; peptide; 15 AA.
 DE Nephila clavipes spider silk protein tandem repeat unit SEQ ID NO:13.
 PN US5728810-A.
 PD 17-MAR-1998.
 PA (UYWY-) UNIV WYOMING.
 Query Match 1.6%; Score 7; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1297
 ID AAY90828 standard; peptide; 15 AA.
 DE Linker amino acid sequence SEQ ID NO:31.
 PN US6054561-A.
 PD 25-APR-2000.
 PA (CHIR-) CHIRON CORP.
 Query Match 1.6%; Score 7; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1298
 ID ABB55909 standard; peptide; 15 AA.
 DE Vascular dementia-associated protein isoform (VPI) 109.
 PN WO200169261-A2.
 PD 20-SEP-2001.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 Query Match 1.6%; Score 7; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1299
 ID AAU08688 standard; peptide; 15 AA.
 DE Antibody L19-Fibronectin-2 (IL-2) fusion protein amino acid linker.
 PN WO200162298-A2.
 PD 30-AUG-2001.

PA (PHIL-) PHILOGEN SRL.
 Query Match 1.6%; Score 7; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1300
 ID RAU04949 standard; peptide; 15 AA.
 DE Humanised anti-p185 antibody/IL-2 fusion protein, linker peptide #2.
 PN WO200153354-A2.
 PD 26-JUL-2001.
 PA (CHIR-) CHIRON CORP.
 PA (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
 PA (HAMI-) HAMILTON REGIONAL CANCER CENT.
 Query Match 1.6%; Score 7; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1301
 ID AAG80185 standard; peptide; 15 AA.
 DE Fusion construct human STAT3/CD4 linker peptide.
 PN WO200178785-A2.
 PD 25-OCT-2001.
 PA (BIOT-) BIOTECHTID GMBH.
 Query Match 1.6%; Score 7; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1302
 ID RAU99372 standard; peptide; 15 AA.
 DE Peptide linker, GLG, used to construct IFN beta single chain dimers.
 PN WO200236628-A2.
 PD 10-MAY-2002.
 PA (MAXY-) MAXYGEN APS.
 Query Match 1.6%; Score 7; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1303
 ID ABG97612 standard; peptide; 15 AA.
 DE Apolipoprotein analogue 1 (Apo A1) associated spacer peptide #6.
 PN WO200236609-A2.
 PD 16-MAY-2002.
 PA (PROT-) PROTEOPHARMA APS.
 Query Match 1.6%; Score 7; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1304
 ID AAU11789 standard; peptide; 15 AA.
 DE Silk fibre forming region repeat unit.
 PN WO200190389-A2.
 PD 29-NOV-2001.
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 7; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1305
 ID ABU08677 standard; peptide; 15 AA.
 DE Human single chain MHC class I polypeptide associated linker #1.
 PN US2003003535-A1.
 PD 02-JAN-2003.
 PA (TECR-) TECHNION RES & DEV FOUND LTD.
 Query Match 1.6%; Score 7; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1306
 ID ABW00718 standard; peptide; 15 AA.
 DE Linker #2, peptide used in the invention.
 PN US2002168375-A1.
 PD 14-NOV-2002.
 PA (CHIR-) CHIRON CORP.
 Query Match 1.6%; Score 7; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1307
 ID ADN60232 standard; protein; 15 AA.
 DE Linker peptide.
 PN US6723517-B1.
 PD 20-APR-2004.
 PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
 Query Match 1.6%; Score 7; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 RESULT 1308
 ID ADR40520 standard; protein; 15 AA.
 DE Spider silk dragline peptide formula #2.
 PN WO2004073644-A2.

PD 02-SEP-2004.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 15;
RESULT 1309
ID AUR38601 standard; peptide; 15 AA.
DE Anti-botulinum neurotoxin antibody associated linker #3.
PN US2004175385-A1.
PD 09-SEP-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 15;
RESULT 1310
ID AAP50321 standard; protein; 17 AA.
DE Spacer peptide between cytotoxic and target cell binding regions.
PN WO8503508-A.
PD 15-AUG-1985.
PA (CETU) CETUS CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 17;
RESULT 1311
ID AAP91928 standard; peptide; 17 AA.
DE Spacer fragment.
PN EP335476-A.
PD 04-OCT-1989.
PA (CETU) CETUS CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 1; Length 17;
RESULT 1312
ID AAY67939 standard; peptide; 17 AA.
DE EPOA-hSA fusion protein peptide linker #2.
PN WO9966054-A2.
PD 23-DEC-1999.
PA (GENZ) GENZYME TRANSGENICS CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 17;
RESULT 1313
ID AAU68114 standard; peptide; 17 AA.
DE Human Breast cancer-associated protein isoform, BPI-317 peptide #2.
PN WO200171357-A2.
PD 27-SEP-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;
RESULT 1314
ID AAU68434 standard; peptide; 17 AA.
DE Human Breast cancer-associated protein isoform, BPI-362 peptide #1.
PN WO200171357-A2.
PD 27-SEP-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;
RESULT 1315
ID AAU68143 standard; peptide; 17 AA.
DE Human Breast cancer-associated protein isoform, BPI-25 peptide #1.
PN WO200171357-A2.
PD 27-SEP-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;
RESULT 1316
ID AAU68451 standard; peptide; 17 AA.
DE Human Breast cancer-associated protein isoform, BPI-367 peptide #1.
PN WO200171357-A2.
PD 27-SEP-2001.
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;
RESULT 1317
ID AAU68344 standard; peptide; 17 AA.
DE Human Breast cancer-associated protein isoform, BPI-343 peptide #1.
PN WO200171357-A2.
PD 27-SEP-2001.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 17;
RESULT 1318
ID AAO17004 standard; peptide; 17 AA.
DE Linker peptide used to construct alpha-MSH concatamer SEQ ID NO: 68.
PN WO200206316-A2.
PD 24-JAN-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 5; Length 17;
RESULT 1319
ID ADB24918 standard; peptide; 17 AA.
DE Peptide linker #4.
PN US2003049801-A1.
PD 13-MAR-2003.
PA (WUCC) WU C.
PA (LINR) LIN R.
PA (HSUP) HSU P.
Query Match
Best Local Similarity 1.6%; Score 7; DB 6; Length 17;
RESULT 1320
ID ADB24915 standard; peptide; 17 AA.
DE Peptide linker #4.
PN US2003049694-A1.
PD 13-MAR-2003.
PA (WUCC) WU C.
PA (LINR) LIN R.
PA (HSUP) HSU P.
Query Match
Best Local Similarity 1.6%; Score 7; DB 7; Length 17;
RESULT 1321
ID ABU10017 standard; peptide; 17 AA.
DE Alpha-MSH concatamer related linker peptide #5.
PN US200219332-A1.
PD 13-DEC-2002.
PA (HEDL) HEDLEY M L.
Query Match
Best Local Similarity 1.6%; Score 7; DB 7; Length 17;
RESULT 1322
ID ADQ28276 standard; peptide; 17 AA.
DE Peptide linker #4.
PN US2004117863-A1.
PD 17-JUN-2004.
PA (EDGE) EDGE M D.
PA (POLL) POLLOCK D.
PA (SCHE) ECHELARD Y.
PA (NEAD) MEADE H M.
PA (RYBA) RYBAK S M.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 17;
RESULT 1323
ID AAY71888 standard; peptide; 18 AA.
DE Linker peptide #7, to construct human OPG-Fc fragment fusion protein.
PN WO200118203-A1.
PD 15-MAR-2001.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 18;
RESULT 1324
ID AAW49208 standard; peptide; 19 AA.
DE Human leucocyte antigen DQ4 binding peptide #99.
PN JP08151396-A.
PD 11-JUN-1996.
PA (TEIJ) TEIJIN LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 2; Length 19;
RESULT 1325
ID ADH47607 standard; peptide; 20 AA.
DE Human lung tumour clone peptide, SEQ ID NO 2088.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.

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Query Match      1.6%; Score 7; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1326
ID ADH47608 standard; peptide; 20 AA.
DE Human lung tumour clone peptide, SEQ ID NO 2089.
PN W02003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1327
ID ADJ21527 standard; peptide; 20 AA.
DE Human lung cancer-related L978P peptide fragment - SEQ ID 2089.
PN US2003211510-A1.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1328
ID ADJ21526 standard; peptide; 20 AA.
DE Human lung cancer-related L978P peptide fragment - SEQ ID 2088.
PN US2003211510-A1.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match      1.6%; Score 7; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
RESULT 1329
ID AA53348 standard; peptide; 21 AA.
DE Nephila clavipes spider silk protein tandem repeat unit SEQ ID NO:5.
PN US5728810-A.
PD 17-MAR-1998.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1330
ID AAY59072 standard; peptide; 21 AA.
DE N. clavipes spider silk protein repeat unit.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
RESULT 1331
ID ADN37739 standard; peptide; 22 AA.
DE Soft segment found in a monomer unit of DP-1B SEQ ID NO:8.
PN W02004035750-A2.
PD 29-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match      1.6%; Score 7; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
RESULT 1332
ID AAY79554 standard; peptide; 23 AA.
DE Linker peptide used in single chain polyspecific binding molecule.
PN W0200023087-A1.
PD 27-APR-2000.
PA (SUNO-) SUNOL MOLECULAR CORP.
Query Match      1.6%; Score 7; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1333
ID AA636907 standard; peptide; 23 AA.
DE N. senegalensis major ampullate spidroin 1 (MaSp1) consensus peptide.
PN W02003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
RESULT 1334
ID AAY59101 standard; peptide; 25 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match      1.6%; Score 7; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1335
ID AAU8959 standard; peptide; 26 AA.
DE Insulin/insulin-like growth factor receptor-binding peptide #915.
PN W0200172771-A2.
PD 04-OCT-2001.
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO) NOVO NORDISK AS.
Query Match      1.6%; Score 7; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1336
ID ADA03793 standard; peptide; 26 AA.
DE Insulin receptor (IR) related Formula 1 motif peptide SEQ ID NO:424.
PN W02003027246-A2.
PD 03-APR-2003.
PA (NOVO) NOVO NORDISK AS.
PA (DGIB-) DGI BIOTECHNOLOGIES.
Query Match      1.6%; Score 7; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1337
ID ADH95006 standard; protein; 26 AA.
DE Insulin receptor motif polypeptide, SEQ ID NO 424.
PN W02003070747-A2.
PD 28-AUG-2003.
PA (NOVO) NOVO NORDISK AS.
PA (DGIB-) DGI BIOTECHNOLOGIES.
Query Match      1.6%; Score 7; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1338
ID ADL67697 standard; peptide; 26 AA.
DE TGF-IR/IR binding peptide seq id 424.
PN US2004023887-A1.
PD 05-FEB-2004.
PA (PILL/) PILLUTLA R.
PA (DEDO/) DEDOVA O.
PA (BLUM/) BLUME A J.
PA (GOLD/) GOLDSTEIN N I.
PA (BRIS/) BRISSETTE R.
PA (WANG/) WANG P.
PA (LIUH/) LIU H.
PA (HSIA/) HSIAO K.
PA (LENN/) LENNICK M.
PA (FLET/) FLETCHER P.
Query Match      1.6%; Score 7; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1339
ID ADM37542 standard; peptide; 26 AA.
DE Anti-IR formula 1 motif peptide #280.
PN US2003236190-A1.
PD 25-DEC-2003.
PA (PILL/) PILLUTLA R.
PA (BRIS/) BRISSETTE R.
PA (BLUM/) BLUME A J.
PA (SCHA/) SCHAFFER L.
PA (BRAN/) BRANDT J.
PA (GOLD/) GOLDSTEIN N I.
PA (SPET/) SPETZLER J.
PA (OSTE/) OSTERGAARD S.
PA (HANS/) HANSEN P H.
Query Match      1.6%; Score 7; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
RESULT 1340
ID ADJ81392 standard; peptide; 27 AA.
DE Self-assembling polymer peptide #247.
PN W02003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match      1.6%; Score 7; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
RESULT 1341
ID ADJ81262 standard; peptide; 27 AA.
DE Self-assembling polymer peptide #117.
PN W02003056297-A2.
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PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match
Best Local Similarity 1.6%; Score 7; DB 7; Length 27;
RESULT 1342
ID A081106 standard; peptide; 27 AA.
DE Self-assembling polymer peptide #161.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match
Best Local Similarity 1.6%; Score 7; DB 7; Length 27;
RESULT 1343
ID A081168 standard; peptide; 27 AA.
DE Self-assembling polymer peptide #23.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match
Best Local Similarity 1.6%; Score 7; DB 7; Length 27;
RESULT 1344
ID A015297 standard; peptide; 28 AA.
DE N clavipes spider silk consensus peptide #1.
PN WO2004041172-A2.
PD 27-MAY-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 28;
RESULT 1345
ID ADR40519 standard; protein; 28 AA.
DE Spider silk dragline peptide formula #1.
PN WO2004073644-A2.
PD 02-SEP-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 28;
RESULT 1346
ID AAU11792 standard; peptide; 29 AA.
DE Silk fibre forming region repeat monomer.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 1.6%; Score 7; DB 5; Length 29;
RESULT 1347
ID AAY59111 standard; peptide; 30 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 30;
RESULT 1348
ID AAY59124 standard; peptide; 30 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 30;
RESULT 1349
ID AAY59123 standard; peptide; 30 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 30;
RESULT 1350
ID AAB15670 standard; peptide; 31 AA.
DE Alpha.v beta 3 receptor-specific peptide.
PN WO200403783-A2.
PD 27-JUL-2000.

PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 31;
RESULT 1351
ID AAO22543 standard; peptide; 31 AA.
DE GRGDS-containing peptide.
PN WO200239999-A2.
PD 23-MAY-2002.
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 5; Length 31;
RESULT 1352
ID ABP97039 standard; peptide; 31 AA.
DE Vitronectin derived GRGDS motif peptide #2.
PN WO2003020280-A2.
PD 13-MAR-2003.
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 6; Length 31;
RESULT 1353
ID ADN60233 standard; protein; 31 AA.
DE Minimal activation motif-1X-Linker-1X peptide.
PN US6723517-B1.
PD 20-APR-2004.
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 31;
RESULT 1354
ID ADO57972 standard; peptide; 31 AA.
DE MHC multimer linker peptide SEQ ID 7.
PN DE10247014-A1.
PD 22-APR-2004.
PA (ERFL/) ERFLE V.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 31;
RESULT 1355
ID AAY59107 standard; peptide; 32 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 32;
RESULT 1356
ID AAW53350 standard; peptide; 33 AA.
DE Nephila clavipes spider silk protein tandem repeat unit SEQ ID NO.7.
PN US5728810-A.
PD 17-MAR-1998.
PA (UYWY-) UNIV WYOMING.
Query Match
Best Local Similarity 1.6%; Score 7; DB 2; Length 33;
RESULT 1357
ID AAY59074 standard; peptide; 33 AA.
DE N. clavipes spider silk protein repeat unit.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match
Best Local Similarity 1.6%; Score 7; DB 3; Length 33;
RESULT 1358
ID AAE18322 standard; peptide; 33 AA.
DE Spider silk protein monomer sequence used to construct NcDS.24.
PN WO200200016-A1.
PD 03-JAN-2002.
PA (LUMI-) LUMINIS PTY LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 5; Length 33;
RESULT 1359
ID AAE36905 standard; peptide; 33 AA.
DE Nephila clavipes major ampullate spidroin 1 (Maspl) consensus peptide.
PN WO2003020916-A2.
PD 13-MAR-2003.

PA (UYWY-) UNIV WYOMING.
Query Match 1.6%; Score 7; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1360
ID ADJ81265 standard; peptide; 33 AA.
DE Self-assembling polymer peptide #120.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1361
ID ADJ81253 standard; peptide; 33 AA.
DE Self-assembling polymer peptide #108.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1362
ID ADJ81383 standard; peptide; 33 AA.
DE Self-assembling polymer peptide #238.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1363
ID ADJ81395 standard; peptide; 33 AA.
DE Self-assembling polymer peptide #250.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 3e+02;
RESULT 1364
ID AA06201 standard; protein; 34 AA.
DE Spider dragline variant, DP-1 consensus sequence.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1365
ID AA933400 standard; peptide; 34 AA.
DE N. clavipes spidroin 1 long repeat peptide motif.
PN WO9947661-A2.
PD 23-SEP-1999.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 1.6%; Score 7; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1366
ID AA959115 standard; peptide; 34 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 1.6%; Score 7; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1367
ID AA959117 standard; peptide; 34 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 1.6%; Score 7; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1368
ID AA959105 standard; peptide; 34 AA.
DE N. clavipes spider silk protein 1 repeat fragment.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.

Query Match 1.6%; Score 7; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1369
ID AAU09054 standard; peptide; 34 AA.
DE Silk spider spidroin 1 34 amino acid long repeat motif.
PN WO200156626-A1.
PD 09-AUG-2001.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 1.6%; Score 7; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1370
ID ABP56042 standard; peptide; 34 AA.
DE Proopiomelanocortin related sequence SEQ ID NO:12.
PN WO200256022-A2.
PD 18-JUL-2002.
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
Query Match 1.6%; Score 7; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1371
ID AAU11788 standard; peptide; 34 AA.
DE Silk fibre forming region repeat consensus sequence.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1372
ID ADB61295 standard; peptide; 34 AA.
DE Dragline silk protein, Nephila spidroin I (MasP 1) peptide region.
PN WO200306099-A2.
PD 24-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
PA (ALWA/) ALWATTARI A.
Query Match 1.6%; Score 7; DB 7; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1373
ID ADC35267 standard; peptide; 34 AA.
DE Silk protein motif, SEQ ID 28.
PN WO2003057727-A1.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 1.6%; Score 7; DB 7; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1374
ID ADJ81402 standard; peptide; 34 AA.
DE Self-assembling polymer peptide #257.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1375
ID ADJ81272 standard; peptide; 34 AA.
DE Self-assembling polymer peptide #127.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1376
ID ADM46123 standard; peptide; 34 AA.
DE Nephila clavipes spidroin 1 (MasPI) repeat motif peptide.
PN WO2003057720-A2.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 1.6%; Score 7; DB 7; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1377
ID ADN37738 standard; peptide; 34 AA.
DE Monomer unit of DP-1B conserved consensus motif SEQ ID NO:7.
PN WO2004035750-A2.
PD 29-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.

Query Match 1.6%; Score 7; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
RESULT 1378
ID AAR10318 standard; protein; 36 AA.
DE Bovine BMP - exon 4.
PN EP409472-A.
PD 23-JAN-1991.
PA (CHIR-) CHIRON CORP.
Query Match
Best Local Similarity 1.6%; Score 7; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
RESULT 1379
ID AAU79502 standard; peptide; 38 AA.
DE Fragment for resistance against dehydration stress, peptide #1.
PN WO200226800-A1.
PD 04-APR-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 1380
ID ABP60376 standard; peptide; 38 AA.
DE Sericin derived peptide SEQ ID NO 1.
PN WO200286133-A1.
PD 31-OCT-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match
Best Local Similarity 1.6%; Score 7; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
RESULT 1381
ID AAM20105 standard; protein; 42 AA.
DE Peptide #6539 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1382
ID ABB40301 standard; peptide; 42 AA.
DE Peptide #7807 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1383
ID AAM33987 standard; protein; 42 AA.
DE Peptide #8024 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1384
ID AAB67213 standard; peptide; 42 AA.
DE HPER2 peptide ligand #2.
PN WO200102440-A1.
PD 11-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1385
ID ABB24705 standard; protein; 42 AA.
DE Protein #6704 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1386
ID AAM73800 standard; protein; 42 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34106.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 42;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1387
ID AAM61095 standard; protein; 42 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33200.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1388
ID AGS55548 standard; peptide; 42 AA.
DE Human liver peptide, SEQ ID No 34196.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1389
ID ABG43687 standard; peptide; 42 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33352.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
RESULT 1390
ID AAM86005 standard; protein; 43 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:13598.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HOMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
RESULT 1391
ID ABB70984 standard; protein; 44 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39744.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 1.6%; Score 7; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
RESULT 1392
ID ABO57991 standard; protein; 47 AA.
DE Human genome derived single exon protein #4225.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENNY) PENN S G.
PA (RANK) RANK D R.
PA (HANZ) HANZEL D K.
Query Match
Best Local Similarity 1.6%; Score 7; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
RESULT 1393
ID AAR65749 standard; peptide; 49 AA.
DE Linker sequence used in IL-3 containing fusion protein.
PN WO9521254-A1.
PD 10-AUG-1995.
PA (SEAR) SEARLE & CO G D.
Query Match
Best Local Similarity 1.6%; Score 7; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1394
ID AAE14027 standard; protein; 49 AA.
DE Chemically modified myelopietin (MPO) conjugate related protein #16.
PN WO200176639-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA CORP.
PA (FINN) FINN R.
PA (GOKA) GOKARN Y.
PA (HILL) HILLS R.
PA (NICA) NICASTRO P.
PA (QIHH) QI H.
PA (SEDO) SEDO K.
PA (SIEG) SIEGEL N.
PA (WALT) WALTER S.

Query Match 1.6%; Score 7; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1395
ID ABG97800 standard; peptide; 49 AA.
DE Human interleukin-3 associated protein #11.
PN US6436387-B1.
PD 20-AUG-2002.
PA (SEAR) SEARLE & CO G D.
Query Match 1.6%; Score 7; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1396
ID ADJ14406 standard; protein; 49 AA.
DE Protein related to human interleukin-3 (IL-3) mutant protein SEQ ID 169.
PN US2003185790-A1.
PD 02-OCT-2003.
PA (BAUE) BAUER S C.
PA (ABRA) ABRAMS M A.
PA (BRA) BRAFORD-GOLDBERG S R.
PA (CAPA) CAPARON M H.
PA (EAST) EASTON A M.
PA (KLEI) KLEIN B K.
PA (MCKE) MCKEARN J P.
PA (OLIN) OLINS P O.
PA (PAIK) PAIK K.
PA (THOM) THOMAS J W.
Query Match 1.6%; Score 7; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
RESULT 1397
ID AB234488 standard; protein; 50 AA.
DE Protein #5487 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 03-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1398
ID AAM58929 standard; protein; 50 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31034.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
RESULT 1399
ID AAU54145 standard; protein; 54 AA.
DE Propionibacterium acnes immunogenic protein #15041.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
RESULT 1400
ID ABM50664 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15340.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
RESULT 1401
ID AAU82104 standard; peptide; 56 AA.
DE T-cell specific binding ligand peptide construct #38.
PN WO200189286-A2.
PD 29-NOV-2001.
PA (CELS-) CEL-SCI CORP.
Query Match 1.6%; Score 7; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
RESULT 1402
ID AAU82108 standard; peptide; 58 AA.
DE T-cell specific binding ligand peptide construct #42.
PN WO200189286-A2.
PD 29-NOV-2001.
PA (CELS-) CEL-SCI CORP.

Query Match 1.6%; Score 7; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
RESULT 1403
ID AAR65750 standard; peptide; 60 AA.
DE Linker sequence used in IL-3 containing fusion protein.
PN WO9521254-A1.
PD 10-AUG-1995.
PA (SEAR) SEARLE & CO G D.
Query Match 1.6%; Score 7; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1404
ID AAE14028 standard; protein; 60 AA.
DE Chemically modified myelopoietin (MPO) conjugate related protein #17.
PN WO200176639-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA CORP.
PA (FINN) FINN R.
PA (GOKA) GOKARN Y.
PA (HILL) HILLS R.
PA (NICA) NICASTRO P.
PA (QIHH) QI H.
PA (SEDO) SEDO K.
PA (SIEG) SIEGEL N.
PA (WALT) WALTER S.
Query Match 1.6%; Score 7; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1405
ID ABG97801 standard; peptide; 60 AA.
DE Human interleukin-3 associated protein #12.
PN US6436387-B1.
PD 20-AUG-2002.
PA (SEAR) SEARLE & CO G D.
Query Match 1.6%; Score 7; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1406
ID ADJ14407 standard; protein; 60 AA.
DE Protein related to human interleukin-3 (IL-3) mutant protein SEQ ID 170.
PN US2003185790-A1.
PD 02-OCT-2003.
PA (BAUE) BAUER S C.
PA (ABRA) ABRAMS M A.
PA (BRA) BRAFORD-GOLDBERG S R.
PA (CAPA) CAPARON M H.
PA (EAST) EASTON A M.
PA (KLEI) KLEIN B K.
PA (MCKE) MCKEARN J P.
PA (OLIN) OLINS P O.
PA (PAIK) PAIK K.
PA (THOM) THOMAS J W.
Query Match 1.6%; Score 7; DB 8; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1407
ID AAM17952 standard; protein; 61 AA.
DE Peptide #4386 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1408
ID AB36983 standard; peptide; 61 AA.
DE Peptide #4489 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1409
ID AAM70123 standard; protein; 61 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30429.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 1.6%; Score 7; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1410
ID AAM57714 standard; protein; 61 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29819.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1411
ID AAM05593 standard; protein; 61 AA.
DE Peptide #4275 encoded by probe for measuring breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
RESULT 1412
ID ABP35879 standard; protein; 65 AA.
DE CTRB BOVIN positions predicted to confer specificity.
PN EPI096411-A2.
PD 02-MAY-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 1.6%; Score 7; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1413
ID ABP35882 standard; protein; 65 AA.
DE CTRA BOVIN positions predicted to confer specificity.
PN EPI096411-A2.
PD 02-MAY-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 1.6%; Score 7; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
RESULT 1414
ID ABB71482 standard; protein; 67 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41238.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 7; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
RESULT 1415
ID AAM90305 standard; protein; 67 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:17898.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
RESULT 1416
ID AAU49753 standard; protein; 68 AA.
DE Propionibacterium acnes immunogenic protein #10649.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1417
ID ABM46272 standard; protein; 68 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #10948.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1418
ID AAM15299 standard; protein; 69 AA.
DE Peptide #1733 encoded by probe for measuring cervical gene expression.
PN W0200157278-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1419
ID ABB34296 standard; peptide; 69 AA.
DE Peptide #1802 encoded by human foetal liver single exon probe.
PN W0200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1420
ID AAM27771 standard; protein; 69 AA.
DE Peptide #1808 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1421
ID ABB29135 standard; peptide; 69 AA.
DE Peptide #1786 encoded by breast cell single exon nucleic acid probe.
PN W0200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1422
ID ABB19723 standard; protein; 69 AA.
DE Protein #1722 encoded by probe for measuring heart cell gene expression.
PN W0200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1423
ID AAM67483 standard; protein; 69 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27789.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1424
ID AAM55090 standard; protein; 69 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27195.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1425
ID ASG49131 standard; peptide; 69 AA.
DE Human liver peptide, SEQ ID NO 27779.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1426
ID AAM03053 standard; protein; 69 AA.
DE Peptide #1735 encoded by probe for measuring breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
RESULT 1427
ID AAG77385 standard; protein; 71 AA.
DE Human colon cancer antigen protein SEQ ID NO:8151.
PN W0200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 7; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1428
ID AAM83108 standard; protein; 71 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:10701.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
RESULT 1429
ID RAU22890 standard; protein; 73 AA.
DE Human prostate cancer antigen, Seq ID No 409.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1430
ID ABP08745 standard; protein; 73 AA.
DE Human ORFX protein sequence SEQ ID NO:17472.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 7; DB 5; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1431
ID ADJ09463 standard; protein; 73 AA.
DE Human prostate cancer associated polypeptide SeqID409.
PN US2003054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1432
ID ABM81841 standard; protein; 75 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82696, SEQ:4740.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.6%; Score 7; DB 8; Length 75;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1433
ID AAU79903 standard; protein; 76 AA.
DE Fragment for resistance against dehydration stress, protein #1.
PN WO200226800-A1.
PD 04-APR-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match 1.6%; Score 7; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1434
ID ABP60378 standard; peptide; 76 AA.
DE Sericin derived peptide SEQ ID NO 4.
PN WO200286133-A1.
PD 31-OCT-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match 1.6%; Score 7; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
RESULT 1435
ID AAG57943 standard; protein; 77 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74738.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.6%; Score 7; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 1436
ID ABT18385 standard; protein; 80 AA.
DE Breast specific related amino acid sequence SEQ ID No 194.
PN WO200277232-A2.
PD 03-OCT-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 1.6%; Score 7; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;

RESULT 1437
ID RAU53680 standard; protein; 81 AA.
DE Propionibacterium acnes immunogenic protein #14576.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 1438
ID ABM50199 standard; protein; 81 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14875.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
RESULT 1439
ID AAM92148 standard; protein; 82 AA.
DE Human digestive system antigen SEQ ID NO: 1497.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1440
ID ADA57125 standard; protein; 82 AA.
DE Human secreted protein #408.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1441
ID ADA40986 standard; protein; 82 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1442
ID ABR47868 standard; protein; 82 AA.
DE Human secreted protein, SEQ ID 759.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1443
ID AAB38342 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 22 clone, HOFNY91.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 3; Length 83;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
RESULT 1444
ID AAU43383 standard; protein; 84 AA.
DE Propionibacterium acnes immunogenic protein #4279.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1445
ID ABM39902 standard; protein; 84 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4578.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1446

ID AAU47347 standard; protein; 86 AA.
DE Propionibacterium acnes immunogenic protein #8243.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 86;
Query Match 100.0%; Pred. No. 7e+02;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1447
ID ABM43866 standard; protein; 86 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8542.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 86;
Query Match 100.0%; Pred. No. 7e+02;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1448
ID AAG59693 standard; protein; 87 AA.
DE Zsa mays protein fragment SEQ ID NO: 77238.
PN EF1033405-A2.
PD 06-SEP-2000.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 3; Length 87;
Query Match 100.0%; Pred. No. 7e+02;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1449
ID AAU42282 standard; protein; 87 AA.
DE Propionibacterium acnes immunogenic protein #3178.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 87;
Query Match 100.0%; Pred. No. 7e+02;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1450
ID ABM38801 standard; protein; 87 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3477.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 87;
Query Match 100.0%; Pred. No. 7e+02;
Best Local Similarity 100.0%; Pred. No. 7e+02;
RESULT 1451
ID AAU41961 standard; protein; 88 AA.
DE Propionibacterium acnes immunogenic protein #2857.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 88;
Query Match 100.0%; Pred. No. 7.1e+02;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1452
ID ABP04934 standard; protein; 88 AA.
DE Human ORFX protein sequence SEQ ID NO: 9850.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP. 1.6%; Score 7; DB 5; Length 88;
Query Match 100.0%; Pred. No. 7.1e+02;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1453
ID ABM38480 standard; protein; 88 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3156.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 88;
Query Match 100.0%; Pred. No. 7.1e+02;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
RESULT 1454
ID ABP63999 standard; protein; 91 AA.
DE Human ORF369.
PN US2002082206-A1.
PD 27-JUN-2002.
PA (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.
Query Match 1.6%; Score 7; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1455
ID AAU17791 standard; protein; 92 AA.
DE Novel human respiratory antigen #107.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 1.6%; Score 7; DB 4; Length 92;
Query Match 100.0%; Pred. No. 7.4e+02;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 1456
ID AAU79904 standard; protein; 92 AA.
DE Fragment for resistance against dehydration stress, protein #2.
PN WO200226800-A1.
PD 04-APR-2002.
PA (SEIR-) SEIREN CO LTD. 1.6%; Score 7; DB 5; Length 92;
Query Match 100.0%; Pred. No. 7.4e+02;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 1457
ID ADG41171 standard; protein; 92 AA.
DE Human respiratory system associated protein seq id 409.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 1.6%; Score 7; DB 7; Length 92;
Query Match 100.0%; Pred. No. 7.4e+02;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 1458
ID ADI96945 standard; protein; 92 AA.
DE Human respiratory system associated polypeptide SeqID409.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 1.6%; Score 7; DB 7; Length 92;
Query Match 100.0%; Pred. No. 7.4e+02;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
RESULT 1459
ID AAU51144 standard; protein; 94 AA.
DE Propionibacterium acnes immunogenic protein #12040.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 4; Length 94;
Query Match 100.0%; Pred. No. 7.5e+02;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1460
ID ABP01010 standard; protein; 94 AA.
DE Human ORFX protein sequence SEQ ID NO: 2002.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP. 1.6%; Score 7; DB 5; Length 94;
Query Match 100.0%; Pred. No. 7.5e+02;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1461
ID ABM47663 standard; protein; 94 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12339.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP. 1.6%; Score 7; DB 6; Length 94;
Query Match 100.0%; Pred. No. 7.5e+02;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
RESULT 1462
ID AAB82467 standard; protein; 96 AA.
DE Mouse PAR-3 exodomain region of GPAR4.
PN WO200144496-A2.
PD 21-JUN-2001.
PA (NOVS) NOVARTIS RES FOUND. 1.6%; Score 7; DB 4; Length 96;
Query Match 100.0%; Pred. No. 7.7e+02;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1463
ID AAU09714 standard; protein; 96 AA.
DE Polymorphic variant #1 of human SCV1 protein.
PN WO200179236-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISSANCE PHARM INC. 1.6%; Score 7; DB 5; Length 96;
Query Match 100.0%; Pred. No. 7.7e+02;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;

RESULT 1464
ID AAU56422 standard; protein; 97 AA.
DE Propionibacterium acnes immunogenic protein #17318.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1465
ID ABG60129 standard; protein; 97 AA.
DE Human DITHP polypeptide #187.
PN WO200220754-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.6%; Score 7; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1466
ID ABM52941 standard; protein; 97 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #17617.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 1.6%; Score 7; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1467
ID ADF61799 standard; protein; 97 AA.
DE Human DI-1 extracellular portion protein.
PN WO2003091447-A2.
PD 06-NOV-2003.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 1.6%; Score 7; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
RESULT 1468
ID ABB41047 standard; peptide; 98 AA.
DE Peptide #8553 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1469
ID AAM34822 standard; protein; 98 AA.
DE Peptide #8859 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1470
ID ABB25117 standard; protein; 98 AA.
DE Protein #7116 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1471
ID AAM74706 standard; protein; 98 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35012.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1472
ID AAM61904 standard; protein; 98 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34009.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1473
ID AAM11790 standard; protein; 101 AA.

ID ABG56491 standard; peptide; 98 AA.
DE Human liver peptide, SEQ ID NO 35139.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1474
ID ABG44514 standard; peptide; 98 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34179.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.6%; Score 7; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
RESULT 1475
ID ABP04110 standard; protein; 100 AA.
DE Human ORFX protein sequence SEQ ID NO:8202.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 7; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
RESULT 1476
ID ADK35275 standard; protein; 100 AA.
DE Novel human polypeptide SeqID7357.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 1.6%; Score 7; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
RESULT 1477
ID AAR99054 standard; protein; 101 AA.
DE Spider dragline variant, DP-1B.9 monomer.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1478
ID AAR99056 standard; protein; 101 AA.
DE Spider dragline variant, DP-1B.16 monomer.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1479
ID AAR99052 standard; protein; 101 AA.
DE Spider dragline variant, DP-1A.9 monomer.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1480
ID AAR86229 standard; protein; 101 AA.
DE Foxvirus ORF-1 truncated fragment 4.
PN WO9849300-A2.
PD 05-NOV-1998.
PA (COLL-) COLLATERAL THERAPEUTICS.
Query Match 1.6%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1481
ID AAU11791 standard; protein; 101 AA.
DE Dragline protein 1 analogue DP-1B.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1482
ID AAU11790 standard; protein; 101 AA.

DE Dragline protein 1 analogue DP-1A.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (HUMA-) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1483
ID ADN37737 standard; protein; 101 AA.
DE Monomer unit of DP-1B SLP amino acid sequence SEQ ID NO:6.
PN WO2004035750-A2.
PD 29-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1484
ID ADN37734 standard; protein; 101 AA.
DE Spider silk-like protein SEQ ID NO:3.
PN WO2004035750-A2.
PD 29-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1485
ID ADO15295 standard; protein; 101 AA.
DE N clavipes spider silk DP-1B6 analogue protein SeqID3.
PN WO2004044172-A2.
PD 27-MAY-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1486
ID ADO15294 standard; protein; 101 AA.
DE N clavipes spider silk DP-1B9 analogue protein SeqID2.
PN WO2004044172-A2.
PD 27-MAY-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1487
ID ADO15293 standard; protein; 101 AA.
DE N clavipes spider silk DP-1A analogue protein SeqID1.
PN WO2004044172-A2.
PD 27-MAY-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1488
ID ADR40516 standard; protein; 101 AA.
DE Monomer of spider silk DP-1B.9 analog protein.
PN WO2004073644-A2.
PD 02-SEP-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1489
ID ADR40515 standard; protein; 101 AA.
DE Monomer of spider silk DP-1A analog protein.
PN WO2004073644-A2.
PD 02-SEP-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1490
ID ADR40517 standard; protein; 101 AA.
DE Monomer of spider silk DP-1B.16 analog protein.
PN WO2004073644-A2.
PD 02-SEP-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 7; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 8e+02;
RESULT 1491
ID AAM84388 standard; protein; 102 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:11981.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
RESULT 1492
ID AAG11758 standard; protein; 103 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10600.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HELI-) HELIX RES INST.
Query Match 1.6%; Score 7; DB 3; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
RESULT 1493
ID AAB94623 standard; protein; 103 AA.
DE Human protein sequence SEQ ID NO:15479.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 1.6%; Score 7; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
RESULT 1494
ID ADM07515 standard; protein; 105 AA.
DE Canine immunoglobulin lambda variable domain protein 19.
PN WO2003060080-A2.
PD 24-JUL-2003.
PA (IDEX-) IDEXX LAB INC.
Query Match 1.6%; Score 7; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
RESULT 1495
ID AAW86228 standard; protein; 106 AA.
DE Poxvirus ORF-1 truncated fragment 3.
PN WO9849300-A2.
PD 05-NOV-1998.
PA (COLL-) COLLATERAL THERAPEUTICS.
Query Match 1.6%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
RESULT 1496
ID ADK98991 standard; protein; 106 AA.
DE S agalactiae SAG1473 (cell wall surface anchor family)-related protein 4.
PN WO2004018646-A2.
PD 04-MAR-2004.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 1.6%; Score 7; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
RESULT 1497
ID AAM92113 standard; protein; 107 AA.
DE Human digestive system antigen SEQ ID NO: 1462.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 7; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
RESULT 1498
ID ABB76673 standard; protein; 107 AA.
DE Protein related to Bombyx mori silk fibroin.
PN WO200240528-A1.
PD 23-MAY-2002.
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Query Match 1.6%; Score 7; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
RESULT 1499
ID ADJ81412 standard; peptide; 109 AA.
DE Self-assembling polymer peptide #267.
PN WO2003056297-A2.
PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
RESULT 1500
ID ADJ81177 standard; peptide; 109 AA.
DE Self-assembling polymer peptide #32.
PN WO2003056297-A2.

PD 10-JUL-2003.
PA (TUFT) TUFTS COLLEGE.
Query Match 1.6%; Score 7; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;

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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:25:38 ; Search time 44 Seconds
(without alignments)
746.491 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 440

Sequence: 1 MKPQGLACLLALCLGSGE.....KLGFINWDINKQRRSRIP 440

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	19.5	230	4	US-09-673-395A-256
2	25	5.7	72	4	US-09-513-999C-5563
3	25	5.7	72	4	US-09-513-999C-5564
4	14	3.2	250	4	US-09-248-796A-22487
5	12	2.7	80	4	US-09-248-796A-23892
6	11	2.5	663	4	US-09-949-016-7198
7	10	2.3	180	4	US-09-248-796A-22352
8	10	2.3	214	4	US-09-949-016-9109
9	10	2.3	441	4	US-09-949-016-6315
10	10	2.3	541	4	US-09-248-796A-26119
11	9	2.0	60	4	US-09-134-000C-6510
12	9	2.0	184	4	US-09-107-532A-5997
13	9	2.0	406	4	US-09-248-796A-14345
14	9	2.0	512	4	US-09-270-767-43154
15	9	2.0	529	4	US-09-381-656-1
16	9	2.0	607	4	US-09-328-352-6716
17	9	2.0	714	4	US-09-949-016-11158
18	9	2.0	1306	4	US-09-538-092-330
19	9	2.0	1712	4	US-09-949-016-9450
20	8	1.8	28	1	US-08-425-069-50
21	8	1.8	28	2	US-08-317-844B-50
22	8	1.8	30	1	US-08-425-069-58
23	8	1.8	30	2	US-08-317-844B-58
24	8	1.8	31	1	US-08-425-069-46
25	8	1.8	31	2	US-08-317-844B-46
26	8	1.8	62	3	US-09-247-155-127
27	8	1.8	67	4	US-09-583-110-3048
28	8	1.8	8	1	US-09-107-433-3523
29	8	1.8	95	4	US-09-513-999C-7096
30	8	1.8	103	4	US-09-513-999C-7639
31	8	1.8	104	4	US-08-809-955-3
32	8	1.8	111	4	US-08-809-955-4
33	8	1.8	117	4	US-09-270-767-56847
34	8	1.8	117	4	US-09-270-767-61204
35	8	1.8	164	4	US-09-270-767-43682
36	8	1.8	172	4	US-09-270-767-45749
37	8	1.8	205	4	US-09-270-767-37829
38	8	1.8	205	4	US-09-270-767-53046
39	8	1.8	231	4	US-09-248-796A-14281
40	8	1.8	262	4	US-09-949-016-7209
41	8	1.8	272	4	US-09-270-767-44311
42	8	1.8	278	3	US-09-260-283-2
43	8	1.8	291	4	US-09-270-767-41613
44	8	1.8	298	4	US-09-270-767-45683
45	8	1.8	316	4	US-09-538-092-997
46	8	1.8	319	3	US-09-100-664A-10
47	8	1.8	319	4	US-09-335-983-10
48	8	1.8	319	4	US-09-553-867A-10
49	8	1.8	319	4	US-09-270-767-42282
50	8	1.8	334	4	US-09-646-028-53
51	8	1.8	339	4	US-09-646-028-55
52	8	1.8	348	4	US-09-646-028-51
53	8	1.8	368	3	US-08-591-685-13
54	8	1.8	392	4	US-09-949-016-6078
55	8	1.8	410	4	US-09-248-796A-18461
56	8	1.8	412	3	US-09-027-064-4
57	8	1.8	412	3	US-09-271-815-4
58	8	1.8	426	1	US-08-476-008-63
59	8	1.8	426	1	US-08-306-063-63
60	8	1.8	426	1	US-08-833-485-63
61	8	1.8	426	3	US-09-137-440-63
62	8	1.8	436	4	US-09-252-991A-30636
63	8	1.8	442	2	US-08-693-457-2
64	8	1.8	442	2	US-08-693-457-4
65	8	1.8	442	3	US-09-265-731-2
66	8	1.8	442	3	US-09-265-731-4
67	8	1.8	452	4	US-09-252-991A-25818
68	8	1.8	528	4	US-09-490-291-8
69	8	1.8	532	4	US-09-328-352-7229
70	8	1.8	536	4	US-09-463-712C-10
71	8	1.8	543	2	US-08-469-412A-7
72	8	1.8	543	3	US-09-021-715-7
73	8	1.8	548	2	US-08-469-412A-2
74	8	1.8	548	3	US-09-021-715-2
75	8	1.8	575	4	US-09-248-796A-17507
76	8	1.8	584	4	US-09-270-767-43419
77	8	1.8	609	4	US-09-198-452A-579
78	8	1.8	649	3	US-09-066-047-5
79	8	1.8	651	3	US-08-556-978B-19
80	8	1.8	651	3	US-09-247-806-1
81	8	1.8	651	4	US-09-863-859-1
82	8	1.8	663	4	US-09-949-016-6046
83	8	1.8	673	4	US-09-949-016-7834
84	8	1.8	718	1	US-08-425-069-2
85	8	1.8	718	2	US-08-317-844B-2
86	8	1.8	747	3	US-09-034-177-3
87	8	1.8	763	2	US-08-577-862-2
88	8	1.8	763	2	US-09-252-571-2
89	8	1.8	763	3	US-09-434-065-2
90	8	1.8	763	3	US-08-789-275-4
91	8	1.8	763	3	US-08-789-275-5
92	8	1.8	765	4	US-09-575-326-4
93	8	1.8	765	4	US-10-217-357-4
94	8	1.8	766	4	US-09-975-326-2
95	8	1.8	766	4	US-10-217-357-2
96	8	1.8	816	2	US-08-820-170A-37
97	8	1.8	816	3	US-09-055-699-37
98	8	1.8	816	3	US-09-273-565-37
99	8	1.8	816	3	US-09-565-538-37
100	8	1.8	816	3	US-09-661-468-37

101	8	1.8	816	4	US-09-976-165-37	Sequence 37, Appl	174	7	1.6	60	3	US-08-468-609A-195	Sequence 195, App
102	8	1.8	928	4	US-08-635-872A-1	Sequence 1, Appli	175	7	1.6	60	3	US-08-446-872A-195	Sequence 195, App
103	8	1.8	928	4	US-09-636-077A-1	Sequence 1, Appli	176	7	1.6	60	4	US-08-762-227A-195	Sequence 195, App
104	8	1.8	928	4	US-09-636-060C-1	Sequence 1, Appli	177	7	1.6	60	5	PCT-US95-01185-195	Sequence 195, App
105	8	1.8	928	4	US-09-986-552-1	Sequence 1, Appli	178	7	1.6	64	4	US-09-270-767-37216	Sequence 37216, A
106	8	1.8	928	4	US-09-636-596C-1	Sequence 1, Appli	179	7	1.6	64	4	US-09-270-767-52433	Sequence 52433, A
107	8	1.8	928	4	US-10-023-894-4	Sequence 4, Appli	180	7	1.6	79	4	US-09-270-767-37592	Sequence 37592, A
108	8	1.8	928	4	US-10-306-686-1	Sequence 1, Appli	181	7	1.6	79	4	US-09-270-767-52809	Sequence 52809, A
109	8	1.8	1141	1	US-08-131-365B-54	Sequence 54, Appl	182	7	1.6	100	4	US-09-411-067C-5	Sequence 5, Appli
110	8	1.8	1141	2	US-08-668-123-54	Sequence 54, Appl	183	7	1.6	101	3	US-08-556-978B-20	Sequence 20, Appl
111	8	1.8	1199	4	US-10-023-894-2	Sequence 2, Appli	184	7	1.6	101	3	US-08-556-978B-22	Sequence 22, Appl
112	8	1.8	1233	4	US-09-645-456A-35	Sequence 35, Appl	185	7	1.6	101	3	US-08-556-978B-62	Sequence 62, Appl
113	8	1.8	1233	4	US-09-425-324A-35	Sequence 35, Appl	186	7	1.6	101	3	US-09-247-806-3	Sequence 3, Appli
114	8	1.8	1233	4	US-09-645-791-35	Sequence 35, Appl	187	7	1.6	101	3	US-09-247-806-5	Sequence 5, Appli
115	8	1.8	1233	4	US-09-688-188B-89	Sequence 89, Appl	188	7	1.6	101	3	US-09-247-806-7	Sequence 7, Appli
116	8	1.8	1233	4	US-09-291-417D-89	Sequence 89, Appl	189	7	1.6	101	3	US-09-863-859-10	Sequence 10, Appl
117	8	1.8	1239	4	US-09-688-188B-13	Sequence 13, Appl	190	7	1.6	101	4	US-09-863-859-11	Sequence 11, Appl
118	8	1.8	1239	4	US-09-291-417D-13	Sequence 13, Appl	191	7	1.6	102	4	US-09-248-796A-27799	Sequence 27799, A
119	8	1.8	1349	3	US-08-938-291A-6	Sequence 6, Appli	192	7	1.6	118	4	US-09-513-999C-4979	Sequence 4979, Ap
120	8	1.8	1349	4	US-09-589-619-6	Sequence 6, Appli	193	7	1.6	121	4	US-09-539-333D-41	Sequence 41, Appl
121	8	1.8	1744	4	US-09-438-185A-542	Sequence 542, App	194	7	1.6	124	4	US-09-621-976-5096	Sequence 5096, Ap
122	8	1.8	2142	4	US-09-538-092-1142	Sequence 1142, Ap	195	7	1.6	126	4	US-09-621-976-4117	Sequence 4117, Ap
123	7	1.6	13	1	US-08-257-341-1	Sequence 1, Appli	196	7	1.6	127	4	US-09-621-976-5097	Sequence 5097, Ap
124	7	1.6	13	1	US-08-425-069-39	Sequence 39, Appl	197	7	1.6	133	4	US-09-431-888-2	Sequence 2, Appli
125	7	1.6	13	2	US-08-317-844B-39	Sequence 39, Appl	198	7	1.6	139	4	US-09-270-767-36667	Sequence 36667, A
126	7	1.6	15	1	US-08-133-804-8	Sequence 8, Appli	199	7	1.6	139	4	US-09-270-767-51884	Sequence 51884, A
127	7	1.6	15	1	US-08-425-069-13	Sequence 13, Appl	200	7	1.6	139	4	US-09-248-796A-15962	Sequence 15962, A
128	7	1.6	15	1	US-08-461-838-8	Sequence 8, Appli	201	7	1.6	142	4	US-09-270-767-60758	Sequence 60758, A
129	7	1.6	15	2	US-08-461-386-8	Sequence 8, Appli	202	7	1.6	145	4	US-09-621-976-4037	Sequence 4037, Ap
130	7	1.6	15	2	US-08-356-786-12	Sequence 12, Appl	203	7	1.6	149	3	US-08-808-599A-40	Sequence 40, Appl
131	7	1.6	15	2	US-08-665-202-3	Sequence 3, Appli	204	7	1.6	151	4	US-09-270-767-37869	Sequence 37869, A
132	7	1.6	15	2	US-08-317-844B-13	Sequence 13, Appl	205	7	1.6	151	4	US-09-270-767-53086	Sequence 53086, A
133	7	1.6	15	3	US-08-483-749A-31	Sequence 31, Appl	206	7	1.6	152	4	US-09-270-767-35204	Sequence 35204, A
134	7	1.6	15	3	US-08-556-978B-2	Sequence 2, Appli	207	7	1.6	152	4	US-09-270-767-50421	Sequence 50421, A
135	7	1.6	15	4	US-09-315-574-3	Sequence 3, Appli	208	7	1.6	155	3	US-09-315-794-12	Sequence 12, Appl
136	7	1.6	15	4	US-09-863-859-9	Sequence 9, Appli	209	7	1.6	155	3	US-09-389-341-12	Sequence 34016, A
137	7	1.6	15	4	US-09-324-258-18	Sequence 18, Appl	210	7	1.6	157	4	US-09-270-767-49233	Sequence 49233, A
138	7	1.6	17	4	US-09-333-213-4	Sequence 4, Appli	211	7	1.6	157	3	US-09-027-449-53	Sequence 53, Appl
139	7	1.6	17	4	US-10-077-210-4	Sequence 4, Appli	212	7	1.6	159	3	US-08-804-444A-53	Sequence 53, Appl
140	7	1.6	21	1	US-08-425-069-5	Sequence 5, Appli	213	7	1.6	159	3	US-09-026-985-53	Sequence 53, Appl
141	7	1.6	21	2	US-08-317-844B-5	Sequence 5, Appli	214	7	1.6	159	4	US-09-121-952A-53	Sequence 53, Appl
142	7	1.6	23	4	US-09-422-375-4	Sequence 4, Appli	215	7	1.6	159	4	US-09-234-340A-53	Sequence 53, Appl
143	7	1.6	25	1	US-08-425-069-38	Sequence 38, Appl	216	7	1.6	163	3	US-09-025-769B-282	Sequence 282, App
144	7	1.6	25	2	US-08-317-844B-38	Sequence 38, Appl	217	7	1.6	163	4	US-09-490-070A-282	Sequence 282, App
145	7	1.6	29	4	US-09-863-859-12	Sequence 12, Appl	218	7	1.6	163	4	US-09-490-153-282	Sequence 282, App
146	7	1.6	30	1	US-08-425-069-48	Sequence 48, Appl	219	7	1.6	163	4	US-09-490-324-282	Sequence 282, App
147	7	1.6	30	1	US-08-425-069-60	Sequence 60, Appl	220	7	1.6	166	4	US-09-270-767-37190	Sequence 37190, A
148	7	1.6	30	1	US-08-425-069-61	Sequence 61, Appl	221	7	1.6	166	4	US-09-270-767-52407	Sequence 52407, A
149	7	1.6	30	2	US-08-317-844B-48	Sequence 48, Appl	222	7	1.6	167	2	US-08-993-228-8	Sequence 8, Appli
150	7	1.6	30	2	US-08-317-844B-60	Sequence 60, Appl	223	7	1.6	175	4	US-09-252-991A-26111	Sequence 26111, A
151	7	1.6	30	2	US-08-317-844B-61	Sequence 61, Appl	224	7	1.6	186	4	US-09-502-540-14288	Sequence 14288, A
152	7	1.6	31	3	US-08-556-978B-26	Sequence 26, Appl	225	7	1.6	186	4	US-09-270-767-45033	Sequence 45033, A
153	7	1.6	31	3	US-08-556-978B-69	Sequence 69, Appl	226	7	1.6	198	4	US-09-919-039-258	Sequence 258, App
154	7	1.6	31	3	US-08-556-978B-89	Sequence 89, Appl	227	7	1.6	205	4	US-09-919-039-258	Sequence 9411, Ap
155	7	1.6	31	4	US-09-324-258-19	Sequence 19, Appl	228	7	1.6	205	4	US-09-949-016-9411	Sequence 60040, A
156	7	1.6	32	1	US-08-425-069-44	Sequence 44, Appl	229	7	1.6	208	4	US-09-270-767-60040	Sequence 60040, A
157	7	1.6	32	2	US-08-317-844B-44	Sequence 44, Appl	230	7	1.6	209	4	US-09-543-681A-5814	Sequence 5814, Ap
158	7	1.6	33	1	US-08-425-069-7	Sequence 7, Appli	231	7	1.6	210	4	US-09-543-681A-8215	Sequence 8215, Ap
159	7	1.6	33	2	US-08-317-844B-7	Sequence 7, Appli	232	7	1.6	211	1	US-08-276-852-34	Sequence 34, Appl
160	7	1.6	34	1	US-08-425-069-52	Sequence 42, Appl	233	7	1.6	211	1	US-08-133-011-16	Sequence 16, Appl
161	7	1.6	34	1	US-08-425-069-42	Sequence 52, Appl	234	7	1.6	211	1	US-08-322-730A-16	Sequence 16, Appl
162	7	1.6	34	1	US-08-425-069-54	Sequence 54, Appl	235	7	1.6	211	1	US-08-387-874-16	Sequence 16, Appl
163	7	1.6	34	2	US-08-317-844B-42	Sequence 42, Appl	236	7	1.6	211	1	US-08-899-575-34	Sequence 34, Appl
164	7	1.6	34	2	US-08-317-844B-52	Sequence 52, Appl	237	7	1.6	211	1	US-08-899-575-34	Sequence 34, Appl
165	7	1.6	34	2	US-08-317-844B-54	Sequence 54, Appl	238	7	1.6	211	2	US-08-383-619-16	Sequence 16, Appl
166	7	1.6	34	3	US-08-556-978B-1	Sequence 1, Appli	239	7	1.6	211	3	US-08-907-739-16	Sequence 16, Appl
167	7	1.6	34	4	US-09-863-859-8	Sequence 8, Appli	240	7	1.6	211	4	US-09-729-597-16	Sequence 16, Appl
168	7	1.6	49	3	US-08-469-318-194	Sequence 194, App	241	7	1.6	211	5	PCT-US93-08364-16	Sequence 16, Appl
169	7	1.6	49	3	US-08-468-609A-194	Sequence 194, App	242	7	1.6	211	5	PCT-US95-08743-34	Sequence 34, Appl
170	7	1.6	49	3	US-08-446-872A-194	Sequence 194, App	243	7	1.6	213	4	US-09-252-991A-28745	Sequence 28745, A
171	7	1.6	49	4	US-08-762-227A-194	Sequence 194, App	244	7	1.6	216	4	US-09-795-872-5	Sequence 5, Appli
172	7	1.6	49	5	PCT-US95-01185-194	Sequence 194, App	245	7	1.6	217	4	US-09-270-767-31877	Sequence 31877, A
173	7	1.6	60	3	US-08-469-318-195	Sequence 195, App	246	7	1.6	217	4	US-09-270-767-47094	Sequence 47094, A

247	7	1.6	217	4	US-09-248-796A-25844	Sequence 25844, A	320	7	1.6	314	4	US-09-902-540-14533	Sequence 14533, A
248	7	1.6	218	4	US-09-902-540-15127	Sequence 15127, A	321	7	1.6	316	1	US-07-828-980A-2	Sequence 2, Appl1
249	7	1.6	219	4	US-09-809-517A-24	Sequence 24, Appl1	322	7	1.6	326	4	US-09-252-991A-17002	Sequence 17002, A
250	7	1.6	219	4	US-09-809-517A-24	Sequence 24, Appl1	323	7	1.6	329	4	US-09-248-796A-17561	Sequence 17561, A
251	7	1.6	223	4	US-09-270-767-33945	Sequence 33945, A	324	7	1.6	331	4	US-09-270-767-44610	Sequence 44610, A
252	7	1.6	223	4	US-09-270-767-49162	Sequence 49162, A	325	7	1.6	331	4	US-09-270-767-45830	Sequence 45830, A
253	7	1.6	226	4	US-09-533-029-88	Sequence 88, Appl1	326	7	1.6	335	3	US-08-469-318-143	Sequence 143, App
254	7	1.6	228	3	US-09-134-001C-4694	Sequence 4694, Ap	327	7	1.6	335	3	US-08-468-609A-143	Sequence 143, App
255	7	1.6	228	3	US-09-134-001C-5495	Sequence 5495, Ap	328	7	1.6	335	3	US-08-446-872A-143	Sequence 143, App
256	7	1.6	229	4	US-09-270-767-35290	Sequence 35290, A	329	7	1.6	335	4	US-08-762-227A-143	Sequence 143, App
257	7	1.6	229	4	US-09-270-767-50507	Sequence 50507, A	330	7	1.6	335	5	PCT-US95-01185-143	Sequence 143, App
258	7	1.6	229	4	US-09-248-796A-17127	Sequence 17127, A	331	7	1.6	337	3	US-08-469-318-148	Sequence 148, App
259	7	1.6	232	2	US-08-829-876-103	Sequence 103, App	332	7	1.6	337	3	US-08-468-609A-148	Sequence 148, App
260	7	1.6	232	3	US-09-234-874A-103	Sequence 103, App	333	7	1.6	337	3	US-08-446-872A-148	Sequence 148, App
261	7	1.6	232	4	US-09-234-873A-103	Sequence 103, App	334	7	1.6	337	4	US-08-762-227A-148	Sequence 148, App
262	7	1.6	233	2	US-08-829-876-101	Sequence 101, App	335	7	1.6	337	4	US-09-270-767-46550	Sequence 46550, A
263	7	1.6	233	2	US-08-829-876-105	Sequence 105, App	336	7	1.6	337	5	PCT-US95-01185-148	Sequence 148, App
264	7	1.6	233	3	US-09-234-874A-101	Sequence 101, App	337	7	1.6	345	4	US-09-270-767-45833	Sequence 45833, A
265	7	1.6	233	3	US-09-234-874A-105	Sequence 105, App	338	7	1.6	348	4	US-09-902-540-16155	Sequence 16155, A
266	7	1.6	233	4	US-09-234-873A-101	Sequence 101, App	339	7	1.6	348	3	US-08-469-318-139	Sequence 139, App
267	7	1.6	233	4	US-09-234-873A-105	Sequence 105, App	340	7	1.6	349	3	US-08-468-609A-139	Sequence 139, App
268	7	1.6	234	3	US-09-605-858-32	Sequence 32, Appl1	341	7	1.6	349	3	US-08-468-609A-151	Sequence 151, App
269	7	1.6	237	4	US-09-270-767-56912	Sequence 56912, A	342	7	1.6	349	3	US-08-446-872A-139	Sequence 139, App
270	7	1.6	238	4	US-09-495-880A-42	Sequence 42, Appl1	343	7	1.6	349	3	US-08-446-872A-151	Sequence 151, App
271	7	1.6	239	4	US-09-949-016-11583	Sequence 11583, A	344	7	1.6	349	3	US-08-762-227A-151	Sequence 151, App
272	7	1.6	241	4	US-09-270-767-34316	Sequence 34316, A	345	7	1.6	349	4	US-08-762-227A-151	Sequence 151, App
273	7	1.6	241	4	US-09-270-767-49533	Sequence 49533, A	346	7	1.6	349	4	US-08-762-227A-151	Sequence 151, App
274	7	1.6	243	1	US-08-133-804-6	Sequence 6, Appl1	347	7	1.6	349	5	PCT-US95-01185-139	Sequence 139, App
275	7	1.6	243	1	US-08-461-838-6	Sequence 6, Appl1	348	7	1.6	349	5	PCT-US95-01185-151	Sequence 151, App
276	7	1.6	243	2	US-08-461-886-6	Sequence 6, Appl1	349	7	1.6	350	4	US-09-248-796A-20605	Sequence 20605, A
277	7	1.6	243	2	US-08-356-786-4	Sequence 4, Appl1	350	7	1.6	360	4	US-09-252-991A-31993	Sequence 31993, A
278	7	1.6	244	4	US-09-248-796A-20707	Sequence 20707, A	351	7	1.6	361	4	US-09-902-540-16412	Sequence 16412, A
279	7	1.6	246	1	US-08-257-341-7	Sequence 7, Appl1	352	7	1.6	362	2	US-09-985-090-5	Sequence 5, Appl1
280	7	1.6	246	4	US-09-270-767-43642	Sequence 43642, A	353	7	1.6	362	3	US-09-165-543-32	Sequence 32, Appl1
281	7	1.6	250	1	US-08-133-804-2	Sequence 2, Appl1	354	7	1.6	363	4	US-09-270-767-45265	Sequence 45265, A
282	7	1.6	250	1	US-08-461-884-8	Sequence 8, Appl1	355	7	1.6	367	1	US-08-257-341-5	Sequence 5, Appl1
283	7	1.6	250	1	US-08-463-675-8	Sequence 8, Appl1	356	7	1.6	369	4	US-09-198-452A-1001	Sequence 1001, Ap
284	7	1.6	250	1	US-08-464-589-8	Sequence 8, Appl1	357	7	1.6	369	4	US-09-328-352-7459	Sequence 7459, A
285	7	1.6	250	1	US-08-461-838-2	Sequence 2, Appl1	358	7	1.6	372	4	US-09-252-991A-23226	Sequence 23226, A
286	7	1.6	250	2	US-08-461-886-2	Sequence 2, Appl1	359	7	1.6	372	4	US-09-252-991A-22016	Sequence 22016, A
287	7	1.6	252	1	US-08-133-804-4	Sequence 4, Appl1	360	7	1.6	374	2	US-09-438-185A-931	Sequence 931, App
288	7	1.6	252	1	US-08-461-838-4	Sequence 4, Appl1	361	7	1.6	374	2	US-08-446-875-4	Sequence 4, Appl1
289	7	1.6	252	2	US-08-461-886-4	Sequence 4, Appl1	362	7	1.6	375	2	US-08-102-385G-4	Sequence 4, Appl1
290	7	1.6	258	4	US-09-252-991A-30124	Sequence 30124, A	363	7	1.6	375	2	US-08-446-875-10	Sequence 10, Appl1
291	7	1.6	258	4	US-09-270-767-43580	Sequence 43580, A	364	7	1.6	376	4	US-09-248-796A-15097	Sequence 15097, A
292	7	1.6	259	4	US-09-543-681A-6390	Sequence 6390, Ap	365	7	1.6	377	4	US-09-252-991A-22016	Sequence 22016, A
293	7	1.6	266	4	US-09-495-880A-26	Sequence 26, Appl1	366	7	1.6	378	4	US-09-395-017B-1	Sequence 1, Appl1
294	7	1.6	268	4	US-09-906-393A-20	Sequence 20, Appl1	367	7	1.6	379	4	US-09-902-540-15163	Sequence 15163, A
295	7	1.6	273	4	US-09-134-000C-3441	Sequence 3441, Ap	368	7	1.6	391	4	US-09-395-017B-2	Sequence 2, Appl1
296	7	1.6	274	4	US-09-252-991A-31410	Sequence 31410, A	369	7	1.6	395	4	US-09-270-767-61223	Sequence 61223, A
297	7	1.6	281	4	US-09-134-000C-3432	Sequence 3432, Ap	370	7	1.6	399	1	US-08-530-950-10	Sequence 10, Appl1
298	7	1.6	281	4	US-10-101-464A-799	Sequence 799, App	371	7	1.6	399	2	US-08-874-186-92	Sequence 92, Appl1
299	7	1.6	281	4	US-09-490-291-2	Sequence 2, Appl1	372	7	1.6	399	3	US-08-888-429A-10	Sequence 10, Appl1
300	7	1.6	291	4	US-09-949-016-11416	Sequence 11416, A	373	7	1.6	399	3	US-09-149-879-10	Sequence 10, Appl1
301	7	1.6	291	6	5194600-2	Sequence 11416, A	374	7	1.6	399	4	US-09-057-009-10	Sequence 10, Appl1
302	7	1.6	291	6	5194600-2	Patent No. 5194600	375	7	1.6	399	4	US-09-593-653-10	Sequence 10, Appl1
303	7	1.6	292	2	US-08-353-476-111	Sequence 111, App	376	7	1.6	399	4	US-09-538-092-11239	Sequence 1129, Ap
304	7	1.6	292	4	US-09-134-000C-4591	Sequence 4591, Ap	377	7	1.6	405	4	US-09-949-016-10726	Sequence 10726, A
305	7	1.6	293	3	US-08-438-745-4	Sequence 4, Appl1	378	7	1.6	406	4	US-09-252-991A-22163	Sequence 22163, A
306	7	1.6	293	3	US-08-438-745-6	Sequence 6, Appl1	379	7	1.6	410	4	US-09-270-767-44592	Sequence 44592, A
307	7	1.6	293	3	US-09-219-019-4	Sequence 4, Appl1	380	7	1.6	415	3	US-09-025-769B-280	Sequence 280, App
308	7	1.6	293	3	US-09-219-019-6	Sequence 6, Appl1	381	7	1.6	415	4	US-09-490-153-280	Sequence 280, App
309	7	1.6	293	4	US-09-252-991A-20791	Sequence 20791, A	382	7	1.6	415	4	US-09-490-324-280	Sequence 280, App
310	7	1.6	293	5	PCT-US94-05669A-4	Sequence 4, Appl1	383	7	1.6	415	4	US-09-248-796A-18691	Sequence 18691, A
311	7	1.6	293	5	PCT-US94-05669A-6	Sequence 6, Appl1	384	7	1.6	428	4	US-09-134-000C-3817	Sequence 3817, Ap
312	7	1.6	298	4	US-09-583-110-4607	Sequence 4607, Ap	385	7	1.6	429	4	US-09-252-991A-32661	Sequence 32661, A
313	7	1.6	300	4	US-09-107-433-2774	Sequence 2774, Ap	386	7	1.6	430	4	US-09-583-110-4297	Sequence 4297, Ap
314	7	1.6	301	3	US-08-469-318-142	Sequence 142, App	387	7	1.6	430	4	US-09-306-595C-8	Sequence 8, Appl1
315	7	1.6	301	3	US-08-468-609A-142	Sequence 142, App	388	7	1.6	432	3	US-09-403-089A-1	Sequence 1, Appl1
316	7	1.6	301	3	US-08-446-872A-142	Sequence 142, App	389	7	1.6	432	4	US-09-925-388-8	Sequence 8, Appl1
317	7	1.6	301	4	US-08-762-227A-142	Sequence 142, App	390	7	1.6	432	4	US-09-809-517A-25	Sequence 25, Appl1
318	7	1.6	301	5	PCT-US95-01185-142	Sequence 142, App	391	7	1.6	432	4	US-09-807-258-32	Sequence 32, Appl1
319	7	1.6	306	4	US-09-248-796A-21212	Sequence 21212, A	392	7	1.6	433	4		

393	7	1.6	433	4	US-09-524-101D-20	Sequence 20, Appl	466	7	1.6	494	4	US-09-198-452A-13	Sequence 13, Appl
394	7	1.6	434	4	US-09-809-517A-23	Sequence 23, Appl	467	7	1.6	494	4	US-09-438-185A-4	Sequence 4, Appl
395	7	1.6	435	4	US-09-809-517A-26	Sequence 26, Appl	468	7	1.6	496	4	US-09-540-236-3821	Sequence 3821, Ap
396	7	1.6	436	4	US-09-794-422-2	Sequence 2, Appl	469	7	1.6	503	1	US-07-612-673-2	Sequence 2, Appl
397	7	1.6	437	4	US-09-107-433-4475	Sequence 4475, Ap	470	7	1.6	506	2	US-08-820-170A-19	Sequence 19, Appl
398	7	1.6	441	4	US-09-370-767-60990	Sequence 60990, A	471	7	1.6	506	3	US-09-055-699-19	Sequence 19, Appl
399	7	1.6	441	4	US-09-794-422-4	Sequence 4, Appl	472	7	1.6	506	3	US-09-273-565-19	Sequence 19, Appl
400	7	1.6	442	4	US-09-248-796A-21400	Sequence 21400, A	473	7	1.6	506	3	US-09-565-538-19	Sequence 19, Appl
401	7	1.6	445	2	US-08-985-090-2	Sequence 2, Appl	474	7	1.6	506	3	US-09-661-468-19	Sequence 19, Appl
402	7	1.6	445	3	US-09-165-543-2	Sequence 2, Appl	475	7	1.6	506	4	US-09-976-165-19	Sequence 19, Appl
403	7	1.6	445	3	US-09-165-543-5	Sequence 5, Appl	476	7	1.6	506	4	US-09-538-092-1381	Sequence 1381, Ap
404	7	1.6	445	3	US-09-167-354-7	Sequence 7, Appl	477	7	1.6	506	4	US-09-949-016-11518	Sequence 11518, A
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406	7	1.6	445	4	US-08-642-514-7	Sequence 7, Appl	479	7	1.6	507	4	US-09-107-433-4015	Sequence 4015, Ap
407	7	1.6	445	4	US-09-891-053-25	Sequence 25, Appl	480	7	1.6	511	4	US-09-328-352-5220	Sequence 5220, Ap
408	7	1.6	446	4	US-09-252-991A-27110	Sequence 27110, A	481	7	1.6	513	4	US-09-248-796A-25078	Sequence 25078, A
409	7	1.6	448	4	US-09-107-532A-3962	Sequence 3962, Ap	482	7	1.6	515	4	US-09-134-000C-3767	Sequence 3767, Ap
410	7	1.6	449	4	US-09-949-016-10930	Sequence 10930, A	483	7	1.6	516	3	US-08-746-559A-4	Sequence 4, Appl
411	7	1.6	453	4	US-09-891-053-20	Sequence 20, Appl	484	7	1.6	521	1	US-07-796-361A-11	Sequence 11, Appl
412	7	1.6	455	4	US-09-370-767-45531	Sequence 45531, A	485	7	1.6	521	1	US-08-539-666-2	Sequence 2, Appl
413	7	1.6	455	4	US-09-248-796A-17535	Sequence 17535, A	486	7	1.6	522	4	US-09-252-991A-30451	Sequence 30451, A
414	7	1.6	458	4	US-09-248-796A-18424	Sequence 18424, A	487	7	1.6	522	4	US-09-949-016-7190	Sequence 7190, Ap
415	7	1.6	461	2	US-08-463-587A-26	Sequence 26, Appl	488	7	1.6	523	2	US-08-482-728A-19	Sequence 19, Appl
416	7	1.6	461	2	US-08-463-667A-4	Sequence 4, Appl	489	7	1.6	523	3	US-09-028-366-4	Sequence 4, Appl
417	7	1.6	461	3	US-08-923-854-26	Sequence 26, Appl	490	7	1.6	523	3	US-09-715-285-4	Sequence 4, Appl
418	7	1.6	461	5	PCT-US91-09133-27	Sequence 27, Appl	491	7	1.6	524	4	US-09-242-913B-15	Sequence 15, Appl
419	7	1.6	462	4	US-09-270-767-43057	Sequence 43057, A	492	7	1.6	528	4	US-09-270-767-43914	Sequence 42914, A
420	7	1.6	464	4	US-09-949-016-10505	Sequence 10505, A	493	7	1.6	536	4	US-09-270-767-43766	Sequence 43766, A
421	7	1.6	465	4	US-09-370-767-46340	Sequence 46340, A	494	7	1.6	539	2	US-08-818-024-4	Sequence 4, Appl
422	7	1.6	466	2	US-08-726-136-28	Sequence 28, Appl	495	7	1.6	539	3	US-09-334-775A-4	Sequence 4, Appl
423	7	1.6	466	3	US-09-103-434-28	Sequence 28, Appl	496	7	1.6	539	3	US-08-789-275-6	Sequence 6, Appl
424	7	1.6	466	3	US-09-687-594-28	Sequence 28, Appl	497	7	1.6	545	4	US-09-949-016-10504	Sequence 10504, A
425	7	1.6	466	4	US-09-489-039A-9530	Sequence 9530, Ap	498	7	1.6	550	4	US-09-242-913B-14	Sequence 14, Appl
426	7	1.6	468	4	US-09-248-796A-19502	Sequence 19502, A	499	7	1.6	551	4	US-09-252-991A-18403	Sequence 18403, A
427	7	1.6	471	1	US-08-257-341-9	Sequence 9, Appl	500	7	1.6	551	4	US-09-252-991A-27787	Sequence 27787, A
428	7	1.6	472	1	US-08-278-091-5	Sequence 5, Appl	501	7	1.6	552	4	US-09-242-913B-19	Sequence 19, Appl
429	7	1.6	472	1	US-08-483-859-5	Sequence 5, Appl	502	7	1.6	554	4	US-08-809-802-8	Sequence 8, Appl
430	7	1.6	472	1	US-08-472-173-5	Sequence 5, Appl	503	7	1.6	556	4	US-09-275-252A-8	Sequence 8, Appl
431	7	1.6	472	2	US-08-487-167-5	Sequence 5, Appl	504	7	1.6	556	4	US-09-270-767-41922	Sequence 41922, A
432	7	1.6	472	2	US-08-482-816-5	Sequence 5, Appl	505	7	1.6	558	4	US-09-252-991A-24047	Sequence 24047, A
433	7	1.6	472	2	US-08-296-149-5	Sequence 5, Appl	506	7	1.6	560	4	US-09-252-991A-23548	Sequence 23548, A
434	7	1.6	472	2	US-08-801-499-5	Sequence 5, Appl	507	7	1.6	560	4	US-09-252-991A-28159	Sequence 28159, A
435	7	1.6	472	2	US-08-615-271-5	Sequence 5, Appl	508	7	1.6	561	4	US-09-134-000C-4759	Sequence 4759, Ap
436	7	1.6	472	3	US-09-074-660-5	Sequence 5, Appl	509	7	1.6	572	4	US-09-252-991A-16924	Sequence 16924, A
437	7	1.6	472	3	US-09-074-659-5	Sequence 5, Appl	510	7	1.6	587	4	US-09-270-767-45702	Sequence 45702, A
438	7	1.6	472	3	US-09-106-468-5	Sequence 5, Appl	511	7	1.6	604	3	US-08-556-978B-21	Sequence 21, Appl
439	7	1.6	472	3	US-09-106-466A-5	Sequence 5, Appl	512	7	1.6	606	3	US-08-556-978B-23	Sequence 23, Appl
440	7	1.6	472	3	US-09-106-467-5	Sequence 5, Appl	513	7	1.6	606	3	US-09-247-806-4	Sequence 4, Appl
441	7	1.6	474	4	US-09-702-705-1812	Sequence 1812, Ap	514	7	1.6	606	3	US-09-247-806-6	Sequence 6, Appl
442	7	1.6	474	4	US-09-736-457-1812	Sequence 1812, Ap	515	7	1.6	606	3	US-09-247-806-8	Sequence 8, Appl
443	7	1.6	474	4	US-09-671-325-1812	Sequence 1279, Ap	516	7	1.6	606	3	US-09-247-806-8	Sequence 8, Appl
444	7	1.6	474	4	US-09-538-092-1279	Sequence 1279, Ap	517	7	1.6	606	3	US-09-247-806-8	Sequence 8, Appl
445	7	1.6	480	4	US-08-358-160-5	Sequence 5, Appl	518	7	1.6	609	4	US-09-949-016-6846	Sequence 6846, Ap
446	7	1.6	482	1	US-08-358-160-5	Sequence 5, Appl	519	7	1.6	618	4	US-09-252-991A-25459	Sequence 25459, A
447	7	1.6	484	1	US-08-358-160-7	Sequence 7, Appl	520	7	1.6	622	2	US-08-356-786-16	Sequence 16, Appl
448	7	1.6	484	4	US-09-302-540-13700	Sequence 13700, A	521	7	1.6	622	2	US-09-252-991A-19802	Sequence 19802, A
449	7	1.6	485	3	US-09-009-494-2	Sequence 2, Appl	522	7	1.6	625	4	US-09-270-767-42376	Sequence 42376, A
450	7	1.6	485	3	US-09-010-233-8	Sequence 8, Appl	523	7	1.6	632	4	US-09-270-767-42178	Sequence 42178, A
451	7	1.6	485	3	US-09-010-232-4	Sequence 4, Appl	524	7	1.6	633	4	US-09-270-767-6	Sequence 6, Appl
452	7	1.6	485	4	US-09-710-279-1346	Sequence 1346, Ap	525	7	1.6	637	4	US-09-569-611C-35	Sequence 35, Appl
453	7	1.6	485	4	US-10-138-701-28	Sequence 28, Appl	526	7	1.6	637	4	US-09-949-016-8152	Sequence 8152, Ap
454	7	1.6	486	4	US-09-302-540-16779	Sequence 16779, A	527	7	1.6	643	3	US-09-538-092-844	Sequence 844, Ap
455	7	1.6	487	3	US-08-361-083-42	Sequence 42, Appl	528	7	1.6	647	3	US-09-753-007A-32	Sequence 32, Appl
456	7	1.6	487	4	US-09-536-784-42	Sequence 42, Appl	529	7	1.6	647	3	US-09-398-496-32	Sequence 32, Appl
457	7	1.6	488	4	US-09-252-991A-26323	Sequence 26323, A	530	7	1.6	656	4	US-09-252-991A-25135	Sequence 25135, A
458	7	1.6	488	4	US-09-328-352-7203	Sequence 7203, Ap	531	7	1.6	666	2	US-08-737-716-14	Sequence 14, Appl
459	7	1.6	488	4	US-09-583-110-3891	Sequence 3891, Ap	532	7	1.6	666	4	US-09-270-767-46736	Sequence 46736, A
460	7	1.6	490	3	US-08-896-346-2	Sequence 2, Appl	533	7	1.6	673	4	US-09-107-532A-5134	Sequence 5134, Ap
461	7	1.6	491	3	US-08-923-454A-14	Sequence 14, Appl	534	7	1.6	674	3	US-08-653-648A-14	Sequence 14, Appl
462	7	1.6	491	3	US-09-134-001C-4677	Sequence 4677, Ap	535	7	1.6	675	4	US-09-564-418-12	Sequence 12, Appl
463	7	1.6	492	1	US-08-350-741-3	Sequence 3, Appl	536	7	1.6	676	1	US-08-282-141-4	Sequence 4, Appl
464	7	1.6	492	2	US-08-463-875A-3	Sequence 3, Appl	537	7	1.6	681	4	US-09-490-291-4	Sequence 4, Appl
465	7	1.6	492	3	US-09-413-814-72	Sequence 72, Appl	538	7	1.6	691	4	US-09-490-291-6	Sequence 6, Appl

539	7	1.6	701	4	US-09-248-796A-16628	Sequence 16628, A	612	7	1.6	1367	3	US-08-864-641B-18	Sequence 18, Appl
540	7	1.6	703	3	US-08-910-925-4	Sequence 4, Appl	613	7	1.6	1367	4	US-09-343-551-2	Sequence 2, Appl
541	7	1.6	706	4	US-09-270-767-40994	Sequence 40994, A	614	7	1.6	1367	4	US-09-949-001-18	Sequence 18, Appl
542	7	1.6	706	4	US-09-270-767-56210	Sequence 56210, A	615	7	1.6	1377	4	US-09-949-001-21	Sequence 21, Appl
543	7	1.6	716	4	US-09-270-767-41668	Sequence 41668, A	616	7	1.6	1402	4	US-09-248-796A-14503	Sequence 14503, A
544	7	1.6	717	3	US-08-910-925-1	Sequence 1, Appl	617	7	1.6	1492	4	US-09-697-898-5	Sequence 5, Appl
545	7	1.6	726	4	US-09-392-714-21	Sequence 21, Appl	618	7	1.6	1493	3	US-09-423-890-8	Sequence 8, Appl
546	7	1.6	731	4	US-09-949-016-9763	Sequence 9763, Ap	619	7	1.6	1584	3	US-09-457-040B-27	Sequence 27, Appl
547	7	1.6	732	3	US-08-914-999-8	Sequence 8, Appl	620	7	1.6	1593	3	US-08-628-829-4	Sequence 4, Appl
548	7	1.6	737	4	US-09-902-540-16346	Sequence 16346, A	621	7	1.6	1617	4	US-09-863-859-14	Sequence 14, Appl
549	7	1.6	739	3	US-09-022-983-2	Sequence 2, Appl	622	7	1.6	1626	4	US-09-863-859-24	Sequence 24, Appl
550	7	1.6	741	4	US-09-854-856-60	Sequence 60, Appl	623	7	1.6	1911	4	US-09-854-856-64	Sequence 64, Appl
551	7	1.6	743	3	US-08-910-925-3	Sequence 3, Appl	624	7	1.6	1912	4	US-09-949-016-10490	Sequence 10490, A
552	7	1.6	743	4	US-09-949-016-6261	Sequence 6261, Ap	625	7	1.6	1939	4	US-09-854-856-48	Sequence 48, Appl
553	7	1.6	745	2	US-08-674-887A-8	Sequence 8, Appl	626	7	1.6	1971	4	US-09-854-856-32	Sequence 32, Appl
554	7	1.6	745	3	US-08-951-844-8	Sequence 8, Appl	627	7	1.6	1999	4	US-09-854-856-16	Sequence 16, Appl
555	7	1.6	745	4	US-09-412-347-8	Sequence 8, Appl	628	7	1.6	2004	4	US-09-854-856-58	Sequence 58, Appl
556	7	1.6	745	4	US-09-270-767-45481	Sequence 45481, A	629	7	1.6	2032	4	US-09-854-856-42	Sequence 42, Appl
557	7	1.6	749	4	US-09-949-016-8645	Sequence 8645, Ap	630	7	1.6	2048	4	US-09-854-856-62	Sequence 62, Appl
558	7	1.6	749	4	US-09-949-016-8646	Sequence 8646, Ap	631	7	1.6	2064	4	US-09-854-856-26	Sequence 26, Appl
559	7	1.6	749	4	US-09-949-016-8647	Sequence 8647, Ap	632	7	1.6	2071	3	US-09-415-522-6	Sequence 6, Appl
560	7	1.6	749	4	US-09-949-016-8648	Sequence 8648, Ap	633	7	1.6	2076	4	US-09-854-856-46	Sequence 46, Appl
561	7	1.6	754	4	US-09-392-714-20	Sequence 20, Appl	634	7	1.6	2092	4	US-09-854-856-10	Sequence 10, Appl
562	7	1.6	766	4	US-08-311-731A-258	Sequence 258, App	635	7	1.6	2108	4	US-09-854-856-30	Sequence 30, Appl
563	7	1.6	766	4	US-09-949-016-11355	Sequence 11355, A	636	7	1.6	2110	4	US-09-270-767-46547	Sequence 46547, A
564	7	1.6	766	4	US-09-949-016-11356	Sequence 11356, A	637	7	1.6	2119	4	US-09-583-110-4893	Sequence 4893, Ap
565	7	1.6	766	4	US-09-949-016-11357	Sequence 11357, A	638	7	1.6	2123	4	US-09-107-433-3728	Sequence 3728, Ap
566	7	1.6	766	4	US-09-949-016-11358	Sequence 11358, A	639	7	1.6	2136	4	US-09-854-856-14	Sequence 14, Appl
567	7	1.6	769	4	US-09-854-856-44	Sequence 44, Appl	640	7	1.6	2141	4	US-09-854-856-56	Sequence 56, Appl
568	7	1.6	779	4	US-09-270-767-42332	Sequence 42332, A	641	7	1.6	2157	4	US-09-854-856-52	Sequence 52, Appl
569	7	1.6	785	4	US-09-538-092-872	Sequence 872, App	642	7	1.6	2169	4	US-09-854-856-40	Sequence 40, Appl
570	7	1.6	801	4	US-09-854-856-28	Sequence 28, Appl	643	7	1.6	2179	4	US-09-949-016-8129	Sequence 8129, Ap
571	7	1.6	801	4	US-09-949-016-6588	Sequence 6588, Ap	644	7	1.6	2182	2	US-08-487-826B-16	Sequence 16, Appl
572	7	1.6	809	4	US-09-863-859-13	Sequence 13, Appl	645	7	1.6	2185	4	US-09-854-856-36	Sequence 36, Appl
573	7	1.6	810	4	US-09-949-016-11152	Sequence 11152, A	646	7	1.6	2201	4	US-09-854-856-24	Sequence 24, Appl
574	7	1.6	818	4	US-09-863-859-22	Sequence 22, Appl	647	7	1.6	2217	4	US-09-854-856-20	Sequence 20, Appl
575	7	1.6	820	4	US-09-583-110-4219	Sequence 4219, Ap	648	7	1.6	2229	4	US-09-854-856-8	Sequence 8, Appl
576	7	1.6	821	1	US-09-377-465A-2	Sequence 2, Appl	649	7	1.6	2245	4	US-09-854-856-4	Sequence 4, Appl
577	7	1.6	827	4	US-10-101-464A-915	Sequence 915, App	650	7	1.6	2294	4	US-09-854-856-50	Sequence 50, Appl
578	7	1.6	829	4	US-09-854-856-12	Sequence 12, Appl	651	7	1.6	2322	4	US-09-854-856-34	Sequence 34, Appl
579	7	1.6	834	2	US-09-107-433-4760	Sequence 4760, Ap	652	7	1.6	2354	4	US-09-854-856-18	Sequence 18, Appl
580	7	1.6	846	2	US-07-728-215-33	Sequence 33, Appl	653	7	1.6	2382	4	US-09-854-856-2	Sequence 2, Appl
581	7	1.6	846	3	US-08-938-085A-33	Sequence 33, Appl	654	7	1.6	2472	4	US-09-252-991A-17052	Sequence 17052, A
582	7	1.6	846	4	US-10-072-844-33	Sequence 33, Appl	655	7	1.6	2710	2	US-08-568-459A-12	Sequence 12, Appl
583	7	1.6	846	4	US-10-072-838-33	Sequence 33, Appl	656	7	1.6	2710	2	US-08-487-826B-12	Sequence 12, Appl
584	7	1.6	846	4	US-10-072-841A-33	Sequence 33, Appl	657	7	1.6	2710	3	US-09-210-288-12	Sequence 12, Appl
585	7	1.6	846	4	US-10-219-631A-33	Sequence 33, Appl	658	7	1.6	3025	6	523423-3	Patent No. 523423
586	7	1.6	894	4	US-09-854-856-54	Sequence 54, Appl	659	7	1.6	3025	6	523423-3	Patent No. 523423
587	7	1.6	907	4	US-09-949-016-9750	Sequence 9750, Ap	660	7	1.6	3060	2	US-08-487-826B-14	Sequence 14, Appl
588	7	1.6	907	4	US-09-949-016-9751	Sequence 9751, Ap	661	6	1.4	6	2	US-08-463-667A-15	Sequence 15, Appl
589	7	1.6	922	4	US-09-854-856-38	Sequence 38, Appl	662	6	1.4	6	3	US-09-330-970-25	Sequence 25, Appl
590	7	1.6	954	4	US-09-854-856-22	Sequence 22, Appl	663	6	1.4	6	4	US-08-537-871A-62	Sequence 62, Appl
591	7	1.6	956	4	US-09-914-259-17	Sequence 17, Appl	664	6	1.4	7	1	US-08-062-024B-1	Sequence 1, Appl
592	7	1.6	966	1	US-08-571-758-2	Sequence 2, Appl	665	6	1.4	7	2	US-08-756-407-1	Sequence 1, Appl
593	7	1.6	966	1	US-08-909-984A-2	Sequence 2, Appl	666	6	1.4	7	3	US-09-020-880-35	Sequence 35, Appl
594	7	1.6	966	1	US-08-909-983-2	Sequence 2, Appl	667	6	1.4	7	3	US-09-101-544-35	Sequence 35, Appl
595	7	1.6	982	4	US-09-854-856-6	Sequence 6, Appl	668	6	1.4	7	4	US-09-755-630B-276	Sequence 276, App
596	7	1.6	1004	3	US-08-916-352-2	Sequence 2, Appl	669	6	1.4	7	4	US-09-755-274-17	Sequence 17, Appl
597	7	1.6	1004	4	US-09-949-016-6495	Sequence 6496, Ap	670	6	1.4	7	5	PCr-US94-05014-1	Sequence 1, Appl
598	7	1.6	1039	4	US-09-252-991A-28966	Sequence 28966, A	671	6	1.4	8	2	US-08-955-848A-38	Sequence 38, Appl
599	7	1.6	1060	3	US-08-911-393-2	Sequence 2, Appl	672	6	1.4	8	2	US-08-833-167-61	Sequence 61, Appl
600	7	1.6	1060	4	US-09-955-909-2	Sequence 2, Appl	673	6	1.4	8	3	US-08-481-968A-20	Sequence 20, Appl
601	7	1.6	1072	4	US-09-949-016-8072	Sequence 8072, Ap	674	6	1.4	8	3	US-08-154-712B-20	Sequence 20, Appl
602	7	1.6	1073	4	US-09-252-991A-27341	Sequence 27341, A	675	6	1.4	8	3	US-09-344-837A-61	Sequence 61, Appl
603	7	1.6	1093	4	US-09-248-796A-17108	Sequence 17108, A	676	6	1.4	8	4	US-09-947-925A-20	Sequence 20, Appl
604	7	1.6	1114	4	US-09-252-991A-24965	Sequence 24965, A	677	6	1.4	8	4	US-09-510-238A-242	Sequence 242, App
605	7	1.6	1146	3	US-08-914-999-6	Sequence 6, Appl	678	6	1.4	8	4	US-09-989-025A-17	Sequence 17, Appl
606	7	1.6	1160	3	US-08-808-599A-24	Sequence 24, Appl	679	6	1.4	8	4	US-09-770-564A-35	Sequence 35, Appl
607	7	1.6	1246	4	US-09-252-991A-23140	Sequence 23140, A	680	6	1.4	9	1	US-08-425-069-11	Sequence 11, Appl
608	7	1.6	1302	3	US-09-423-890-2	Sequence 2, Appl	681	6	1.4	9	2	US-08-317-844B-11	Sequence 11, Appl
609	7	1.6	1367	2	US-08-249-687C-2	Sequence 2, Appl	682	6	1.4	9	3	US-08-582-333A-2	Sequence 2, Appl
610	7	1.6	1367	2	US-08-625-819-2	Sequence 2, Appl	683	6	1.4	9	3	US-09-305-923A-5	Sequence 5, Appl
611	7	1.6	1367	3	US-08-746-559A-2	Sequence 2, Appl	684	6	1.4	9	4	US-09-790-317-5	Sequence 5, Appl

685	6	1.4	9	4	US-09-239-043D-379	Sequence 379, App	758	6	1.4	13	2	US-08-248-839C-32	Sequence 32, Appl
686	6	1.4	10	1	US-08-442-542-32	Sequence 32, Appl	759	6	1.4	13	2	US-08-484-905-6	Sequence 6, Appli
687	6	1.4	10	1	US-08-575-361A-35	Sequence 35, Appl	760	6	1.4	13	3	US-08-481-985B-6	Sequence 6, Appli
688	6	1.4	10	2	US-08-207-481-7	Sequence 7, Appl	761	6	1.4	13	3	US-08-370-476-6	Sequence 6, Appli
689	6	1.4	10	2	US-08-596-387B-1	Sequence 1, Appli	762	6	1.4	13	3	US-09-248-588-97	Sequence 97, Appl
690	6	1.4	10	2	US-08-647-449-29	Sequence 29, Appl	763	6	1.4	13	3	US-08-525-539A-66	Sequence 66, Appl
691	6	1.4	10	3	US-08-765-469-32	Sequence 32, Appl	764	6	1.4	13	4	US-09-554-941-13	Sequence 13, Appl
692	6	1.4	10	3	US-09-281-792B-29	Sequence 29, Appl	765	6	1.4	14	1	US-08-430-633-5	Sequence 5, Appli
693	6	1.4	10	3	US-09-067-615-1	Sequence 1, Appli	766	6	1.4	14	2	US-08-448-418-89	Sequence 89, Appl
694	6	1.4	10	4	US-09-470-191-96	Sequence 96, Appl	767	6	1.4	14	2	US-08-448-418-101	Sequence 101, App
695	6	1.4	10	4	US-08-406-824A-29	Sequence 29, Appl	768	6	1.4	14	2	US-08-373-190-3	Sequence 3, Appli
696	6	1.4	10	4	US-09-223-040-9	Sequence 9, Appli	769	6	1.4	14	2	US-08-373-190-5	Sequence 5, Appli
697	6	1.4	10	4	US-09-287-849-45	Sequence 45, Appl	770	6	1.4	14	2	US-08-620-694A-5	Sequence 5, Appli
698	6	1.4	10	4	US-09-790-317-6	Sequence 6, Appli	771	6	1.4	14	2	US-08-936-854-5	Sequence 5, Appli
699	6	1.4	10	4	US-09-239-043D-380	Sequence 380, App	772	6	1.4	14	2	US-08-438-190A-3	Sequence 3, Appli
700	6	1.4	10	4	US-09-239-043D-1433	Sequence 1433, Ap	773	6	1.4	14	2	US-08-438-190A-5	Sequence 5, Appli
701	6	1.4	10	4	US-10-077-210-1	Sequence 1, Appli	774	6	1.4	14	2	US-08-656-906-26	Sequence 26, Appl
702	6	1.4	10	4	US-09-798-689-19	Sequence 19, Appl	775	6	1.4	14	2	US-08-818-253-46	Sequence 46, Appl
703	6	1.4	10	5	PCT-US95-02689-7	Sequence 7, Appli	776	6	1.4	14	3	US-08-350-215-3	Sequence 3, Appli
704	6	1.4	10	5	PCT-US95-09818A-1	Sequence 1, Appli	777	6	1.4	14	3	US-08-350-215-5	Sequence 5, Appli
705	6	1.4	11	1	US-08-323-474-5	Sequence 5, Appli	778	6	1.4	14	3	US-09-022-255-5	Sequence 5, Appli
706	6	1.4	11	1	US-08-086-335C-13	Sequence 13, Appl	779	6	1.4	14	3	US-09-287-145A-3	Sequence 3, Appli
707	6	1.4	11	1	US-08-641-704-1	Sequence 1, Appli	780	6	1.4	14	3	US-09-287-145A-5	Sequence 5, Appli
708	6	1.4	11	1	US-08-336-918A-17	Sequence 17, Appl	781	6	1.4	14	3	US-09-022-696-5	Sequence 5, Appli
709	6	1.4	11	2	US-08-385-335A-5	Sequence 5, Appli	782	6	1.4	14	3	US-09-022-253-5	Sequence 5, Appli
710	6	1.4	11	2	US-08-556-906-18	Sequence 18, Appl	783	6	1.4	14	3	US-09-022-260-5	Sequence 5, Appli
711	6	1.4	11	2	US-08-656-906-20	Sequence 20, Appl	784	6	1.4	14	3	US-09-046-992-6	Sequence 6, Appli
712	6	1.4	11	3	US-09-217-847-18	Sequence 18, Appl	785	6	1.4	14	3	US-09-022-259-5	Sequence 5, Appli
713	6	1.4	11	3	US-09-217-847-20	Sequence 20, Appl	786	6	1.4	14	3	US-09-022-257-5	Sequence 5, Appli
714	6	1.4	11	3	US-09-150-864A-17	Sequence 17, Appl	787	6	1.4	14	3	US-08-818-252-46	Sequence 46, Appl
715	6	1.4	11	4	US-08-829-558-5	Sequence 5, Appli	788	6	1.4	14	3	US-09-217-847-26	Sequence 26, Appl
716	6	1.4	11	4	US-09-039-642B-4	Sequence 4, Appli	789	6	1.4	14	3	US-08-960-190A-29	Sequence 29, Appl
717	6	1.4	11	4	US-08-406-824A-23	Sequence 23, Appl	790	6	1.4	14	3	US-08-849-488-16	Sequence 16, Appl
718	6	1.4	11	4	US-09-333-213-2	Sequence 2, Appli	791	6	1.4	14	3	US-09-362-805-8	Sequence 8, Appli
719	6	1.4	11	4	US-09-239-043D-1077	Sequence 1077, Ap	792	6	1.4	14	3	US-09-173-190-8	Sequence 8, Appli
720	6	1.4	11	4	US-09-239-043D-1545	Sequence 1545, Ap	793	6	1.4	14	3	US-09-556-111-3	Sequence 3, Appli
721	6	1.4	11	4	US-10-077-210-2	Sequence 2, Appli	794	6	1.4	14	3	US-09-556-111-5	Sequence 5, Appli
722	6	1.4	11	5	PCT-US95-08533-1	Sequence 1, Appli	795	6	1.4	14	4	US-09-316-919-62	Sequence 62, Appl
723	6	1.4	12	1	US-08-482-530-13	Sequence 13, Appl	796	6	1.4	14	4	US-09-146-979-89	Sequence 89, Appl
724	6	1.4	12	1	US-08-050-058B-13	Sequence 13, Appl	797	6	1.4	14	4	US-09-146-979-101	Sequence 101, App
725	6	1.4	12	2	US-08-463-587A-12	Sequence 12, Appl	798	6	1.4	14	4	US-09-125-576B-9	Sequence 9, Appli
726	6	1.4	12	2	US-08-441-871-16	Sequence 16, Appl	799	6	1.4	14	4	US-09-033-525-6	Sequence 6, Appli
727	6	1.4	12	2	US-08-224-591-7	Sequence 7, Appli	800	6	1.4	14	4	US-09-832-297A-8	Sequence 8, Appli
728	6	1.4	12	2	US-08-392-338A-1	Sequence 1, Appli	801	6	1.4	14	4	US-09-549-679-5	Sequence 5, Appli
729	6	1.4	12	2	US-08-955-848A-39	Sequence 39, Appl	802	6	1.4	14	4	US-09-316-920A-62	Sequence 62, Appl
730	6	1.4	12	2	US-08-591-196-56	Sequence 56, Appl	803	6	1.4	14	4	US-09-883-777-16	Sequence 16, Appl
731	6	1.4	12	2	US-08-926-789-7	Sequence 7, Appli	804	6	1.4	14	4	US-09-937-837-16	Sequence 16, Appl
732	6	1.4	12	2	US-08-818-253-41	Sequence 41, Appl	805	6	1.4	15	1	US-07-664-989B-11	Sequence 11, Appl
733	6	1.4	12	3	US-09-166-750-1	Sequence 1, Appli	806	6	1.4	15	1	US-07-664-989B-18	Sequence 18, Appl
734	6	1.4	12	3	US-09-166-093-1	Sequence 1, Appli	807	6	1.4	15	1	US-07-988-194A-43	Sequence 43, Appl
735	6	1.4	12	3	US-08-923-854-12	Sequence 12, Appl	808	6	1.4	15	1	US-07-843-125-13	Sequence 13, Appl
736	6	1.4	12	3	US-08-833-167-62	Sequence 62, Appl	809	6	1.4	15	1	US-08-346-293-15	Sequence 15, Appl
737	6	1.4	12	3	US-09-172-019-1	Sequence 1, Appli	810	6	1.4	15	1	US-08-164-151-23	Sequence 23, Appl
738	6	1.4	12	3	US-09-166-094-1	Sequence 1, Appli	811	6	1.4	15	1	US-08-133-804-7	Sequence 7, Appli
739	6	1.4	12	3	US-08-818-252-41	Sequence 41, Appl	812	6	1.4	15	1	US-08-331-398A-32	Sequence 32, Appl
740	6	1.4	12	3	US-09-362-805-3	Sequence 3, Appli	813	6	1.4	15	1	US-08-478-312-22	Sequence 22, Appl
741	6	1.4	12	3	US-09-173-190-3	Sequence 3, Appli	814	6	1.4	15	1	US-08-485-302-22	Sequence 22, Appl
742	6	1.4	12	3	US-09-069-821-6	Sequence 6, Appli	815	6	1.4	15	1	US-08-476-163-18	Sequence 18, Appl
743	6	1.4	12	3	US-09-344-837A-62	Sequence 62, Appl	816	6	1.4	15	1	US-08-484-083-18	Sequence 18, Appl
744	6	1.4	12	4	US-09-316-919-57	Sequence 57, Appl	817	6	1.4	15	1	US-08-077-252B-23	Sequence 23, Appl
745	6	1.4	12	4	US-09-443-213-1	Sequence 1, Appli	818	6	1.4	15	1	US-08-461-838-7	Sequence 7, Appli
746	6	1.4	12	4	US-09-832-297A-3	Sequence 3, Appli	819	6	1.4	15	2	US-08-575-361A-27	Sequence 27, Appl
747	6	1.4	12	4	US-09-316-920A-57	Sequence 57, Appl	820	6	1.4	15	2	US-08-564-955-67	Sequence 67, Appl
748	6	1.4	12	4	US-09-883-777-12	Sequence 12, Appl	821	6	1.4	15	2	US-08-448-418-98	Sequence 98, Appl
749	6	1.4	12	4	US-09-510-238A-243	Sequence 243, App	822	6	1.4	15	2	US-08-461-386-7	Sequence 7, Appli
750	6	1.4	12	4	US-09-956-086-6	Sequence 6, Appli	823	6	1.4	15	2	US-08-373-190-1	Sequence 1, Appli
751	6	1.4	12	4	US-09-956-087-6	Sequence 6, Appli	824	6	1.4	15	2	US-08-373-190-2	Sequence 2, Appli
752	6	1.4	12	4	US-09-937-837-11	Sequence 11, Appl	825	6	1.4	15	2	US-08-373-190-4	Sequence 4, Appli
753	6	1.4	12	4	US-09-869-445-1	Sequence 1, Appli	826	6	1.4	15	2	US-08-480-774A-5	Sequence 5, Appli
754	6	1.4	12	4	US-09-625-049A-42	Sequence 42, Appl	827	6	1.4	15	2	US-08-356-786-14	Sequence 14, Appl
755	6	1.4	12	4	US-09-830-748B-12	Sequence 12, Appl	828	6	1.4	15	2	US-08-621-751A-17	Sequence 17, Appl
756	6	1.4	12	5	PCT-US91-09133-13	Sequence 13, Appl	829	6	1.4	15	2	US-08-385-335A-7	Sequence 7, Appli
757	6	1.4	12	5	PCT-US93-11138-7	Sequence 7, Appli	830	6	1.4	15	2	US-08-647-449-21	Sequence 21, Appl

831	6	1.4	15	2	US-08-902-623-1	Sequence 1, Appl	904	6	1.4	15	4	US-09-440-344-4	Sequence 4, Appl
832	6	1.4	15	2	US-08-752-844-45	Sequence 45, Appl	905	6	1.4	15	4	US-08-840-713-49	Sequence 49, Appl
833	6	1.4	15	2	US-08-465-473B-17	Sequence 17, Appl	906	6	1.4	15	4	US-09-696-322-67	Sequence 67, Appl
834	6	1.4	15	2	US-08-891-848-19	Sequence 19, Appl	907	6	1.4	15	4	US-09-717-391-67	Sequence 67, Appl
835	6	1.4	15	2	US-08-438-190A-1	Sequence 1, Appl	908	6	1.4	15	4	US-09-293-533-45	Sequence 45, Appl
836	6	1.4	15	2	US-08-438-190A-2	Sequence 2, Appl	909	6	1.4	15	4	US-09-315-574-1	Sequence 1, Appl
837	6	1.4	15	2	US-08-438-190A-4	Sequence 4, Appl	910	6	1.4	15	4	US-09-696-313-67	Sequence 67, Appl
838	6	1.4	15	2	US-08-955-848A-45	Sequence 45, Appl	911	6	1.4	15	4	US-09-422-375-2	Sequence 2, Appl
839	6	1.4	15	2	US-08-656-906-27	Sequence 27, Appl	912	6	1.4	15	4	US-09-254-832B-21	Sequence 21, Appl
840	6	1.4	15	2	US-08-484-905-8	Sequence 8, Appl	913	6	1.4	15	4	US-09-491-894A-9	Sequence 9, Appl
841	6	1.4	15	2	US-08-484-905-18	Sequence 18, Appl	914	6	1.4	15	4	US-09-223-040-10	Sequence 10, Appl
842	6	1.4	15	2	US-08-591-196-45	Sequence 45, Appl	915	6	1.4	15	4	US-09-657-274-23	Sequence 23, Appl
843	6	1.4	15	2	US-08-665-202-1	Sequence 1, Appl	916	6	1.4	15	4	US-09-240-307-67	Sequence 67, Appl
844	6	1.4	15	2	US-08-331-397B-32	Sequence 32, Appl	917	6	1.4	15	4	US-09-411-067C-3	Sequence 3, Appl
845	6	1.4	15	2	US-08-759-804A-32	Sequence 32, Appl	918	6	1.4	15	4	US-09-746-359A-72	Sequence 72, Appl
846	6	1.4	15	2	US-08-889-291-31	Sequence 31, Appl	919	6	1.4	15	4	US-09-703-399A-80	Sequence 80, Appl
847	6	1.4	15	2	US-08-350-215-1	Sequence 1, Appl	920	6	1.4	15	4	US-09-700-820C-1	Sequence 1, Appl
848	6	1.4	15	2	US-08-350-215-2	Sequence 2, Appl	921	6	1.4	15	4	US-09-549-067A-34	Sequence 34, Appl
849	6	1.4	15	2	US-08-350-215-4	Sequence 4, Appl	922	6	1.4	15	4	US-09-287-849-46	Sequence 46, Appl
850	6	1.4	15	2	US-08-654-623-13	Sequence 13, Appl	923	6	1.4	15	4	US-09-380-484A-16	Sequence 16, Appl
851	6	1.4	15	2	US-08-654-623-29	Sequence 29, Appl	924	6	1.4	15	4	US-10-108-077-4	Sequence 4, Appl
852	6	1.4	15	2	US-08-481-985B-8	Sequence 8, Appl	925	6	1.4	15	4	US-09-719-243-11	Sequence 11, Appl
853	6	1.4	15	2	US-08-481-985B-18	Sequence 18, Appl	926	6	1.4	15	4	US-09-719-243-12	Sequence 12, Appl
854	6	1.4	15	2	US-08-920-610-9	Sequence 9, Appl	927	6	1.4	15	4	US-09-239-043D-2100	Sequence 2100, App
855	6	1.4	15	2	US-08-483-749A-29	Sequence 29, Appl	928	6	1.4	15	4	US-09-724-108-25	Sequence 25, Appl
856	6	1.4	15	2	US-09-287-145A-1	Sequence 1, Appl	929	6	1.4	15	4	US-09-867-262-4	Sequence 4, Appl
857	6	1.4	15	2	US-09-287-145A-2	Sequence 2, Appl	930	6	1.4	15	4	US-09-009-388C-25	Sequence 25, Appl
858	6	1.4	15	2	US-09-287-145A-4	Sequence 4, Appl	931	6	1.4	15	4	US-10-087-426-4	Sequence 4, Appl
859	6	1.4	15	2	US-08-881-037-111	Sequence 111, App	932	6	1.4	15	4	US-09-498-557-17	Sequence 17, Appl
860	6	1.4	15	2	US-08-949-758-1	Sequence 1, Appl	933	6	1.4	15	4	US-10-099-816B-4	Sequence 4, Appl
861	6	1.4	15	2	US-08-621-859-67	Sequence 67, Appl	934	6	1.4	15	4	US-09-885-551A-4	Sequence 4, Appl
862	6	1.4	15	2	US-09-046-985-13	Sequence 13, Appl	935	6	1.4	15	4	US-10-309-587A-2	Sequence 2, Appl
863	6	1.4	15	2	US-09-296-595-18	Sequence 18, Appl	936	6	1.4	15	4	US-09-554-941-14	Sequence 14, Appl
864	6	1.4	15	2	US-09-070-637-12	Sequence 12, Appl	937	6	1.4	15	4	US-09-726-219A-15	Sequence 15, Appl
865	6	1.4	15	2	US-08-501-253A-9	Sequence 9, Appl	938	6	1.4	15	4	US-09-726-219A-269	Sequence 269, App
866	6	1.4	15	2	US-09-002-753A-23	Sequence 23, Appl	939	6	1.4	15	4	US-09-726-219A-270	Sequence 270, App
867	6	1.4	15	2	US-08-370-476-8	Sequence 8, Appl	940	6	1.4	15	4	US-09-726-219A-271	Sequence 271, App
868	6	1.4	15	2	US-08-370-476-18	Sequence 18, Appl	941	6	1.4	15	4	US-09-726-219A-272	Sequence 272, App
869	6	1.4	15	2	US-09-075-511-67	Sequence 67, Appl	942	6	1.4	15	4	US-09-581-345-6	Sequence 6, Appl
870	6	1.4	15	2	US-09-098-244-31	Sequence 31, Appl	943	6	1.4	15	4	US-09-798-689-17	Sequence 17, Appl
871	6	1.4	15	2	US-09-099-015-67	Sequence 67, Appl	944	6	1.4	15	4	US-09-936-885A-42	Sequence 42, Appl
872	6	1.4	15	2	US-08-737-629-13	Sequence 13, Appl	945	6	1.4	15	4	US-08-537-871A-59	Sequence 59, Appl
873	6	1.4	15	2	US-09-217-847-27	Sequence 27, Appl	946	6	1.4	15	5	PCT-US95-15696-14	Sequence 6, Appl
874	6	1.4	15	2	US-08-646-265A-111	Sequence 111, App	947	6	1.4	15	5	PCT-US96-10435-6	Sequence 14, Appl
875	6	1.4	15	2	US-08-487-761-2	Sequence 2, Appl	948	6	1.4	16	1	US-08-331-398A-54	Sequence 54, Appl
876	6	1.4	15	2	US-09-474-743-13	Sequence 13, Appl	949	6	1.4	16	2	US-08-442-461D-21	Sequence 21, Appl
877	6	1.4	15	2	US-08-890-929-9	Sequence 9, Appl	950	6	1.4	16	2	US-08-385-335A-6	Sequence 6, Appl
878	6	1.4	15	2	US-09-281-792B-21	Sequence 21, Appl	951	6	1.4	16	2	US-08-750-128-9	Sequence 9, Appl
879	6	1.4	15	2	US-08-743-168B-6	Sequence 6, Appl	952	6	1.4	16	2	US-08-331-397B-54	Sequence 54, Appl
880	6	1.4	15	2	US-09-227-693-32	Sequence 32, Appl	953	6	1.4	16	3	US-09-434-774-13	Sequence 13, Appl
881	6	1.4	15	2	US-09-367-953B-21	Sequence 21, Appl	954	6	1.4	16	3	US-09-440-325A-3	Sequence 3, Appl
882	6	1.4	15	2	US-09-165-060-67	Sequence 67, Appl	955	6	1.4	16	3	US-09-528-760A-4	Sequence 4, Appl
883	6	1.4	15	2	US-08-635-928-34	Sequence 34, Appl	956	6	1.4	16	3	US-08-983-035A-54	Sequence 54, Appl
884	6	1.4	15	2	US-09-140-084-20	Sequence 20, Appl	957	6	1.4	16	3	US-09-397-992A-20	Sequence 20, Appl
885	6	1.4	15	2	US-08-525-539A-67	Sequence 67, Appl	958	6	1.4	16	3	US-09-347-504-15	Sequence 15, Appl
886	6	1.4	15	2	US-08-479-737-45	Sequence 45, Appl	959	6	1.4	16	4	US-09-493-565-8	Sequence 8, Appl
887	6	1.4	15	2	US-09-240-310-67	Sequence 67, Appl	960	6	1.4	16	4	US-09-240-179-56	Sequence 56, Appl
888	6	1.4	15	2	US-09-556-111-1	Sequence 1, Appl	961	6	1.4	16	4	US-09-715-994-4	Sequence 4, Appl
889	6	1.4	15	2	US-09-556-111-2	Sequence 2, Appl	962	6	1.4	16	4	US-09-347-926-23	Sequence 23, Appl
890	6	1.4	15	2	US-09-556-111-4	Sequence 4, Appl	963	6	1.4	16	4	US-09-229-007A-7	Sequence 7, Appl
891	6	1.4	15	2	US-09-375-314-31	Sequence 31, Appl	964	6	1.4	16	4	US-09-796-110-4	Sequence 4, Appl
892	6	1.4	15	2	US-09-590-778-67	Sequence 67, Appl	965	6	1.4	16	4	US-09-712-529-7	Sequence 7, Appl
893	6	1.4	15	2	US-09-192-838B-5	Sequence 5, Appl	966	6	1.4	16	4	US-09-731-558-10	Sequence 10, Appl
894	6	1.4	15	2	US-09-535-754-4	Sequence 4, Appl	967	6	1.4	16	4	US-09-716-793A-4	Sequence 4, Appl
895	6	1.4	15	2	US-09-590-774-67	Sequence 67, Appl	968	6	1.4	16	4	US-09-846-996A-3	Sequence 3, Appl
896	6	1.4	15	2	US-09-619-550-67	Sequence 67, Appl	969	6	1.4	16	4	US-09-229-037-12	Sequence 12, Appl
897	6	1.4	15	2	US-08-475-442A-45	Sequence 45, Appl	970	6	1.4	16	4	US-09-971-843-20	Sequence 20, Appl
898	6	1.4	15	4	US-09-240-734-67	Sequence 67, Appl	971	6	1.4	16	4	US-09-740-510-4	Sequence 4, Appl
899	6	1.4	15	4	US-09-724-297-25	Sequence 25, Appl	972	6	1.4	16	4	US-09-555-352-34	Sequence 34, Appl
900	6	1.4	15	4	US-09-470-191-97	Sequence 97, Appl	973	6	1.4	16	4	US-09-951-843-4	Sequence 4, Appl
901	6	1.4	15	4	US-09-495-052-32	Sequence 32, Appl	974	6	1.4	16	4	US-09-395-448-12	Sequence 12, Appl
902	6	1.4	15	4	US-09-767-395-31	Sequence 31, Appl	975	6	1.4	16	4	US-09-478-681-12	Sequence 12, Appl
903	6	1.4	15	4	US-09-146-979-98	Sequence 98, Appl	976	6	1.4	16	4	US-09-634-368-17	Sequence 17, Appl

977	6	1.4	16	4	US-10-161-499-15	Sequence 15, Appl	1050	6	1.4	20	3	US-09-025-769B-1	Sequence 1, Appl
978	6	1.4	16	4	US-09-779-233-35	Sequence 35, Appl	1051	6	1.4	20	3	US-09-067-615-81	Sequence 81, Appl
979	6	1.4	16	4	US-09-873-135-4	Sequence 4, Appl	1052	6	1.4	20	3	US-09-067-615-89	Sequence 89, Appl
980	6	1.4	16	4	US-10-212-101A-7	Sequence 7, Appl	1053	6	1.4	20	3	US-09-425-585-12	Sequence 12, Appl
981	6	1.4	16	4	US-09-582-761B-48	Sequence 48, Appl	1054	6	1.4	20	4	US-09-603-663-75	Sequence 75, Appl
982	6	1.4	16	4	US-09-925-796-12	Sequence 12, Appl	1055	6	1.4	20	4	US-09-603-658-75	Sequence 75, Appl
983	6	1.4	16	4	US-09-941-450-12	Sequence 12, Appl	1056	6	1.4	20	4	US-09-602-373A-75	Sequence 75, Appl
984	6	1.4	16	4	US-10-113-424-7	Sequence 7, Appl	1057	6	1.4	20	4	US-08-716-249-9	Sequence 9, Appl
985	6	1.4	16	4	US-09-716-637-10	Sequence 10, Appl	1058	6	1.4	20	4	US-09-422-375-1	Sequence 1, Appl
986	6	1.4	16	4	US-09-968-362A-23	Sequence 23, Appl	1059	6	1.4	20	4	US-09-333-213-3	Sequence 3, Appl
987	6	1.4	16	4	US-09-625-049A-39	Sequence 39, Appl	1060	6	1.4	20	4	US-09-953-321-12	Sequence 12, Appl
988	6	1.4	16	4	US-09-706-243A-12	Sequence 12, Appl	1061	6	1.4	20	4	US-09-490-070A-1	Sequence 1, Appl
989	6	1.4	16	4	US-10-212-355-7	Sequence 7, Appl	1062	6	1.4	20	4	US-09-490-153-1	Sequence 1, Appl
990	6	1.4	17	1	US-08-463-163-5	Sequence 5, Appl	1063	6	1.4	20	4	US-08-302-758B-10	Sequence 10, Appl
991	6	1.4	17	2	US-08-484-905-10	Sequence 10, Appl	1064	6	1.4	20	4	US-10-077-210-3	Sequence 3, Appl
992	6	1.4	17	3	US-08-481-985B-10	Sequence 10, Appl	1065	6	1.4	20	4	US-09-490-324-1	Sequence 1, Appl
993	6	1.4	17	3	US-08-370-476-10	Sequence 10, Appl	1066	6	1.4	20	5	PCT-US95-04468-55	Sequence 55, Appl
994	6	1.4	17	3	US-08-890-929-1	Sequence 1, Appl	1067	6	1.4	20	5	PCT-US95-09816A-81	Sequence 81, Appl
995	6	1.4	17	4	US-09-646-028-57	Sequence 57, Appl	1068	6	1.4	20	5	PCT-US95-09816A-89	Sequence 89, Appl
996	6	1.4	17	4	US-09-634-368-21	Sequence 21, Appl	1069	6	1.4	21	1	US-07-679-052A-9	Sequence 9, Appl
997	6	1.4	17	4	US-09-634-368-32	Sequence 32, Appl	1070	6	1.4	21	2	US-08-484-905-14	Sequence 14, Appl
998	6	1.4	17	4	US-08-346-293-9	Sequence 9, Appl	1071	6	1.4	21	3	US-08-851-749-1	Sequence 1, Appl
999	6	1.4	18	1	US-07-972-032-84	Sequence 84, Appl	1072	6	1.4	21	3	US-08-481-985B-14	Sequence 14, Appl
1000	6	1.4	18	1	US-08-207-169A-7	Sequence 7, Appl	1073	6	1.4	21	3	US-08-370-476-14	Sequence 14, Appl
1001	6	1.4	18	1	US-08-642-255-135	Sequence 135, Appl	1074	6	1.4	21	4	US-09-446-787B-4	Sequence 4, Appl
1002	6	1.4	18	3	US-08-469-318-188	Sequence 188, Appl	1075	6	1.4	21	4	US-08-406-824A-17	Sequence 17, Appl
1003	6	1.4	18	3	US-08-469-318-189	Sequence 189, Appl	1076	6	1.4	21	4	US-09-512-563C-26	Sequence 26, Appl
1004	6	1.4	18	3	US-08-469-318-190	Sequence 190, Appl	1077	6	1.4	21	4	US-09-625-049A-38	Sequence 38, Appl
1005	6	1.4	18	3	US-08-468-609A-188	Sequence 188, Appl	1078	6	1.4	21	4	US-09-625-049A-38	Sequence 38, Appl
1006	6	1.4	18	3	US-08-468-609A-189	Sequence 189, Appl	1079	6	1.4	21	6	5182195-7	Patent No. 5182195
1007	6	1.4	18	3	US-08-468-609A-190	Sequence 190, Appl	1080	6	1.4	22	1	US-08-264-002-14	Sequence 14, Appl
1008	6	1.4	18	3	US-08-949-758-2	Sequence 2, Appl	1081	6	1.4	22	1	US-08-225-224-56	Sequence 56, Appl
1009	6	1.4	18	3	US-08-446-872A-188	Sequence 188, Appl	1082	6	1.4	22	3	US-08-722-258-56	Sequence 56, Appl
1010	6	1.4	18	3	US-08-446-872A-189	Sequence 189, Appl	1083	6	1.4	22	3	US-08-469-318-196	Sequence 196, Appl
1011	6	1.4	18	3	US-08-446-872A-190	Sequence 190, Appl	1084	6	1.4	22	3	US-08-468-609A-196	Sequence 196, Appl
1012	6	1.4	18	3	US-09-215-212-6	Sequence 6, Appl	1085	6	1.4	22	3	US-08-446-872A-196	Sequence 196, Appl
1013	6	1.4	18	4	US-08-762-227A-188	Sequence 188, Appl	1086	6	1.4	22	4	US-08-762-227A-196	Sequence 196, Appl
1014	6	1.4	18	4	US-08-762-227A-189	Sequence 189, Appl	1087	6	1.4	22	4	US-08-406-824A-24	Sequence 24, Appl
1015	6	1.4	18	4	US-08-762-227A-190	Sequence 190, Appl	1088	6	1.4	22	5	PCT-US95-01185-196	Sequence 196, Appl
1016	6	1.4	18	4	US-09-634-368-19	Sequence 19, Appl	1089	6	1.4	22	5	PCT-US95-04468-56	Sequence 56, Appl
1017	6	1.4	18	5	PCT-US95-01185-188	Sequence 188, Appl	1090	6	1.4	23	3	US-09-215-213-5	Sequence 5, Appl
1018	6	1.4	18	5	PCT-US95-01185-189	Sequence 189, Appl	1091	6	1.4	24	2	US-08-256-156A-2	Sequence 2, Appl
1019	6	1.4	18	5	PCT-US95-01185-190	Sequence 190, Appl	1092	6	1.4	24	2	US-08-623-16	Sequence 16, Appl
1020	6	1.4	18	6	5182195-2	Patent No. 5182195	1093	6	1.4	24	4	US-09-643-657-35	Sequence 35, Appl
1021	6	1.4	18	6	5182195-2	Patent No. 5182195	1094	6	1.4	24	4	US-09-643-657-35	Sequence 35, Appl
1022	6	1.4	19	1	US-07-679-052A-1	Sequence 1, Appl	1095	6	1.4	24	4	US-09-851-271A-12	Sequence 12, Appl
1023	6	1.4	19	2	US-08-448-418-90	Sequence 90, Appl	1096	6	1.4	25	4	US-09-254-832B-22	Sequence 22, Appl
1024	6	1.4	19	2	US-08-484-905-12	Sequence 12, Appl	1097	6	1.4	25	4	US-09-376-463-4	Sequence 4, Appl
1025	6	1.4	19	2	US-09-018-760-2	Sequence 2, Appl	1098	6	1.4	26	1	US-08-281-702A-6	Sequence 6, Appl
1026	6	1.4	19	3	US-08-481-985B-12	Sequence 12, Appl	1099	6	1.4	26	2	US-08-618-917-6	Sequence 6, Appl
1027	6	1.4	19	3	US-08-993-380-2	Sequence 2, Appl	1100	6	1.4	26	2	US-08-596-387B-97	Sequence 97, Appl
1028	6	1.4	19	3	US-08-370-476-12	Sequence 12, Appl	1101	6	1.4	26	3	US-08-545-196B-58	Sequence 58, Appl
1029	6	1.4	19	4	US-08-716-249-1	Sequence 1, Appl	1102	6	1.4	26	3	US-09-439-897-63	Sequence 63, Appl
1030	6	1.4	19	4	US-09-368-819A-6	Sequence 6, Appl	1103	6	1.4	26	3	US-09-067-615-97	Sequence 97, Appl
1031	6	1.4	19	4	US-09-146-979-90	Sequence 90, Appl	1104	6	1.4	26	5	PCT-US95-09816A-97	Sequence 97, Appl
1032	6	1.4	19	4	US-09-634-368-25	Sequence 25, Appl	1105	6	1.4	27	4	US-09-270-767-59868	Sequence 59868, A
1033	6	1.4	19	4	US-08-302-758B-5	Sequence 5, Appl	1106	6	1.4	28	1	US-08-478-312-16	Sequence 16, Appl
1034	6	1.4	19	4	US-09-376-463-22	Sequence 22, Appl	1107	6	1.4	28	1	US-08-485-302-16	Sequence 16, Appl
1035	6	1.4	20	1	US-07-987-286-18	Sequence 18, Appl	1108	6	1.4	28	1	US-08-476-169-12	Sequence 12, Appl
1036	6	1.4	20	1	US-08-225-224-55	Sequence 55, Appl	1109	6	1.4	28	1	US-08-484-083-12	Sequence 12, Appl
1037	6	1.4	20	2	US-08-596-387B-81	Sequence 81, Appl	1110	6	1.4	28	2	US-08-400-115-21	Sequence 21, Appl
1038	6	1.4	20	2	US-08-596-387B-89	Sequence 89, Appl	1111	6	1.4	28	3	US-08-957-001B-25	Sequence 25, Appl
1039	6	1.4	20	2	US-08-614-626-18	Sequence 18, Appl	1112	6	1.4	28	3	US-09-496-301-25	Sequence 25, Appl
1040	6	1.4	20	2	US-08-934-915-19	Sequence 19, Appl	1113	6	1.4	28	3	US-09-215-212-4	Sequence 4, Appl
1041	6	1.4	20	2	US-08-934-915-95	Sequence 95, Appl	1114	6	1.4	28	4	US-09-235-230-12	Sequence 12, Appl
1042	6	1.4	20	2	US-08-751-767A-14	Sequence 14, Appl	1115	6	1.4	29	1	US-08-478-312-14	Sequence 14, Appl
1043	6	1.4	20	3	US-08-851-749-6	Sequence 6, Appl	1116	6	1.4	29	1	US-08-478-312-17	Sequence 17, Appl
1044	6	1.4	20	3	US-08-654-623-15	Sequence 15, Appl	1117	6	1.4	29	1	US-08-485-302-17	Sequence 17, Appl
1045	6	1.4	20	3	US-08-722-258-55	Sequence 55, Appl	1118	6	1.4	29	1	US-08-485-302-17	Sequence 17, Appl
1046	6	1.4	20	3	US-09-046-985-14	Sequence 14, Appl	1119	6	1.4	29	1	US-08-476-169-10	Sequence 10, Appl
1047	6	1.4	20	3	US-09-474-743-14	Sequence 14, Appl	1120	6	1.4	29	1	US-08-476-169-13	Sequence 13, Appl
1048	6	1.4	20	3	US-09-178-115-116	Sequence 116, Appl	1121	6	1.4	29	1	US-08-484-083-10	Sequence 10, Appl
1049	6	1.4	20	3	US-09-177-776-116	Sequence 116, Appl	1122	6	1.4	29	1	US-08-484-083-13	Sequence 13, Appl

1123	6	1.4	29	4	US-09-270-767-35666	Sequence 35666, A	1196	6	1.4	36	4	US-08-762-227A-50	Sequence 50, Appl
1124	6	1.4	29	4	US-09-270-767-50883	Sequence 50883, A	1197	6	1.4	36	4	US-09-140-749-12	Sequence 12, Appl
1125	6	1.4	29	4	US-09-419-381-48	Sequence 48, Appl	1198	6	1.4	36	4	US-09-510-238A-9	Sequence 9, Appl
1126	6	1.4	30	1	US-08-478-312-18	Sequence 18, Appl	1199	6	1.4	36	4	US-09-936-885A-5	Sequence 5, Appl
1127	6	1.4	30	1	US-08-485-302-18	Sequence 18, Appl	1200	6	1.4	36	5	PCT-US95-01185-50	Sequence 50, Appl
1128	6	1.4	30	1	US-08-476-169-14	Sequence 14, Appl	1201	6	1.4	37	1	US-08-346-293-26	Sequence 26, Appl
1129	6	1.4	30	1	US-08-484-083-14	Sequence 14, Appl	1202	6	1.4	37	4	US-09-975-413A-14	Sequence 14, Appl
1130	6	1.4	31	1	US-08-478-312-15	Sequence 15, Appl	1203	6	1.4	37	4	US-09-975-413A-17	Sequence 17, Appl
1131	6	1.4	31	1	US-08-478-312-19	Sequence 19, Appl	1204	6	1.4	37	4	US-09-975-413A-23	Sequence 23, Appl
1132	6	1.4	31	1	US-08-485-302-15	Sequence 15, Appl	1205	6	1.4	38	4	US-09-446-787B-1	Sequence 1, Appl
1133	6	1.4	31	1	US-08-485-302-19	Sequence 19, Appl	1206	6	1.4	39	3	US-08-941-445A-37	Sequence 37, Appl
1134	6	1.4	31	1	US-08-476-169-11	Sequence 11, Appl	1207	6	1.4	39	3	US-09-314-268-98	Sequence 98, Appl
1135	6	1.4	31	1	US-08-476-169-15	Sequence 15, Appl	1208	6	1.4	39	4	US-09-857-401B-4	Sequence 4, Appl
1136	6	1.4	31	1	US-08-484-083-11	Sequence 11, Appl	1209	6	1.4	40	3	US-08-815-190A-17	Sequence 17, Appl
1137	6	1.4	31	1	US-08-484-083-15	Sequence 15, Appl	1210	6	1.4	40	4	US-09-333-213-1	Sequence 1, Appl
1138	6	1.4	31	3	US-08-789-333F-12	Sequence 12, Appl	1211	6	1.4	42	1	US-08-078-683A-12	Sequence 39, Appl
1139	6	1.4	31	3	US-09-169-015-22	Sequence 22, Appl	1212	6	1.4	42	1	US-08-377-687-39	Sequence 39, Appl
1140	6	1.4	31	3	US-08-743-168B-5	Sequence 5, Appl	1213	6	1.4	42	2	US-08-777-192-39	Sequence 39, Appl
1141	6	1.4	31	3	US-09-133-944-12	Sequence 12, Appl	1214	6	1.4	42	2	US-08-143-311B-4	Sequence 4, Appl
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1435 6 1.4 105 1 US-08-477-484B-157 Sequence 157, App
1436 6 1.4 105 1 US-08-107-669D-21 Sequence 21, Appl
1437 6 1.4 105 1 US-08-472-788A-21 Sequence 21, Appl
1438 6 1.4 105 2 US-08-477-531B-21 Sequence 21, App
1439 6 1.4 105 2 US-08-646-360-157 Sequence 157, App
1440 6 1.4 105 2 US-08-082-842A-21 Sequence 21, Appl
1441 6 1.4 105 3 US-08-839-765-157 Sequence 157, App
1442 6 1.4 105 3 US-09-136-389-157 Sequence 157, App
1443 6 1.4 105 3 US-09-610-938-157 Sequence 157, App
1444 6 1.4 105 4 US-09-711-485-157 Sequence 157, App
1445 6 1.4 106 4 US-09-270-767-57470 Sequence 57470, A
1446 6 1.4 106 4 US-09-240-274-47 Sequence 47, Appl
1447 6 1.4 106 3 US-09-240-274-48 Sequence 48, Appl
1448 6 1.4 106 4 US-09-489-039A-8560 Sequence 8560, App
1449 6 1.4 106 4 US-09-489-039A-8914 Sequence 8914, App
1450 6 1.4 106 4 US-09-270-767-34548 Sequence 34548, A
1451 6 1.4 106 4 US-09-270-767-49765 Sequence 49765, A
1452 6 1.4 107 1 US-08-276-852-90 Sequence 90, Appl
1453 6 1.4 107 1 US-08-899-575-90 Sequence 90, Appl
1454 6 1.4 107 1 US-08-899-575-90 Sequence 90, Appl
1455 6 1.4 107 3 US-08-894-173-69 Sequence 69, Appl
1456 6 1.4 107 3 US-08-894-173-83 Sequence 83, Appl
1457 6 1.4 107 3 US-09-398-193-69 Sequence 69, Appl
1458 6 1.4 107 3 US-09-398-193-83 Sequence 83, Appl
1459 6 1.4 107 4 US-09-740-002-20 Sequence 20, Appl
1460 6 1.4 107 4 US-09-248-796A-21742 Sequence 21742, A
1461 6 1.4 107 5 PCT-US95-08743-90 Sequence 90, Appl
1462 6 1.4 108 1 US-08-360-125-12 Sequence 12, Appl
1463 6 1.4 108 2 US-08-450-578-12 Sequence 12, Appl
1464 6 1.4 108 2 US-08-997-080-166 Sequence 166, App
1465 6 1.4 108 2 US-08-997-362-166 Sequence 166, App
1466 6 1.4 108 2 US-09-017-628-12 Sequence 12, Appl
1467 6 1.4 108 2 US-09-014-880-12 Sequence 12, Appl
1468 6 1.4 108 3 US-09-095-855-166 Sequence 166, App
1469 6 1.4 108 3 US-09-324-542-166 Sequence 166, App
1470 6 1.4 108 4 US-09-205-426-166 Sequence 166, App
1471 6 1.4 108 4 US-08-450-363-12 Sequence 12, Appl
1472 6 1.4 108 4 US-09-270-767-41095 Sequence 41095, A
1473 6 1.4 108 4 US-09-270-767-56311 Sequence 56311, A
1474 6 1.4 108 4 US-09-467-903-12 Sequence 12, Appl
1475 6 1.4 108 4 US-09-720-493-4 Sequence 4, Appl
1476 6 1.4 108 4 US-09-640-211A-1090 Sequence 1090, Ap
1477 6 1.4 109 2 US-08-002-324-4 Sequence 4, Appl
1478 6 1.4 109 2 US-08-652-816A-16 Sequence 16, Appl
1479 6 1.4 109 2 US-08-665-202-34 Sequence 34, Appl
1480 6 1.4 109 4 US-09-315-574-34 Sequence 34, Appl
1481 6 1.4 109 4 US-09-407-687-41 Sequence 41, Appl
1482 6 1.4 109 4 US-09-270-767-57602 Sequence 57602, A
1483 6 1.4 109 5 PCT-US94-00261-4 Sequence 4, Appl
1484 6 1.4 110 4 US-09-462-843A-3 Sequence 3, Appl
1485 6 1.4 110 4 US-09-172-699-22 Sequence 22, Appl
1486 6 1.4 110 4 US-09-248-796A-19689 Sequence 19689, A
1487 6 1.4 111 1 US-08-466-886-35 Sequence 35, Appl
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Sequence 43, Appl
Sequence 35, Appl
Sequence 43, Appl
Sequence 35, Appl
Sequence 8, Appl
Sequence 21707, A
Sequence 58, Appl
Sequence 6021, Ap
Sequence 34681, A
Sequence 49898, A
Sequence 65, Appl
Sequence 8, Appl

1488 6 1.4 111 2 US-08-665-202-43 Sequence 43, Appl
1489 6 1.4 111 3 US-08-469-617-35 Sequence 35, Appl
1490 6 1.4 111 4 US-09-315-574-43 Sequence 43, Appl
1491 6 1.4 111 4 US-08-469-630-35 Sequence 35, Appl
1492 6 1.4 111 4 US-09-203-768A-8 Sequence 8, Appl
1493 6 1.4 112 4 US-09-252-991A-21707 Sequence 21707, A
1494 6 1.4 112 4 US-09-840-459-58 Sequence 58, Appl
1495 6 1.4 112 4 US-09-497-625A-58 Sequence 58, Appl
1496 6 1.4 112 4 US-09-513-999C-6021 Sequence 6021, Ap
1497 6 1.4 113 4 US-09-270-767-34681 Sequence 34681, A
1498 6 1.4 113 4 US-09-270-767-49898 Sequence 49898, A
1499 6 1.4 113 4 US-09-377-285B-65 Sequence 65, Appl
1500 6 1.4 113 4 US-09-826-312A-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-673-395A-256
; Sequence 256, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 256
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-256

Query Match 19.5%; Score 86; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.8e-65;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 347 SGIOGFRGGVSSNMREISKGNRLGGSDNRYRGSSWGGSDAVGGVNTVNSP 406
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Db 49 SGIOGFRGGVSSNMREISKGNRLGGSDNRYRGSSWGGSDAVGGVNTVNSP 108
|||||

Qy 407 GMFNFTFWKNFKSKLGFINWDANK 432
|||||
Db 109 GMFNFTFWKNFKSKLGFINWDANK 134
|||||

RESULT 2
US-09-513-999C-5563
; Sequence 5563, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5563
; LENGTH: 72


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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 46
; OTHER INFORMATION: Xaa=Phe or Leu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 63
; OTHER INFORMATION: Xaa=Asp or Phe or His or Ile or Leu or Asn or Val or Tyr
US-09-513-999C-5563

Query Match      5.7%; Score 25; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 MFNFDTFWKNFKSKLGFINWDINK 432
Db 1 MFNFDTFWKNFKSKLGFINWDINK 25

RESULT 3
US-09-513-999C-5564
; Sequence 5564, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5564
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 46
; OTHER INFORMATION: Xaa=Phe or Leu
; NAME/KEY: UNSURE
; LOCATION: 63
; OTHER INFORMATION: Xaa=Asp or Phe or His or Ile or Leu or Asn or Val or Tyr
US-09-513-999C-5564

Query Match      5.7%; Score 25; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 MFNFDTFWKNFKSKLGFINWDINK 432
Db 1 MFNFDTFWKNFKSKLGFINWDINK 25

RESULT 4
US-09-248-796A-22487
; Sequence 22487, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725

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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22487
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22487

Query Match      3.2%; Score 14; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 GGSSSGSSSGSSSG 283
Db 68 GGSSSGSSSGSSSG 81

RESULT 5
US-09-248-796A-23892
; Sequence 23892, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23892
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23892

Query Match      2.7%; Score 12; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 GSSSGSSSGSS 290
Db 49 GSSSGSSSGSS 60

RESULT 6
US-09-949-016-7198
; Sequence 7198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7198
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Human

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US-09-949-016-7198

Query Match 2.5%; Score 11; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 GSSGSSGSSG 285

Db 578 GSSGSSGSSG 588

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RESULT 7

US-09-248-796A-22352

; Sequence 22352, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; PRIOR FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 22352

; LENGTH: 180

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-22352

Query Match 2.3%; Score 10; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 270 GSSGSSGSSG 279

Db 68 GSSGSSGSSG 77

|||||

RESULT 8

US-09-949-016-9109

; Sequence 9109, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9109

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-9109

Query Match 2.3%; Score 10; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 SSSGSSGSSG 281

|||||

Db 118 SSSGSSGSSG 127

RESULT 9

US-09-949-016-6315

; Sequence 6315, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6315

; LENGTH: 441

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6315

Query Match 2.3%; Score 10; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 SSSGSSGSSG 281

Db 345 SSSGSSGSSG 354

|||||

RESULT 10

US-09-248-796A-26119

; Sequence 26119, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 26119

; LENGTH: 541

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-26119

Query Match 2.3%; Score 10; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 SSSGSSGSSG 283

Db 407 SSSGSSGSSG 416

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RESULT 11

US-09-134-000C-6510

; Sequence 6510, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

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; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6510
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6510

Query Match      2.0%; Score 9; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACULLALCL 16
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Db      32 ACULLALCL 40

RESULT 12
US-09-107-532A-5997
; Sequence 5997, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Walcham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5997:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...184
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; SEQUENCE DESCRIPTION: SEQ ID NO: 5997:
US-09-107-532A-5997

Query Match      2.0%; Score 9; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACULLALCL 16
      |||||
Db      32 ACULLALCL 40

RESULT 13
US-09-248-796A-14345
; Sequence 14345, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14345
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14345

Query Match      2.0%; Score 9; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      274 SGSSSGSSS 282
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Db      345 SGSSSGSSS 353

RESULT 14
US-09-270-767-43154
; Sequence 43154, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43154
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43154

Query Match      2.0%; Score 9; DB 4; Length 512;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      269 SGSSSGSSS 277
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Db      308 SGSSSGSSS 316

RESULT 15
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US-09-381-656-1
; Sequence 1, Application US/09381656
; Patent No. 6645509
; GENERAL INFORMATION:
; APPLICANT: SERRE, Guy Bruno Rene
; APPLICANT: SIMON, Michel
; APPLICANT: WEBER-VIVAT, Marina
; TITLE OF INVENTION: POLYPEPTIDE EXPRESSED IN THE HORNY LAYER OF EPIDERMIS
; TITLE OF INVENTION: AND USE THEREOF
; FILE REFERENCE: 016800-336
; CURRENT APPLICATION NUMBER: US/09/381,656
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: FR 97/03899
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: FR 97/11317
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Human
US-09-381-656-1

Query Match      2.0%; Score 9; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      273 SSGSSSGSS 281
Db      88 SSGSSSGSS 96

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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566	440	100.0	440	14	US-10-223-088-150
567	440	100.0	440	14	US-10-223-090-150
573	440	100.0	440	14	US-10-223-087-150
586	440	100.0	440	14	US-10-223-083-150
592	440	100.0	440	14	US-10-223-089-150
618	440	100.0	440	14	US-10-174-587-202
688	440	100.0	440	14	US-10-063-742-52
764	440	100.0	440	14	US-10-013-909A-52
769	440	100.0	440	14	US-10-223-081-150
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Job time : 152 secs

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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:25:58 ; Search time 46 Seconds
(without alignments)
920.334 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 440

Sequence: 1 MKFGPLACLLALCLGSGE.....KLGFINWDINKDQRSSRP 440

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	3.0	1428	2 T08852	lustrin A - Califo
2	12	2.7	683	2 A82704	1,4-beta-cellobios
3	11	2.5	644	2 S39356	transcription fact
4	11	2.5	954	1 S68178	mixed-lineage prot
5	11	2.5	1570	2 T18272	1-phosphatidylinos
6	10	2.3	441	2 G01758	transcription fact
7	10	2.3	510	2 T37541	probable glycolipi
8	10	2.3	542	2 T06728	pectate lyase (EC
9	10	2.3	643	1 KRH2	keratin 1, type II
10	10	2.3	710	2 S28014	outD protein - Erw
11	10	2.3	1469	2 T09219	basal transcriptio
12	10	2.3	1891	2 T13594	hypothetical prote
13	10	2.3	1920	2 T13893	gene hindsight pro
14	9	2.0	235	2 D87278	DNA-binding respon
15	9	2.0	275	2 F84088	N-acetylmuramoyl-L
16	9	2.0	326	2 C96735	unknown protein F2
17	9	2.0	502	2 A48679	differentiated ker
18	9	2.0	535	2 S66148	gene pipsqueak pro
19	9	2.0	549	2 T20720	hypothetical prote
20	9	2.0	668	1 S54304	taxis sensor histi
21	9	2.0	668	2 E84253	chemotaxis protein
22	9	2.0	668	2 C71868	hypothetical prote
23	9	2.0	675	2 S25005	dnak-type molecula
24	9	2.0	712	2 B47021	pectic enzyme secr
25	9	2.0	1085	2 S66149	gene pipsqueak pro
26	9	2.0	1097	2 T13033	Cyclin F - fruit f
27	9	2.0	1130	2 T19148	hypothetical prote
28	9	2.0	1306	2 S25370	MSB2 protein - yea
29	9	2.0	1711	1 A47392	chromodomain-helic

30	8	1.8	67	2 E95210	hypothetical prote
31	8	1.8	67	2 H98074	hypothetical prote
32	8	1.8	99	2 D86931	hypothetical prote
33	8	1.8	115	2 D61615	sericin MG-1 - gre
34	8	1.8	120	2 T45451	hypothetical prote
35	8	1.8	179	2 D84259	hypothetical prote
36	8	1.8	183	2 PN0109	keratin-like prote
37	8	1.8	194	2 T45625	hypothetical prote
38	8	1.8	251	2 D96010	hypothetical expor
39	8	1.8	305	2 T02851	probable membrane
40	8	1.8	305	2 JC4525	nucleic acid-bindi
41	8	1.8	315	2 S53589	Sol2 protein - yea
42	8	1.8	316	1 A38743	loricrin - human
43	8	1.8	319	2 A55661	protein kinase ADK
44	8	1.8	336	2 T30757	homeotic protein e
45	8	1.8	392	2 B48423	hypothetical prote
46	8	1.8	392	2 T20268	hypothetical prote
47	8	1.8	396	2 T49109	glycine-rich prote
48	8	1.8	398	2 G90225	hypothetical prote
49	8	1.8	399	1 B49836	transcription fact
50	8	1.8	423	2 H84860	hypothetical prote
51	8	1.8	426	2 I39539	3-phosphoshikimate
52	8	1.8	432	2 S30193	T-cell surface gly
53	8	1.8	441	2 T49265	hypothetical prote
54	8	1.8	442	2 S57710	unusual floral org
55	8	1.8	447	2 G84687	probable disease r
56	8	1.8	471	2 B86170	ADK1 [imported] -
57	8	1.8	471	2 T39571	probable regulator
58	8	1.8	472	1 A49836	transcription fact
59	8	1.8	477	2 D82877	glutamyl-tRNA amid
60	8	1.8	481	2 A35628	loricrin - mouse
61	8	1.8	484	2 G70846	hypothetical glyci
62	8	1.8	506	2 C42725	amidase (EC 3.5.1.
63	8	1.8	506	2 H71253	probable glu-tRNA
64	8	1.8	521	2 D87413	hypothetical prote
65	8	1.8	527	2 T15258	hypothetical prote
66	8	1.8	548	2 S59133	ETS2 repressor fac
67	8	1.8	549	1 S54538	amidase (EC 3.5.1.
68	8	1.8	570	2 S56132	cellulase (EC 3.2.
69	8	1.8	579	2 T37248	probable matrix me
70	8	1.8	589	2 JG0196	protein kinase DYR
71	8	1.8	594	2 A87476	amidase family pro
72	8	1.8	598	2 T32166	hypothetical prote
73	8	1.8	601	2 T15260	hypothetical prote
74	8	1.8	629	2 G0195	protein kinase DYR
75	8	1.8	633	2 F84564	probable protein k
76	8	1.8	645	2 T45482	heat shock protein
77	8	1.8	656	1 QQBET2	UL25 protein - hum
78	8	1.8	661	1 S59633	endo-1,4-beta-xyla
79	8	1.8	663	2 S21912	BRcore-Q1-21 prote
80	8	1.8	694	2 S71786	wingless receptor
81	8	1.8	710	2 C98235	probable hydroxama
82	8	1.8	716	2 A13050	hydroxamate-type f
83	8	1.8	718	2 A36068	major amputate fi
84	8	1.8	728	2 S21913	BRcore-TNT1-Q1-21
85	8	1.8	733	2 S44876	2C21.4 protein - C
86	8	1.8	754	2 JC4898	Down-syndrome-crit
87	8	1.8	772	2 T43034	kinesin-like prote
88	8	1.8	775	2 T43033	kinesin-like prote
89	8	1.8	778	2 F70963	hypothetical glyci
90	8	1.8	805	2 A56199	transcription fact
91	8	1.8	858	2 JG0183	myosin Myok - Dict
92	8	1.8	877	2 T43449	hypothetical prote
93	8	1.8	890	2 A30481	bacteriocin BCN5 -
94	8	1.8	937	2 S58135	hypally regulated
95	8	1.8	965	2 S55658	segment protein 6
96	8	1.8	976	1 TVMSMD	macrophage colony-
97	8	1.8	978	2 S16385	macrophage colony-
98	8	1.8	1024	2 T46016	hypothetical prote
99	8	1.8	1027	2 T46481	hypothetical prote
100	8	1.8	1141	2 A54962	sterol regulatory
101	8	1.8	1230	2 T18256	probable serine/th
102	8	1.8	1230	2 T18259	serine/threonine p

103	8	1.8	1233	2	T30989	serine/threonine p	176	7	1.6	272	2	E95946	periplasmic amino
104	8	1.8	1585	2	T31611	hypothetical prote	177	7	1.6	272	2	S73796	hypothetical prote
105	8	1.8	1723	2	H86357	polymorphic membra	178	7	1.6	273	2	F83221	plant-metabolite d
106	8	1.8	1723	2	E72067	polymorphic membra	179	7	1.6	276	2	F83919	hypothetical prote
107	8	1.8	1732	2	C81601	MHC class III hist	180	7	1.6	277	2	T32460	ribose-phosphate p
108	8	1.8	1870	2	S37671	MHC class III hist	181	7	1.6	282	2	F75020	neutrophil protein
109	8	1.8	1872	2	S36152	MHC class III hist	182	7	1.6	284	2	A35419	CAMP-binding prote
110	8	1.8	2142	2	B35098	MHC class III hist	183	7	1.6	287	2	A49752	hypothetical prote
111	8	1.8	2761	2	T29285	hypothetical prote	184	7	1.6	292	2	C71448	helix-destabilizin
112	8	1.8	3759	2	A35085	trithorax protein	185	7	1.6	293	1	DDBP32	helix-destabilizin
113	7	1.6	91	2	H91035	hypothetical prote	186	7	1.6	293	1	DDBP36	2,5-diketo-D-gluc
114	7	1.6	91	2	B85880	hypothetical prote	187	7	1.6	294	2	AC3642	RNA-binding protei
115	7	1.6	91	2	H97856	hypothetical prote	188	7	1.6	296	2	A47318	gene Merc protein
116	7	1.6	102	2	JC1150	hypothetical prote	189	7	1.6	296	2	I53142	Polyamine transpor
117	7	1.6	118	2	C48806	probable nonspecif	190	7	1.6	297	2	E83194	Fl003.14 protein -
118	7	1.6	133	2	B49530	vascular endotheli	191	7	1.6	297	2	B86161	proteind disulfide-
119	7	1.6	139	2	B96500	hypothetical prote	192	7	1.6	298	2	T31236	hypothetical prote
120	7	1.6	144	2	JC2102	lectin-related pro	193	7	1.6	299	2	T12483	helix-destabilizin
121	7	1.6	145	2	F25929	hemoglobin beta-II	194	7	1.6	301	1	DDBP34	hypothetical prote
122	7	1.6	150	2	C86224	hypothetical prote	195	7	1.6	304	2	T16535	hypothetical prote
123	7	1.6	154	2	A70508	hypothetical prote	196	7	1.6	312	2	G75514	hypothetical prote
124	7	1.6	155	2	S56258	hypothetical prote	197	7	1.6	313	2	A34677	secretory pathway
125	7	1.6	161	2	S71453	glycine-rich RNA-b	198	7	1.6	316	2	S08169	collagen col-12 pr
126	7	1.6	161	2	AE0357	conserved hypotet	199	7	1.6	316	2	S08170	collagen col-13 pr
127	7	1.6	163	2	T28012	hypothetical prote	200	7	1.6	317	2	S01412	hypothetical prote
128	7	1.6	167	2	S21359	keratin, type I, c	201	7	1.6	317	2	T27485	hypothetical prote
129	7	1.6	167	2	D81031	conserved hypotet	202	7	1.6	321	2	D83813	hypothetical prote
130	7	1.6	170	2	JC2213	hypothetical 14.7K	203	7	1.6	324	2	D48423	homotetic protein e
131	7	1.6	175	2	H81975	hypothetical prote	204	7	1.6	329	2	A48805	insulin-like growt
132	7	1.6	175	2	C70326	hypothetical prote	205	7	1.6	329	2	T45972	hypothetical prote
133	7	1.6	175	2	T47463	serine/proline-ric	206	7	1.6	332	2	S15347	transcription fact
134	7	1.6	177	2	AG1467	transcription anti	207	7	1.6	342	2	S51839	D13F(MVASTI) prote
135	7	1.6	177	2	F96739	hypothetical prote	208	7	1.6	343	2	T05221	hypothetical prote
136	7	1.6	178	2	G96667	unknown protein, 5	209	7	1.6	345	2	G83148	DNA polymerase III
137	7	1.6	182	2	A02947	keratin, 60K type	210	7	1.6	351	2	T03946	Xnl like-homeo box
138	7	1.6	182	2	A02946	keratin, 59K type	211	7	1.6	357	2	T02785	probable homeotic
139	7	1.6	190	2	A24713	sericin - silkworm	212	7	1.6	359	2	H90301	hypothetical prote
140	7	1.6	193	2	JC6114	melanocyte-specifi	213	7	1.6	361	2	T48029	hypothetical prote
141	7	1.6	196	2	G87484	acyltransferase fa	214	7	1.6	362	2	T52266	nit-lilase-like pro
142	7	1.6	200	2	I46051	secreted phosphor	215	7	1.6	363	2	TS1341	RNA helicase RH9 l
143	7	1.6	202	2	B87521	Deda family protei	216	7	1.6	366	2	JC7690	Gfi-1-like protein
144	7	1.6	204	2	D84809	hypothetical prote	217	7	1.6	369	2	H72018	chlp3 43 kda prote
145	7	1.6	204	2	B86308	F2023.10 protein	218	7	1.6	369	2	C86606	CHLPS 43 kda prote
146	7	1.6	211	2	S55885	CCHH finger protei	219	7	1.6	369	2	C81521	conserved hypotet
147	7	1.6	216	2	G70447	flagellar I-ring p	220	7	1.6	371	2	T13021	hypothetical prote
148	7	1.6	221	2	AG1961	hypothetical prote	221	7	1.6	372	2	AG2827	hFLK protein (impo
149	7	1.6	223	1	VCBVCA	coat protein - tob	222	7	1.6	373	2	E97605	protease chain h
150	7	1.6	224	2	T19959	hypothetical prote	223	7	1.6	374	2	A45074	Gal beta 1,3(4)Glc
151	7	1.6	231	2	S62530	hypothetical prote	224	7	1.6	375	2	JN0618	Gal beta 1,3(4)Glc
152	7	1.6	233	2	T24714	hypothetical prote	225	7	1.6	379	2	S42543	hypothetical prote
153	7	1.6	234	2	F46449	hypothetical prote	226	7	1.6	382	1	B42333	transcription fact
154	7	1.6	246	2	AB0589	hypothetical prote	227	7	1.6	384	2	E75295	conserved hypotet
155	7	1.6	247	2	T10524	tonoplast intrinsi	228	7	1.6	385	2	S53087	ubiquinol-cytochro
156	7	1.6	248	2	S26198	H+-transporting tw	229	7	1.6	385	2	S40778	ubiquinol-cytochro
157	7	1.6	248	2	T40415	hypothetical prote	230	7	1.6	386	2	T14243	ubiquinol-cytochro
158	7	1.6	248	2	T33230	hypothetical prote	231	7	1.6	387	1	CBASN	ubiquinol-cytochro
159	7	1.6	253	2	T04642	hypothetical prote	232	7	1.6	387	2	T25452	hypothetical prote
160	7	1.6	253	2	B49752	probable membrane	233	7	1.6	391	2	C86347	F24U8.6 protein -
161	7	1.6	254	2	S48547	amidase yedB (impo	234	7	1.6	399	2	I38901	JNK-activating pro
162	7	1.6	256	2	T44452	glycine-rich prote	235	7	1.6	401	2	AE3651	amidase (EC 3.5.1.
163	7	1.6	256	2	T03371	hypothetical prote	236	7	1.6	401	2	T48495	hypothetical prote
164	7	1.6	256	2	T24713	hypothetical prote	237	7	1.6	402	2	JC5270	neuron-specific si
165	7	1.6	257	2	C84533	hypothetical prote	238	7	1.6	405	2	SI9355	hypothetical prote
166	7	1.6	258	2	G96798	hypothetical prote	239	7	1.6	406	2	S38170	SRP40 protein - ye
167	7	1.6	258	2	T09031	hypothetical prote	240	7	1.6	417	2	JC7092	PsuI protein - fis
168	7	1.6	259	2	F86475	hypothetical prote	241	7	1.6	419	2	AC1049	hFLK protein (impo
169	7	1.6	262	2	T47669	hypothetical prote	242	7	1.6	419	2	F86113	probable integral
170	7	1.6	263	2	T49870	probable transcrip	243	7	1.6	419	2	F91272	probable integral
171	7	1.6	264	2	JC7772	aquaporin 10 - hum	244	7	1.6	419	2	B43653	probable integral
172	7	1.6	265	2	B96993	probable membrane	245	7	1.6	423	2	G84243	Glu-tRNA amidotran
173	7	1.6	267	1	CTPGP	corticotropin / li	246	7	1.6	424	1	Z3BPF1	coat protein A pre
174	7	1.6	270	2	A60830	keratin, 70K type	247	7	1.6	424	1	Z3BPF2	coat protein A pre
175	7	1.6	271	2	T04666	hypothetical prote	248	7	1.6	424	1	Z3BPM3	coat protein A pre

249	7	1.6	424	2	T43498	hypotheical prote	322	7	1.6	485	2	T44294	glutamyl-tRNA (Gln
250	7	1.6	426	2	A51309	hypotheical prote	323	7	1.6	486	1	A57601	transcription fact
251	7	1.6	430	2	T21060	hypotheical prote	324	7	1.6	486	2	C86645	Glu-tRNA amidotran
252	7	1.6	433	2	S76485	hypotheical prote	325	7	1.6	486	2	T51582	glutamyl-tRNA (Gln
253	7	1.6	434	1	Z3B9TK	coat protein A - p	326	7	1.6	486	2	AB1938	glutamyl-tRNA (Gln
254	7	1.6	434	2	G64444	amidase - Mechanoc	327	7	1.6	487	1	BWSOGM	glta protein - Str
255	7	1.6	434	2	H71310	amidase - Mechanoc	328	7	1.6	488	1	QXASBI	mRNA maturase bli
256	7	1.6	434	2	S73331	hypotheical prote	329	7	1.6	488	2	A72554	probable Glu-tRNA
257	7	1.6	436	2	A11316	hypotheical prote	330	7	1.6	488	2	F95050	glutamyl-tRNA(Gln)
258	7	1.6	436	2	A11688	hypotheical prote	331	7	1.6	488	2	B97921	glu-tRNAAGln amidot
259	7	1.6	436	2	T15331	hypotheical prote	332	7	1.6	488	2	A55180	homeotic protein H
260	7	1.6	438	2	I50517	retinoid X recepto	333	7	1.6	489	2	D87551	glutamyl-tRNA(Gln)
261	7	1.6	439	2	I57561	transcription fact	334	7	1.6	490	2	B81239	pyruvate kinase II
262	7	1.6	439	2	H86658	N-acetylmutramoyl-L	335	7	1.6	490	2	G82011	pyruvate kinase (E
263	7	1.6	440	2	S37303	sox-4 protein - mo	336	7	1.6	491	2	A81722	glutamyl-tRNA(Gln)
264	7	1.6	442	2	T47788	hypotheical prote	337	7	1.6	491	2	F71568	probable glu-tRNA
265	7	1.6	444	2	T47114	probable 3-carboxy	338	7	1.6	492	2	H72130	glutamyl-tRNA(Gln)
266	7	1.6	445	1	A49447	transcription fact	339	7	1.6	492	2	C86491	Glu tRNA Gln amido
267	7	1.6	446	2	B53376	indoleacetamide hy	340	7	1.6	492	2	AB1030	probable exported
268	7	1.6	447	2	E83465	conserved hypothe	341	7	1.6	493	2	A44761	6-aminohexanoate-c
269	7	1.6	448	2	H90536	hypotheical prote	342	7	1.6	493	2	A44761	6-aminohexanoate-c
270	7	1.6	452	2	T25076	hypotheical prote	343	7	1.6	493	2	B97724	glutamyl-tRNA amid
271	7	1.6	453	1	P64623	amidase - Helicoba	344	7	1.6	493	2	E71725	glutamyl-tRNA amid
272	7	1.6	453	2	A69494	Glu-tRNA amidotran	345	7	1.6	493	2	AG2738	glutamyl-tRNA amid
273	7	1.6	453	2	H81308	Glu-tRNAAGln amidot	346	7	1.6	495	1	S52641	heat shock transcr
274	7	1.6	453	2	A71891	glu-tRNA amidotran	347	7	1.6	495	2	AB3594	glutamyl-tRNA(Gln)
275	7	1.6	454	2	D69066	amidase - Methanob	348	7	1.6	496	2	E70142	glu-tRNA amidotran
276	7	1.6	455	1	B25493	indoleacetamide hy	349	7	1.6	496	2	E97519	glutamyl-tRNA(Gln)
277	7	1.6	455	2	A86306	F20D23.27 protein	350	7	1.6	497	2	T35815	probable Glu-tRNA(
278	7	1.6	457	2	A69541	Glu-tRNA amidotran	351	7	1.6	499	2	F86645	amidase [imported]
279	7	1.6	457	2	E96772	hypotheical prote	352	7	1.6	499	2	T36462	hypotheical prote
280	7	1.6	459	2	S13064	1D-myo-inositol-tr	353	7	1.6	502	2	I52637	Ca2+/calmodulin-de
281	7	1.6	461	2	F70571	hypotheical glyci	354	7	1.6	504	2	S74034	amidase (EC 3.5.1.
282	7	1.6	461	2	JN0129	1D-myo-inositol-tr	355	7	1.6	506	2	S75789	6-aminohexanoate-c
283	7	1.6	461	2	C86679	transcription regu	356	7	1.6	507	2	AB2530	amidase [imported]
284	7	1.6	461	2	H84099	cell wall-binding	357	7	1.6	507	2	S05542	hypotheical prote
285	7	1.6	462	1	S30104	indoleacetamide hy	358	7	1.6	510	2	A45338	connexin-56 - Chic
286	7	1.6	462	2	G70753	probable amidase -	359	7	1.6	515	2	S38270	amidase (EC 3.5.1.
287	7	1.6	464	2	AG1933	Glu-tRNA(Gln) amid	360	7	1.6	516	2	AC1540	ATP-dependent RNA
288	7	1.6	464	2	B87573	pyrazinamide/nic	361	7	1.6	520	2	AB1183	ATP-dependent RNA
289	7	1.6	464	2	E82865	conjugal transfer	362	7	1.6	521	2	A37806	amidase (EC 3.5.1.
290	7	1.6	465	2	AC0396	probable amidase [363	7	1.6	521	2	S15070	amidase (EC 3.5.1.
291	7	1.6	465	2	F75524	hypotheical prote	364	7	1.6	523	2	T23003	hypotheical prote
292	7	1.6	471	2	D95356	probable amidase [365	7	1.6	524	2	S55097	probable membrane
293	7	1.6	474	2	B85500	proteinase DO (EC	366	7	1.6	525	2	D70878	keratin, 54K type
294	7	1.6	474	2	S45229	proteinase DO (EC	367	7	1.6	526	1	KRBOVI	hypotheical glyci
295	7	1.6	474	2	E90849	proteinase DO (EC	368	7	1.6	530	2	T32812	hypotheical prote
296	7	1.6	474	2	I38240	transcription fact	369	7	1.6	534	2	B71445	probable glycerol-
297	7	1.6	475	2	G72274	glutamyl tRNA-Gln	370	7	1.6	536	2	H71563	hypotheical prote
298	7	1.6	475	2	C86863	N-acetylmutramoyl-L	371	7	1.6	537	2	S50344	aspegrillopepsin h
299	7	1.6	476	2	C84643	hypotheical prote	372	7	1.6	543	2	F70726	hypotheical glyci
300	7	1.6	477	2	I64210	hydrolase (aux2) h	373	7	1.6	543	2	B39369	homeotic protein B
301	7	1.6	477	2	T18801	hypotheical prote	374	7	1.6	546	2	B75375	probable amidase -
302	7	1.6	478	1	S73920	amidase homolog G0	375	7	1.6	547	2	C86264	protein F3F19.5 [1
303	7	1.6	478	2	F70322	glutamyl-tRNA (Gln	376	7	1.6	550	1	FGRTA	collagen alpha c
304	7	1.6	478	2	H90246	hypotheical prote	377	7	1.6	551	1	NRECE3	collagen E3 (EC 3.1
305	7	1.6	478	2	D97266	glutamyl-tRNAAGln a	378	7	1.6	552	2	S17551	gamma-aminobutyric
306	7	1.6	480	2	A40815	transcription fact	379	7	1.6	554	2	G01928	gamma-aminobutyric
307	7	1.6	480	2	A86427	probable serine/th	380	7	1.6	555	2	D95139	DNA repair protein
308	7	1.6	481	2	E81091	Glu-tRNA(Gln) amid	381	7	1.6	555	2	C98007	DNA repair and gen
309	7	1.6	481	2	C81849	Glu-tRNA(Gln) amid	382	7	1.6	555	2	F86487	unknown protein [1
310	7	1.6	481	2	A27626	glucose phosphoryl	383	7	1.6	556	2	S06838	gamma-aminobutyric
311	7	1.6	482	2	D75346	glutamyl-tRNA(Gln)	384	7	1.6	556	2	D70940	probable PPS prote
312	7	1.6	483	1	TVRTKA	protein kinase (EC	385	7	1.6	558	2	T23991	hypotheical prote
313	7	1.6	483	1	S77264	amidase slr0877 -	386	7	1.6	560	2	AD1681	formyl-tetrahydrof
314	7	1.6	483	2	AC1294	glutamyl-tRNA(Gln)	387	7	1.6	561	2	C75543	6-aminohexanoate-c
315	7	1.6	483	2	A11665	glutamyl-tRNA(Gln)	388	7	1.6	568	2	S15008	gene disco protein
316	7	1.6	483	2	S27680	Nasopressin recept	389	7	1.6	571	2	T29751	hypotheical prote
317	7	1.6	484	2	H83084	Glu-tRNA(Gln) amid	390	7	1.6	572	2	T08509	trbL protein - Ent
318	7	1.6	484	2	B70586	probable amiA2 pro	391	7	1.6	575	2	T48224	probable homeodoma
319	7	1.6	485	2	C89978	glutamyl-tRNAAGln a	392	7	1.6	575	2	S35327	protein kinase 999
320	7	1.6	485	2	B69795	glutamyl-tRNA(Gln)	393	7	1.6	576	1	S22453	colicin E7 (EC 3.1
321	7	1.6	485	2	F97228	glu-tRNAAGln amidot	394	7	1.6	576	2	A26628	homeotic protein I

395	7	1.6	577	2	Tl6333	hypothetical prote	468	7	1.6	816	2	T00919	hypothetical prote
396	7	1.6	577	2	T01945	hypothetical prote	469	7	1.6	821	2	E95245	penicillin-binding
397	7	1.6	581	1	NDECE2	colicin E2 (EC 3.1	470	7	1.6	821	2	B95110	peptidoglycan gly
398	7	1.6	581	1	KRMS2	keratin, type II c	471	7	1.6	822	2	AB0238	neamin storage sys
399	7	1.6	581	2	H69452	hypothetical prote	472	7	1.6	822	2	T47007	hypothetical prote
400	7	1.6	583	2	T39112	probable amidase -	473	7	1.6	835	2	JP0076	hel protein - chic
401	7	1.6	586	2	T51211	hypothetical prote	474	7	1.6	844	2	AD0047	ribonuclease R (EC
402	7	1.6	586	2	T04716	hypothetical prote	475	7	1.6	846	2	A30889	integrin beta chai
403	7	1.6	586	2	JC6500	hypothetical prote	476	7	1.6	850	2	JC5700	Erbb kinase activa
404	7	1.6	587	2	T00316	hnf-3/forkhead tra	477	7	1.6	853	2	S74279	hypothetical prote
405	7	1.6	590	2	A29904	toxr-regulated lip	478	7	1.6	858	2	T18946	probable phospholi
406	7	1.6	592	2	B82759	keratin 5, type II	479	7	1.6	873	2	B53225	ecdysone-induced p
407	7	1.6	594	2	B86456	endo-1,4-beta-gluc	480	7	1.6	898	2	T42131	probable toxR-regu
408	7	1.6	604	2	A39369	protein trihelix D	481	7	1.6	899	2	S17546	furin (EC 3.4.21-7
409	7	1.6	606	2	H70816	homeotic protein B	482	7	1.6	900	2	C96842	hypothetical prote
410	7	1.6	606	2	S13367	hypothetical glyci	483	7	1.6	927	2	A48085	transcription fact
411	7	1.6	609	2	B84783	Om(1D) protein - f	484	7	1.6	932	1	A31898	hypothetical prote
412	7	1.6	609	2	A49839	probable poly(A) b	485	7	1.6	947	2	T00340	hydroxymethylgluta
413	7	1.6	612	2	S53714	odd-paired - fruit	486	7	1.6	952	2	T52456	hypothetical prote
414	7	1.6	615	2	T20839	probable dinitrifi	487	7	1.6	952	2	T49283	endopeptidase Clp
415	7	1.6	615	2	T34392	hypothetical prote	488	7	1.6	962	2	S60225	AtClpC - Arabidops
416	7	1.6	616	2	A11180	hypothetical prote	489	7	1.6	968	2	T00353	ionotropic glutama
417	7	1.6	618	2	A70989	amidasas homolog 1	490	7	1.6	972	2	T49773	hypothetical prote
418	7	1.6	621	2	S75115	hypothetical glyci	491	7	1.6	980	1	TVCTMD	related to actin-1
419	7	1.6	621	2	JC7278	acetohydroxy acid	492	7	1.6	980	1	T49570	macrophage colony-
420	7	1.6	622	2	I37984	adaptor protein co	493	7	1.6	983	2	B88533	hypothetical prote
421	7	1.6	623	1	S33167	keratin 9, type I,	494	7	1.6	998	2	A96827	glutamate receptor
422	7	1.6	631	1	B83404	gene pointed prote	495	7	1.6	1000	2	C82630	hypothetical prote
423	7	1.6	632	2	T32454	hypothetical prote	496	7	1.6	1002	2	T09438	serine proteinase
424	7	1.6	633	2	T27215	hypothetical prote	497	7	1.6	1008	2	F71727	tox-activated lip
425	7	1.6	638	2	S46499	hypothetical prote	498	7	1.6	1011	2	F70620	acriflavin resista
426	7	1.6	640	1	ZYBTE5	NADP-dependent mal	499	7	1.6	1013	2	B82276	hypothetical glyci
427	7	1.6	641	2	T03095	tail protein pb5 -	500	7	1.6	1018	2	T30986	Tox-activated gen
428	7	1.6	647	2	S06450	homeoprotein Sail	501	7	1.6	1029	2	T28956	period protein - C
429	7	1.6	650	2	F72540	steroid hormone re	502	7	1.6	1036	1	GNLJG2	hypothetical prote
430	7	1.6	655	2	T00768	hypothetical prote	503	7	1.6	1043	2	T13733	HIV-1 retropepsin
431	7	1.6	660	2	S50383	polyadenylate-bind	504	7	1.6	1044	2	G98332	RT2-F1 protein - f
432	7	1.6	663	2	T40493	gamma-glutamyltran	505	7	1.6	1047	2	AD2950	rnd multidrug effl
433	7	1.6	666	2	A42296	hnf-3/forkhead tra	506	7	1.6	1047	2	T34946	RND multidrug effl
434	7	1.6	671	2	A35912	lysozyme 2 (EC 3.2	507	7	1.6	1063	2	A40253	probable isoleucyl
435	7	1.6	673	2	T06294	homeotic protein o	508	7	1.6	1070	2	S19686	HIRA protein - fru
436	7	1.6	673	2	T00328	hypothetical prote	509	7	1.6	1076	2	JC2217	acidic nuclear pro
437	7	1.6	675	2	S19140	hypothetical prote	510	7	1.6	1077	2	A44067	alpha-glucosidase
438	7	1.6	678	2	T49984	dnak-type molecula	511	7	1.6	1079	2	B70807	major surface glyci
439	7	1.6	685	2	T24950	bromodomain protei	512	7	1.6	1079	2	B70807	serine-rich protei
440	7	1.6	703	2	T05632	hypothetical prote	513	7	1.6	1079	2	C96772	hypothetical glyci
441	7	1.6	709	2	T28712	hypothetical prote	514	7	1.6	1096	2	T08619	probable metallopr
442	7	1.6	710	2	T31502	hypothetical prote	515	7	1.6	1110	2	IS1116	probable metallop
443	7	1.6	713	2	T48634	DRH1 DEAD box prot	516	7	1.6	1119	2	AB2239	hypothetical prote
444	7	1.6	714	2	AF2479	ABC transporter AT	517	7	1.6	1121	2	JQ1631	hypothetical prote
445	7	1.6	716	2	AC2449	ABC transporter AT	518	7	1.6	1133	2	A54164	sterol regulatory
446	7	1.6	720	1	A55160	Trg protein - fru1	519	7	1.6	1133	2	T01757	hypothetical prote
447	7	1.6	722	2	AF1956	ABC transporter AT	520	7	1.6	1143	2	T10636	hypothetical prote
448	7	1.6	722	2	S57246	ventral nervous sy	521	7	1.6	1146	2	A55532	myosin-heavy-chain
449	7	1.6	726	2	T34638	hypothetical prote	522	7	1.6	1150	2	T13824	LK6 protein kinase
450	7	1.6	733	2	T28145	RING3 kinase - chi	523	7	1.6	1160	2	T13713	beta3 protein - fr
451	7	1.6	742	2	T00371	hypothetical prote	524	7	1.6	1175	2	S39951	chitin synthase (E
452	7	1.6	749	2	A70812	hypothetical glyci	525	7	1.6	1187	2	C84568	hypothetical prote
453	7	1.6	754	2	T18238	lysophospholipase	526	7	1.6	1189	2	T17088	homodomain-intera
454	7	1.6	754	2	F87185	phosphoribosylform	527	7	1.6	1200	2	C96025	hypothetical expor
455	7	1.6	754	2	A56619	female sterile hom	528	7	1.6	1205	2	AH2486	hypothetical prote
456	7	1.6	759	2	B83474	probable type II s	529	7	1.6	1208	2	T23467	hypothetical prote
457	7	1.6	760	1	S07896	transcription fact	530	7	1.6	1212	2	T44236	hypothetical prote
458	7	1.6	781	1	TVFFDF	protein kinase Dra	531	7	1.6	1215	2	T44051	hypothetical prote
459	7	1.6	781	2	H87531	methy1-accepting c	532	7	1.6	1215	2	IS2882	autautigen - huma
460	7	1.6	781	2	S37032	gene IL5 protein -	533	7	1.6	1217	2	S52714	sericinB - silkw
461	7	1.6	786	2	G85073	probable myosin-li	534	7	1.6	1218	2	J50069	hypothetical p1 op
462	7	1.6	788	2	C84616	similar to mammali	535	7	1.6	1237	2	A34598	ecdysone-induced p
463	7	1.6	788	2	JS0747	regulatory protein	536	7	1.6	1242	2	S14201	probable adenylate
464	7	1.6	795	2	T52516	hypothetical prote	537	7	1.6	1249	2	T26294	hypothetical prote
465	7	1.6	798	2	T21369	hypothetical prote	538	7	1.6	1268	2	G85154	hypothetical prote
466	7	1.6	799	2	T02456	protein kinase hom	539	7	1.6	1269	2	S35366	furin (EC 3.4.21.7
467	7	1.6	806	2	F69899	phage-related pre-	540	7	1.6	1325	1	S73723	probable lipoprote

541	7	1.6	1335	2	A82494	TagA-related prote	614	71	2	T32501	hypothetical prote
542	7	1.6	1361	2	C71403	hypothetical 15.1K	615	71	2	T29977	hypothetical prote
543	7	1.6	1367	1	IGHUR1	insulin-like growt	616	72	2	B90762	hypothetical prote
544	7	1.6	1371	2	A33837	insulin-like growt	617	73	2	T34599	hypothetical prote
545	7	1.6	1394	2	B34598	ecdysone-induced p	618	75	2	D95085	hypothetical prote
546	7	1.6	1403	2	S64142	hypothetical prote	619	75	2	E86841	hypothetical prote
547	7	1.6	1411	2	T48529	hypothetical prote	620	76	2	H0517	ig heavy chain V-A
548	7	1.6	1433	2	S54587	Cat8 protein - yea	621	76	2	D82844	carbon storage reg
549	7	1.6	1436	2	S05979	probable PPE prote	622	77	2	A82966	hypothetical prote
550	7	1.6	1443	2	S05979	steroid hormone re	623	80	2	T10550	hypothetical prote
551	7	1.6	1464	2	T13716	bazooka gene prote	624	81	2	A49736	collagen alpha 3(I
552	7	1.6	1487	2	T02850	hypothetical prote	625	81	2	A95319	SyrA protein invol
553	7	1.6	1489	2	D70807	hypothetical prote	626	82	2	T52378	probable transport
554	7	1.6	1538	2	H70846	hypothetical glyci	627	82	2	T33088	hypothetical prote
555	7	1.6	1584	2	T18276	hypothetical glyci	628	82	2	AF3259	hypothetical prote
556	7	1.6	1612	2	JC5210	protein-tyrosine k	629	82	2	AH2065	hypothetical prote
557	7	1.6	1616	2	T17884	DNA (cytosine-5-) -	630	83	2	G82744	hypothetical prote
558	7	1.6	1677	2	T43021	S-layer protein -	631	85	2	T07090	metallothionein-II
559	7	1.6	1718	2	T14603	vitellogenin precu	632	85	2	T16739	hypothetical prote
560	7	1.6	1726	2	T30810	hypothetical prote	633	86	2	AI2732	conserved hypothet
561	7	1.6	1741	2	T13610	chromatin structur	634	86	2	C97514	hypothetical prote
562	7	1.6	1768	2	T13349	parallel sister ch	635	88	1	WMAD9	hypothetical prote
563	7	1.6	1777	2	T34369	hypothetical prote	636	89	2	E87288	early E1B 9K prote
564	7	1.6	1782	2	S45289	hypothetical prote	637	90	2	C69480	ribosomal protein
565	7	1.6	1791	2	T02345	vitellogenin precu	638	90	2	S00060	phospholipid trans
566	7	1.6	1839	1	OYBYK	hypothetical prote	639	91	2	T31244	hypothetical prote
567	7	1.6	1842	2	T43409	adenylate cyclase	640	92	2	S52277	hypothetical prote
568	7	1.6	1842	2	T38781	probable fatty-aci	641	94	2	C32529	ig lambda chain V
569	7	1.6	1912	2	T29088	fatty acid synthas	642	95	2	PH0864	ig kappa chain V r
570	7	1.6	1969	2	T08875	vitellogenin I pre	643	95	2	E83065	hypothetical prote
571	7	1.6	1970	2	T03284	histidine kinase h	644	96	2	S36060	hypothetical prote
572	7	1.6	2023	2	T13154	myoblast city prot	645	96	2	AG2795	conserved hypothet
573	7	1.6	2038	2	A43742	polycarb protein e	646	96	2	G97574	hypothetical 11.0K
574	7	1.6	2061	2	T13751	female sterile hom	647	98	2	S26933	ig heavy chain V r
575	7	1.6	2064	2	G82562	transcription fact	648	99	2	SL4881	hypothetical prote
576	7	1.6	2174	2	E95365	bacteriocin XP2407	649	100	2	T04807	hypothetical prote
577	7	1.6	2182	2	T28634	hypothetical glyci	650	100	2	A72572	hypothetical prote
578	7	1.6	2406	2	A54148	variant-specific s	651	101	2	I57492	SMW3 protein homol
579	7	1.6	2515	2	S47008	odx protein - fru	652	101	2	C90564	hypothetical prote
580	7	1.6	2528	2	T20719	tenascin-like prot	653	101	2	E72698	lipoprotein (impor
581	7	1.6	2528	2	T20719	hypothetical prote	654	101	2	G75188	hypothetical prote
582	7	1.6	2738	2	E88320	hypothetical prote	655	102	2	C81002	probable periplasm
583	7	1.6	2946	2	T15840	protein F07A11.6 l	656	102	2	E72482	hypothetical prote
584	7	1.6	3016	2	S77300	hypothetical prote	657	103	2	S08462	ig heavy chain V r
585	7	1.6	3078	2	T28432	variant-specific s	658	104	1	KVRBXP	ig kappa chain V r
586	7	1.6	3190	2	T13828	CREB-binding prote	659	104	2	JC4190	holotricin 3 precu
587	7	1.6	3396	2	T22813	hypothetical prote	660	105	1	A46264	thioredoxin 1 - sl
588	7	1.6	13288	2	T03099	mucin, submaxillar	661	105	2	S49533	anti-Sm antibody V
589	6	1.4	15	2	E56978	collagen alpha 2(X	662	105	2	S44838	K02D10.3 protein -
590	6	1.4	28	2	PQ0263	dnak-type molecula	663	105	2	A42694	homeodomain protei
591	6	1.4	29	2	A41683	hyaluronate recept	664	106	1	L4HUKN	ig lambda chain V-
592	6	1.4	42	2	A35494	scatter protein 90	665	106	2	S40091	ig light chain - m
593	6	1.4	47	2	E32529	ig lambda chain V	666	107	1	ERADT1	early EJA 12.5K pr
594	6	1.4	47	2	H90945	hypothetical prote	667	107	2	C72766	hypothetical prote
595	6	1.4	47	2	C85794	hypothetical prote	668	107	2	G83348	hypothetical prote
596	6	1.4	47	2	B64944	hypothetical prote	669	107	2	B85356	glycine-rich prote
597	6	1.4	48	2	T14521	H+-transporting tw	670	108	1	K1HUHU	ig kappa chain V-I
598	6	1.4	52	2	S69113	collagen alpha 3(I	671	108	1	L3HUSH	ig lambda chain V-
599	6	1.4	53	2	S12520	core protein A1 -	672	108	2	S38498	ig lambda chain -
600	6	1.4	53	2	H84193	hypothetical prote	673	108	2	S47184	ig lambda chain -
601	6	1.4	56	2	T02946	hypothetical prote	674	108	2	PS0073	ig kappa chain V r
602	6	1.4	59	2	F69040	hypothetical prote	675	108	2	C72777	hypothetical prote
603	6	1.4	60	1	WZV2A7	5K HindIII-C prote	676	108	2	B72586	hypothetical prote
604	6	1.4	63	2	S26796	ig heavy chain V r	677	109	2	S19663	ig lambda chain V
605	6	1.4	63	2	C83524	probable cold-shoc	678	109	2	F41151	ig kappa chain V r
606	6	1.4	63	2	H70930	probable lppr prot	679	109	2	G72473	hypothetical prote
607	6	1.4	64	2	FC1237	peptidylprolyl iso	680	110	1	R6BY24	60s acidic ribosom
608	6	1.4	64	2	A86333	hypothetical prote	681	110	1	S40402	protein-export pro
609	6	1.4	66	2	S22529	hypothetical prote	682	110	2	S19672	ig lambda chain V
610	6	1.4	67	2	T17658	cold-regulated pro	683	110	2	S36272	ig lambda chain V
611	6	1.4	70	2	T23415	hypothetical prote	684	110	2	A85981	protein export mem
612	6	1.4	70	2	T26824	hypothetical prote	685	110	2	AD0902	protein-export mem
613	6	1.4	70	2	T32870	hypothetical prote	686	110	2	F91135	protein-export pro

687	6	1.4	110	2	S16496	hypothetical prote	760	6	1.4	133	2	A28565	Ig lambda chain pr
688	6	1.4	110	2	B70601	hypothetical prote	761	6	1.4	133	2	B86754	prophage p12 prote
689	6	1.4	111	2	S69911	Ig V-D-J region (R	762	6	1.4	133	2	D86175	hypothetical prote
690	6	1.4	111	2	F82962	hypothetical prote	763	6	1.4	133	2	C86473	arabinogalactan-pr
691	6	1.4	113	2	S43583	F26F3.3 protein -	764	6	1.4	135	2	AB3626	nr1 protein (lmpo
692	6	1.4	113	2	H84725	hypothetical prote	765	6	1.4	135	2	S48141	hypoglycemic hormo
693	6	1.4	113	2	S33779	hypothetical prote	766	6	1.4	135	2	S48142	hypoglycemic hormo
694	6	1.4	113	2	G88947	protein C39F7.3 fi	767	6	1.4	135	2	F83611	hypothetical prote
695	6	1.4	113	2	G95390	protein [imported	768	6	1.4	136	2	T02870	globulin 2 precurs
696	6	1.4	114	2	B45036	Pur beta - human (769	6	1.4	136	2	S37924	hypothetical prote
697	6	1.4	114	2	S44112	Ig heavy chain V r	770	6	1.4	136	2	T31126	hypothetical prote
698	6	1.4	115	2	S13726	Ig lambda chain V	771	6	1.4	136	2	C55291	hypothetical prote
699	6	1.4	116	1	HVRK	Ig heavy chain pre	772	6	1.4	137	2	T04930	glycine-rich cell
700	6	1.4	116	1	Z6BPIK	coat protein D - p	773	6	1.4	137	2	G72666	hypothetical prote
701	6	1.4	116	2	S45909	probable membrane	774	6	1.4	137	2	B82998	hypothetical prote
702	6	1.4	116	2	T48427	hypothetical prote	775	6	1.4	138	2	S24106	envelope protein -
703	6	1.4	117	2	S24658	Ig heavy chain V r	776	6	1.4	138	2	S24082	envelope protein -
704	6	1.4	117	2	S24656	Ig heavy chain V r	777	6	1.4	138	2	JT0593	hypothetical 15K p
705	6	1.4	117	2	S24656	Ig heavy chain V r	778	6	1.4	138	2	C87389	hypothetical prote
706	6	1.4	117	2	F70881	Ig heavy chain V r	779	6	1.4	139	2	B33910	sal homeotic prote
707	6	1.4	117	2	S69301	hypothetical prote	780	6	1.4	139	2	H89287	protein par-1 (lmp
708	6	1.4	117	2	S69471	hypothetical prote	781	6	1.4	139	2	F84701	hypothetical prote
709	6	1.4	117	2	S69471	hypothetical prote	782	6	1.4	139	2	T03372	high mobility grou
710	6	1.4	118	2	A32529	Ig lambda chain pr	783	6	1.4	140	2	JC4607	hydrophobin 1 prec
711	6	1.4	118	2	A72654	hypothetical prote	784	6	1.4	140	2	A64886	ydar protein - Esc
712	6	1.4	118	2	F87447	hypothetical prote	785	6	1.4	141	2	C32536	T-cell receptor al
713	6	1.4	119	2	S24655	Ig heavy chain V r	786	6	1.4	141	2	H86609	kinase [imported]
714	6	1.4	119	2	S24657	Ig heavy chain V r	787	6	1.4	141	2	T17493	citrate utilizatio
715	6	1.4	119	2	S24659	Ig heavy chain V r	788	6	1.4	141	2	A27249	vitelline membrane
716	6	1.4	119	2	PH1533	Ig H chain V regio	789	6	1.4	141	2	T46427	hypothetical prote
717	6	1.4	119	2	S30526	Ig lambda chain V	790	6	1.4	142	1	HARB	hemoglobin alpha c
718	6	1.4	119	2	A97825	S08 ribosomal prot	791	6	1.4	142	2	S00262	sal homeotic prote
719	6	1.4	119	2	D71671	ribosomal protein	792	6	1.4	142	2	C33910	sal homeotic prote
720	6	1.4	120	2	S11090	FK506-binding prot	793	6	1.4	142	2	F70517	hypothetical prote
721	6	1.4	120	2	S24654	Ig heavy chain V r	794	6	1.4	143	2	T12144	hypothetical prote
722	6	1.4	120	2	PS0055	Ig lambda chain pr	795	6	1.4	143	2	G72492	hypothetical prote
723	6	1.4	120	2	PS0056	Ig lambda chain pr	796	6	1.4	144	2	T15047	RNA binding protei
724	6	1.4	120	2	A54256	Ig heavy chain V r	797	6	1.4	144	2	T18867	hypothetical prote
725	6	1.4	120	2	A34871	Ig kappa chain V r	798	6	1.4	144	2	F72556	hypothetical prote
726	6	1.4	120	2	T51754	endo-xyloglucan tr	799	6	1.4	144	2	T25028	hypothetical prote
727	6	1.4	120	2	A31337	hypothetical prote	800	6	1.4	144	2	S68454	SKB7 protein homol
728	6	1.4	121	2	S24660	Ig heavy chain V r	801	6	1.4	145	2	C83639	hypothetical prote
729	6	1.4	122	1	R5HG12	ribosomal protein	802	6	1.4	146	2	S02083	Ig lambda chain V-
730	6	1.4	122	2	T48951	hypothetical prote	803	6	1.4	146	2	S71256	ribosomal protein
731	6	1.4	122	2	AD2072	hypothetical prote	804	6	1.4	146	2	C82254	conserved hypotet
732	6	1.4	123	2	S40378	Ig kappa chain - h	805	6	1.4	146	2	AP2642	conserved hypotet
733	6	1.4	124	1	NRGPA	pancreatic ribonuc	806	6	1.4	147	1	VBHU	transthyretin prec
734	6	1.4	124	1	NROZ	pancreatic ribonuc	807	6	1.4	147	1	VBRT	transthyretin prec
735	6	1.4	124	1	TVVPBJ	small T antigen -	808	6	1.4	147	1	VBRT	transthyretin prec
736	6	1.4	124	2	S24653	Ig heavy chain V r	809	6	1.4	147	2	S05320	transthyretin prec
737	6	1.4	124	2	JS0515	hypothetical 12.4K	810	6	1.4	147	2	C84049	hypothetical prote
738	6	1.4	124	2	T19000	hypothetical prote	811	6	1.4	147	2	B69040	hypothetical prote
739	6	1.4	124	2	AE2521	transposase alr734	812	6	1.4	148	2	S07196	meiosis and sporu
740	6	1.4	125	2	S72665	Ig V-D-J region (R	813	6	1.4	148	2	E87609	hypothetical prote
741	6	1.4	125	2	H90062	conserved hypotet	814	6	1.4	148	2	S10238	leghemoglobin glb3
742	6	1.4	125	2	T49356	hypothetical prote	815	6	1.4	148	2	E95384	protein [imported
743	6	1.4	127	1	VERB	transthyretin - ra	816	6	1.4	149	2	A83696	nitrogen fixation
744	6	1.4	127	2	S40380	Ig kappa chain V-J	817	6	1.4	149	2	S67473	transthyretin prec
745	6	1.4	127	2	PH1420	Ig heavy chain V r	818	6	1.4	149	2	T23179	hypothetical prote
746	6	1.4	127	2	PH1421	Ig heavy chain V r	819	6	1.4	149	2	F75509	hypothetical prote
747	6	1.4	127	2	S70444	Ig lambda chain pr	820	6	1.4	150	2	S17827	transthyretin prec
748	6	1.4	127	2	AB1063	phage immunity rep	821	6	1.4	150	2	S65955	transthyretin prec
749	6	1.4	127	2	F69377	molybdenum-pterin-	822	6	1.4	150	2	F83061	peptide n-acetyltr
750	6	1.4	127	2	G98316	hypothetical prote	823	6	1.4	150	2	C95233	conserved hypotet
751	6	1.4	128	2	JC1273	ribosomal protein	824	6	1.4	150	2	T21489	hypothetical prote
752	6	1.4	129	2	D71328	probable flagellar	825	6	1.4	150	2	F86299	hypothetical prote
753	6	1.4	129	2	T36916	hypothetical prote	826	6	1.4	150	2	AG3397	hypothetical membr
754	6	1.4	129	2	H72806	probable DNA prima	827	6	1.4	151	2	H69991	hypothetical prote
755	6	1.4	130	2	B32456	Ig kappa chain pre	828	6	1.4	151	2	A69823	hypothetical prote
756	6	1.4	130	2	T22004	hypothetical prote	829	6	1.4	152	2	JC1521	synaptobrevin isof
757	6	1.4	132	2	PL0114	Ig lambda chain pr	830	6	1.4	152	2	A97003	probable beta-D-ga
758	6	1.4	132	2	A55410	Ig light chain V r	831	6	1.4	152	2	G96010	hypothetical expor
759	6	1.4	132	2	S04937	Ig lambda chain pr	832	6	1.4	154	2	AH0704	probable lipoprote

833	6	1.4	154	2	F86437	protein F28K20.12	906	6	1.4	178	1	LGBO	beta-lactoglobulin
834	6	1.4	154	2	E96728	hypothetical prote	907	6	1.4	178	2	G97359	fxsA protein (VC26
835	6	1.4	155	2	T00844	hypothetical prote	908	6	1.4	178	2	AH2577	conserved hypotet
836	6	1.4	155	2	G35266	probable membrane	909	6	1.4	178	2	E83025	conserved hypotet
837	6	1.4	155	2	T72580	hypothetical prote	910	6	1.4	178	2	E86637	protein W09G12.6 l
838	6	1.4	156	2	S41771	glycine-rich RNA-b	911	6	1.4	178	2	F87408	hypothetical prote
839	6	1.4	156	2	E36905	conserved hypotet	912	6	1.4	178	2	T05810	hypothetical prote
840	6	1.4	156	2	T16066	hypothetical prote	913	6	1.4	180	1	LWR21	H+-transporting tw
841	6	1.4	156	2	C84688	probable C2H2-type	914	6	1.4	180	1	LGST	beta-lactoglobulin
842	6	1.4	157	2	S18651	variant surface an	915	6	1.4	180	1	LGSH	beta-lactoglobulin
843	6	1.4	157	2	AH1070	probable membrane	916	6	1.4	180	2	E69024	hypothetical prote
844	6	1.4	157	2	S57603	hypothetical prote	917	6	1.4	180	2	S43791	PBX protein - hum
845	6	1.4	157	2	G97424	hypothetical prote	918	6	1.4	181	2	D81450	aminoacyl-tRNA hyd
846	6	1.4	157	2	A70058	conserved hypotet	919	6	1.4	181	2	E84775	hypothetical prote
847	6	1.4	158	2	S74928	ribosomal protein-	920	6	1.4	181	2	T48241	hypothetical prote
848	6	1.4	158	2	S61953	hrpK protein - Pse	921	6	1.4	181	2	H95863	hypothetical prote
849	6	1.4	158	2	S77877	hypothetical prote	922	6	1.4	181	2	E86819	hypothetical prote
850	6	1.4	159	2	AC1103	7,8-dihydro-6-hydr	923	6	1.4	181	2	C85354	RNase L inhibitor-
851	6	1.4	159	2	AC1465	7,8-dihydro-6-hydr	924	6	1.4	182	1	KRBO2A	keratin, 68K type
852	6	1.4	159	2	F86429	protein F26G16.9 l	925	6	1.4	183	1	PWMT1	H+-transporting tw
853	6	1.4	159	2	T04173	heat shock protein	926	6	1.4	183	1	KNRZG2	glycine-rich cell
854	6	1.4	159	2	T31598	hypothetical prote	927	6	1.4	183	2	S57772	early nodulin GRP3
855	6	1.4	159	2	D87658	hypothetical prote	928	6	1.4	183	2	D45392	orf4 protein - por
856	6	1.4	159	2	T48209	hypothetical prote	929	6	1.4	183	2	E36861	orf4 protein - bel
857	6	1.4	160	2	S30056	major allergen Cor	930	6	1.4	183	2	D71828	hypothetical prote
858	6	1.4	160	2	C83048	hypothetical prote	931	6	1.4	183	2	G64689	hypothetical prote
859	6	1.4	161	2	T07639	pEARL1 protein h	932	6	1.4	183	2	AC2632	hypothetical prote
860	6	1.4	161	2	T46048	hypothetical prote	933	6	1.4	183	2	G97414	hypothetical prote
861	6	1.4	161	2	F86303	hypothetical prote	934	6	1.4	183	2	A11562	B. subtilis Ydfe p
862	6	1.4	161	2	E43719	ureg protein - Pro	935	6	1.4	184	1	LMNT1	H+-transporting tw
863	6	1.4	162	2	C85356	glycine-rich prote	936	6	1.4	184	1	PWSP1	H+-transporting tw
864	6	1.4	162	2	F75339	hypothetical prote	937	6	1.4	184	2	JC2429	activin-A protein
865	6	1.4	163	2	B87656	hypothetical prote	938	6	1.4	184	2	AB1206	hypothetical prote
866	6	1.4	163	2	JC6571	cold-inducible RNA	939	6	1.4	184	2	AB1206	B. subtilis Ydfe p
867	6	1.4	163	2	T23076	hypothetical prote	940	6	1.4	185	2	G97156	probable membrane
868	6	1.4	165	1	KNRZG1	glycine-rich cell	941	6	1.4	185	2	G84671	hypothetical prote
869	6	1.4	166	1	KRBO2B	keratin, 68K type	942	6	1.4	187	2	T45176	conserved hypotet
870	6	1.4	166	2	T10463	glycine-rich prote	943	6	1.4	187	2	G70969	precorrin-6B methy
871	6	1.4	166	2	A33637	Xtvi protein - Afr	944	6	1.4	188	1	G97055	probable 2-amino-4
872	6	1.4	167	2	D87431	single-strand bind	945	6	1.4	188	2	AF1295	phosphoribosylglyc
873	6	1.4	167	2	A87150	tuberculin related	946	6	1.4	188	2	F89876	phosphoribosylglyc
874	6	1.4	167	2	S76890	hypothetical prote	947	6	1.4	188	2	S18956	fix23-4 protein -
875	6	1.4	167	2	H72579	hypothetical prote	948	6	1.4	189	2	JC4072	virulence-associat
876	6	1.4	168	2	F844709	hypothetical prote	949	6	1.4	189	2	T28092	hypothetical prote
877	6	1.4	169	1	S38331	glycine-rich RNA-b	950	6	1.4	189	2	T06555	blue copper-bindin
878	6	1.4	169	2	S30148	glycine-rich prote	951	6	1.4	189	2	A86369	hypothetical prote
879	6	1.4	169	2	F84259	hypothetical prote	952	6	1.4	190	2	S25740	Ig lambda chain -
880	6	1.4	170	2	D87707	hypothetical prote	953	6	1.4	190	2	S12674	ribosomal protein
881	6	1.4	171	2	T27371	peptidylprolyl iso	954	6	1.4	190	2	T00735	hypothetical prote
882	6	1.4	171	2	H84709	probable glycine-r	955	6	1.4	190	2	T46985	hypothetical prote
883	6	1.4	171	2	A11280	hypothetical prote	956	6	1.4	190	2	AI0240	conserved hypotet
884	6	1.4	171	2	H84923	hypothetical prote	957	6	1.4	190	2	H85357	hypothetical prote
885	6	1.4	171	2	S57894	laminin - Hydra vu	958	6	1.4	190	2	A87263	hypothetical prote
886	6	1.4	172	2	S66014	single-stranded DN	959	6	1.4	191	2	S56012	XS-2 protein (homo
887	6	1.4	172	2	T39026	conserved hypotet	960	6	1.4	191	2	H87330	hypothetical prote
888	6	1.4	173	2	JQ1064	glycine-rich prote	961	6	1.4	191	2	F75340	conserved hypotet
889	6	1.4	173	2	H82149	crossover junction	962	6	1.4	192	2	S16572	plastoquinol-plast
890	6	1.4	173	2	A47303	FTZ-F1 steroid rec	963	6	1.4	192	2	AH3643	cytochrome b561 [i
891	6	1.4	174	2	S54979	pancreatitis-assoc	964	6	1.4	192	2	S15930	hypothetical 21.5K
892	6	1.4	174	2	E88274	inositol 1,4,5-tri	965	6	1.4	192	2	E71917	hypothetical prote
893	6	1.4	174	2	E84868	hypothetical prote	966	6	1.4	192	2	D64594	hypothetical prote
894	6	1.4	175	2	T01215	protein kinase hom	967	6	1.4	192	2	F72805	gp49 protein - Myc
895	6	1.4	175	2	PH0261	hypothetical 17.8K	968	6	1.4	193	2	C86334	hypothetical prote
896	6	1.4	176	1	A46606	platelet glycoprot	969	6	1.4	193	2	H90364	hypothetical prote
897	6	1.4	176	2	F81098	endopeptidase Clp	970	6	1.4	194	2	D83175	hypothetical prote
898	6	1.4	176	2	S30147	glycine-rich RNA b	971	6	1.4	194	2	AG3177	Mg(2+) transport A
899	6	1.4	176	2	T40121	outer surface prote	972	6	1.4	195	2	A83031	conserved hypotet
900	6	1.4	176	2	G83369	hypothetical prote	973	6	1.4	195	2	E81903	hypothetical prote
901	6	1.4	176	2	D84369	hypothetical prote	974	6	1.4	195	2	B84603	AtRer1B [imported]
902	6	1.4	177	2	H86710	hypothetical prote	975	6	1.4	195	2	T51628	endoplasmatic reti
903	6	1.4	177	2	F81442	hypothetical prote	976	6	1.4	195	2	AD2782	hypothetical prote
904	6	1.4	177	2	A12177	hypothetical prote	977	6	1.4	195	2	G83170	hypothetical prote
905	6	1.4	177	2	I49069	A+U-rich RNA-bind	978	6	1.4	195	2	T03245	G-box binding fact

979	6	1.4	196	2	B28964	platelet-derived g	1052	6	1.4	215	2	C95352	hypothetical prote
980	6	1.4	196	2	A40623	heat shock protein	1053	6	1.4	215	2	G87554	hypothetical prote
981	6	1.4	196	2	E97561	hypothetical prote	1054	6	1.4	216	1	T1APX2	tail fiber protein
982	6	1.4	197	2	S46928	phytochrome - Char	1055	6	1.4	216	2	S61545	transferrin bindin
983	6	1.4	197	2	T03442	glycine-rich prote	1056	6	1.4	216	2	S61544	transferrin bindin
984	6	1.4	197	2	F96799	Similar to 'MADS b	1057	6	1.4	216	2	A11118	dihydroxyacetone k
985	6	1.4	198	2	T49955	40S ribosomal prot	1058	6	1.4	216	2	AF1478	dihydroxyacetone k
986	6	1.4	199	2	T36594	probable single-st	1059	6	1.4	216	2	F70073	hypothetical prote
987	6	1.4	199	2	S41316	coat protein - cuc	1060	6	1.4	216	2	T25025	hypothetical prote
988	6	1.4	200	2	D82698	DNA repair system	1061	6	1.4	216	2	G82532	outer membrane lip
989	6	1.4	200	2	D83997	hypothetical prote	1062	6	1.4	217	2	S74394	phosphoribosylglyc
990	6	1.4	200	2	G86214	protein T6D22.4 [i	1063	6	1.4	217	2	T45364	ribosomal protein
991	6	1.4	200	2	C49529	RNA-directed RNA p	1064	6	1.4	217	2	H70641	probable ribosomal
992	6	1.4	200	2	AD3320	conserved hypothet	1065	6	1.4	217	2	T27524	hypothetical prote
993	6	1.4	201	2	F84596	glycine-rich prote	1066	6	1.4	217	2	H85433	homeodomain protei
994	6	1.4	201	2	D82779	hypothetical prote	1067	6	1.4	218	2	A87142	50S ribosomal prot
995	6	1.4	201	2	T46295	hypothetical prote	1068	6	1.4	218	2	A97237	uncharacterized co
996	6	1.4	201	2	G01204	twist protein homo	1069	6	1.4	218	2	T47889	hypothetical prote
997	6	1.4	201	2	G95852	conserved hypothet	1070	6	1.4	219	2	S71472	endo-1,4-beta-xyla
998	6	1.4	201	2	F95370	hypothetical prote	1071	6	1.4	219	2	A64864	probable 2-hydroxy
999	6	1.4	202	2	E72466	hypothetical prote	1072	6	1.4	219	2	C85696	probable isomerase
1000	6	1.4	203	1	JQ1061	hypothetical prote	1073	6	1.4	219	2	C90838	probable isomerase
1001	6	1.4	203	1	I40890	sarcosine oxidase	1074	6	1.4	219	2	T06302	hypothetical prote
1002	6	1.4	204	2	A81844	endopeptidase Clp	1075	6	1.4	219	2	AH2953	conserved hypothet
1003	6	1.4	204	2	G70029	hypothetical prote	1076	6	1.4	220	2	I55963	Lyt-2.1 lymphocyte
1004	6	1.4	204	2	S50723	hypothetical prote	1077	6	1.4	220	2	B49736	collagen alpha 3(I
1005	6	1.4	204	2	T29489	hypothetical prote	1078	6	1.4	220	2	T50624	hypothetical prote
1006	6	1.4	204	2	T13208	minor capsid prote	1079	6	1.4	220	2	S30977	gene 32 protein -
1007	6	1.4	205	2	T31489	hypothetical prote	1080	6	1.4	221	2	T52622	probable peptidylp
1008	6	1.4	205	2	AF3046	hypothetical prote	1081	6	1.4	221	2	E97834	ABC transporter AT
1009	6	1.4	205	2	D90455	hypothetical prote	1082	6	1.4	221	2	F71676	glutamine transpor
1010	6	1.4	206	2	D85481	hypothetical prote	1083	6	1.4	222	1	CE8CFE	cell division ATP-
1011	6	1.4	206	2	D90630	hypothetical prote	1084	6	1.4	222	2	H83528	phosphoribosylamin
1012	6	1.4	206	2	T34979	probable lipoprote	1085	6	1.4	222	2	A27270	myosin light chain
1013	6	1.4	206	2	F84459	hypothetical prote	1086	6	1.4	222	2	AH0991	cell division ATP-
1014	6	1.4	206	2	I53066	gene M-twist prote	1087	6	1.4	222	2	H86013	cell division ATP-
1015	6	1.4	206	2	C71032	hypothetical prote	1088	6	1.4	222	2	H91167	cell division ATP-
1016	6	1.4	207	2	AE1925	cytochrome c oxida	1089	6	1.4	222	2	AD0464	cell division ATP-
1017	6	1.4	207	2	T51296	phosphoribosylglyc	1090	6	1.4	222	2	T29457	probable two-compo
1018	6	1.4	207	2	T07381	glycine-rich prote	1091	6	1.4	223	1	CSNCM	peptidylprolyl iso
1019	6	1.4	207	2	F84563	hypothetical prote	1092	6	1.4	223	2	T21646	hypothetical prote
1020	6	1.4	208	2	T04884	hypothetical prote	1093	6	1.4	223	2	F98239	hypothetical prote
1021	6	1.4	209	2	T35041	hypothetical prote	1094	6	1.4	224	2	G72746	hypothetical prote
1022	6	1.4	209	2	T17551	methytransferase-	1095	6	1.4	225	2	T35127	hypothetical prote
1023	6	1.4	209	2	B82501	hypothetical prote	1096	6	1.4	225	2	S54391	prohead proteinase
1024	6	1.4	209	2	T20155	hypothetical prote	1097	6	1.4	225	2	F96742	hypothetical prote
1025	6	1.4	209	2	C70630	hypothetical prote	1098	6	1.4	225	2	C85475	hypothetical prote
1026	6	1.4	209	2	JE0154	mitochondrial inne	1099	6	1.4	226	2	A69904	hypothetical prote
1027	6	1.4	210	2	G95328	ABC transporter, A	1100	6	1.4	226	2	C97488	hypothetical 21.6K
1028	6	1.4	210	2	F83450	hypothetical prote.	1101	6	1.4	226	2	T43814	conserved hypothet
1029	6	1.4	210	2	E75315	probable c-type cy	1102	6	1.4	227	2	A64129	probable ABC-type
1030	6	1.4	210	2	C98093	hypothetical prote	1103	6	1.4	227	2	H83288	probable ATP-bindi
1031	6	1.4	210	2	A97693	probable acetyltra	1104	6	1.4	227	2	D83271	probable ATP-bindi
1032	6	1.4	210	2	AE2970	conserved hypothet	1105	6	1.4	227	2	F96964	ABC transporter, A
1033	6	1.4	210	2	AF2918	acetyltransferase	1106	6	1.4	228	2	S25312	plastoquinol-plast
1034	6	1.4	210	2	F98112	hypothetical prote	1107	6	1.4	228	2	C26599	clathrin light cha
1035	6	1.4	211	1	FFHUG1	platelet-derived g	1108	6	1.4	228	2	JC7761	dendritic cell-der
1036	6	1.4	211	2	D96507	hypothetical prote	1109	6	1.4	228	2	G64856	probable ABC-type
1037	6	1.4	212	1	E71111	hypothetical prote	1110	6	1.4	228	2	G90815	hypothetical prote
1038	6	1.4	212	2	A40047	peptidylprolyl iso	1111	6	1.4	228	2	C85675	hypothetical prote
1039	6	1.4	212	2	B95140	uridine kinase [im	1112	6	1.4	228	2	A82147	ABC transporter, A
1040	6	1.4	212	2	A99008	uridine kinase (EC	1113	6	1.4	229	2	S37101	ATAF1 protein - Ar
1041	6	1.4	212	2	AC0074	probable tellurium	1114	6	1.4	231	2	C81107	ABC transporter, A
1042	6	1.4	212	2	I40603	hypothetical prote	1115	6	1.4	231	2	B86154	T6A9.7 protein - A
1043	6	1.4	212	2	AG1050	conserved hypothet	1116	6	1.4	231	2	C81909	probable ABC-trans
1044	6	1.4	213	2	B83420	endopeptidase Clp	1117	6	1.4	231	2	A11262	ABC transporter, A
1045	6	1.4	213	2	S68213	Ig heavy chain (Ma	1118	6	1.4	231	2	AC1625	ABC transporter, A
1046	6	1.4	213	2	H83552	conserved hypothet	1119	6	1.4	232	2	S17399	Ig lambda chain pr
1047	6	1.4	214	1	KNNT25	glycine-rich prote	1120	6	1.4	232	2	D72037	macromolecule tran
1048	6	1.4	214	1	ABBYD	ADE8 protein - yea	1121	6	1.4	232	2	G86588	macromolecule tran
1049	6	1.4	214	2	G84361	hypothetical prote	1122	6	1.4	232	2	F84798	hypothetical prote
1050	6	1.4	214	2	T23593	hypothetical prote	1123	6	1.4	233	2	S25748	Ig lambda chain -
1051	6	1.4	215	2	A86437	F2K820.7 protein -	1124	6	1.4	233	2	S62063	H+-exporting ATPas

1125	6	1.4	233	2	T00566	hypothenical prote	1198	6	1.4	249	1	R3RTS6	ribosomal protein
1126	6	1.4	233	2	E71515	hypothenical prote	1199	6	1.4	249	2	T09297	topoplast intrinsi
1127	6	1.4	233	2	E64412	hypothenical prote	1200	6	1.4	249	2	T25643	hypothenical prote
1128	6	1.4	233	2	F72542	hypothenical prote	1201	6	1.4	249	2	S41374	single chain Fv an
1129	6	1.4	233	2	AC0645	hypothenical prote	1202	6	1.4	249	2	S76327	hypothenical prote
1130	6	1.4	234	1	S15102	ABC transporter At	1203	6	1.4	249	2	A41497	36k antigen pra -
1131	6	1.4	234	2	A39956	eosinophil major b	1204	6	1.4	249	2	T20790	hypothenical prote
1132	6	1.4	234	2	C75639	Ig lambda chain pr	1205	6	1.4	250	2	T45893	hypothenical prote
1133	6	1.4	234	2	T46203	transcription fact	1206	6	1.4	251	1	B60492	homeotic protein H
1134	6	1.4	234	2	T49448	hypothenical prote	1207	6	1.4	251	2	S25186	probable dehydroge
1135	6	1.4	234	2	AF0198	lipoprotein releas	1208	6	1.4	251	2	D70215	hypothenical prote
1136	6	1.4	235	2	S25719	Ig lambda chain -	1209	6	1.4	251	2	T32200	hypothenical prote
1137	6	1.4	235	2	C64744	YaeB protein - Esc	1210	6	1.4	252	1	S01821	glycine-rich prote
1138	6	1.4	235	2	E90653	hypothenical prote	1211	6	1.4	252	2	S50217	multidrug resistan
1139	6	1.4	235	2	B85504	hypothenical prote	1212	6	1.4	252	2	F84607	hypothenical prote
1140	6	1.4	235	2	AG0532	conserved hypotet	1213	6	1.4	252	2	T45737	hypothenical prote
1141	6	1.4	235	2	AD3274	uroporphyrinogen-I	1214	6	1.4	252	2	S31022	gene 77 protein -
1142	6	1.4	236	2	B65088	hypothenical prote	1215	6	1.4	252	2	T03160	capsid protein - a
1143	6	1.4	236	2	H91115	2,5-diketo-D-gluco	1216	6	1.4	253	2	AH3280	histidine/orntin
1144	6	1.4	236	2	H85960	probable enzyme yq	1217	6	1.4	254	2	T44458	hypothenical prote
1145	6	1.4	236	2	C75516	hypothenical prote	1218	6	1.4	254	2	H84017	hypothenical prote
1146	6	1.4	236	2	F75443	probable hydrolase	1219	6	1.4	254	2	E98329	hypothenical prote
1147	6	1.4	236	2	F75375	nodulin 21-related	1220	6	1.4	254	2	T41477	hypothenical prote
1148	6	1.4	237	2	A45587	lectin - Dioclea l	1221	6	1.4	254	2	H97081	proline/glycine be
1149	6	1.4	237	2	JU0176	lectin alpha chain	1222	6	1.4	254	2	A31488	hypothenical prote
1150	6	1.4	238	2	T40820	proline-rich prote	1223	6	1.4	255	2	B84777	amino acid ABC tra
1151	6	1.4	238	2	T34710	hypothenical prote	1224	6	1.4	255	2	F69962	probable amino aci
1152	6	1.4	239	2	T40555	hypothenical prote	1225	6	1.4	255	2	E95931	histidine transpor
1153	6	1.4	239	2	AC0811	probable amidotran	1226	6	1.4	255	2	D83281	hypothenical prote
1154	6	1.4	239	2	D85073	probable polyprote	1227	6	1.4	255	2	C89936	hypothenical prote
1155	6	1.4	240	2	AB1905	phosphoribosylglyc	1228	6	1.4	255	2	A86457	probable peptide c
1156	6	1.4	240	2	B24264	proline-rich prote	1229	6	1.4	255	2	A35026	filaggrin A - mous
1157	6	1.4	240	2	S36797	lectin BMA - Bowri	1230	6	1.4	256	1	TRFF	trypan-like prote
1158	6	1.4	240	2	D71272	hypothenical prote	1231	6	1.4	256	2	D82147	amino acid ABC tra
1159	6	1.4	240	2	A81837	probable dnaJ-fami	1232	6	1.4	256	2	T46871	C-8 sterol isomera
1160	6	1.4	240	2	T20791	hypothenical prote	1233	6	1.4	256	2	S13338	hypothenical prote
1161	6	1.4	240	2	B40520	homeotic protein 1	1234	6	1.4	256	2	B83612	hypothenical prote
1162	6	1.4	241	2	H86719	hypothenical prote	1235	6	1.4	256	2	AC1561	conserved hypotet
1163	6	1.4	241	2	G95928	transcription regu	1236	6	1.4	257	2	G42600	ABC-type transport
1164	6	1.4	242	2	B81719	conserved hypotet	1237	6	1.4	257	2	AB3231	hypothenical prote
1165	6	1.4	242	2	T34767	hypothenical prote	1238	6	1.4	257	2	H65002	histidine transpor
1166	6	1.4	243	2	A53381	hypothenical prote	1239	6	1.4	257	2	G85871	ATP-binding compon
1167	6	1.4	243	2	G97161	conserved membrane	1240	6	1.4	257	2	F91027	ATP-binding compon
1168	6	1.4	243	2	G95928	hypothenical prote	1241	6	1.4	257	2	B69213	protein-export mem
1169	6	1.4	244	2	F64247	triose-phosphate i	1242	6	1.4	257	2	C84890	hypothenical prote
1170	6	1.4	244	2	AD1225	cobalamin biosynth	1243	6	1.4	257	2	T21029	hypothenical prote
1171	6	1.4	244	2	AF1578	cobalamin biosynth	1244	6	1.4	257	2	E83001	probable ATP-bind
1172	6	1.4	244	2	H71873	hypothenical prote	1245	6	1.4	257	2	A96908	ABC transporter, A
1173	6	1.4	245	1	KYBOA	chymotrypsin (EC 3	1246	6	1.4	258	1	QREBPT	histidine transpor
1174	6	1.4	245	1	KYBOB	chymotrypsin (EC 3	1247	6	1.4	258	2	C70885	probable dehydroge
1175	6	1.4	245	2	AB0499	ABC transporter pe	1248	6	1.4	258	2	AE0800	histidine transpor
1176	6	1.4	245	2	C65206	thiF protein - Esc	1249	6	1.4	258	2	AD2867	hypothenical prote
1177	6	1.4	245	2	A86091	thiamin biosynthes	1250	6	1.4	258	2	A97644	hypothenical prote
1178	6	1.4	245	2	C91243	thiamin biosynthes	1251	6	1.4	259	1	WMMS28	complement factor
1179	6	1.4	246	2	A29523	T-cell surface gly	1252	6	1.4	259	2	T15126	hypothenical prote
1180	6	1.4	246	2	T46446	hypothenical prote	1253	6	1.4	259	2	T35284	hypothenical prote
1181	6	1.4	246	2	H97932	glutamine ABC tran	1254	6	1.4	259	2	T49291	hypothenical prote
1182	6	1.4	246	2	D95052	amino acid ABC tra	1255	6	1.4	259	2	S55884	CCH finger protei
1183	6	1.4	246	2	S37959	hypothenical prote	1256	6	1.4	259	2	S01704	merozoite surface
1184	6	1.4	246	2	B96707	hypothenical prote	1257	6	1.4	260	2	H97357	stage 0 sporulatio
1185	6	1.4	246	2	T49305	hypothenical prote	1258	6	1.4	260	2	B96686	probable C2H2-type
1186	6	1.4	246	2	T20792	hypothenical prote	1259	6	1.4	261	2	C84584	probable cAMP-depe
1187	6	1.4	247	1	RMWST2	T-cell surface gly	1260	6	1.4	261	2	E75335	conserved hypotet
1188	6	1.4	247	1	JQ1550	coat protein - Pan	1261	6	1.4	261	2	T40482	apoptosis specific
1189	6	1.4	247	2	T32198	hypothenical prote	1262	6	1.4	261	2	D97334	metallo-beta-lacta
1190	6	1.4	247	2	A34954	T-cell surface gly	1263	6	1.4	261	2	E86354	hypothenical prote
1191	6	1.4	247	2	G64341	hypothenical prote	1264	6	1.4	262	2	AD1239	phosphatidate cyti
1192	6	1.4	247	2	D84448	probable ankryin f	1265	6	1.4	262	2	AH1601	phosphatidate cyti
1193	6	1.4	248	2	C83431	type III export pr	1266	6	1.4	262	2	F87480	indole-3-glycerol
1194	6	1.4	248	2	B95334	probable transcrip	1267	6	1.4	262	2	C41044	octopine transpor
1195	6	1.4	249	1	S05398	granaticin polyket	1268	6	1.4	262	2	T27381	hypothenical prote
1196	6	1.4	249	1	R3H06	ribosomal protein	1269	6	1.4	263	2	B83025	probable enoyl-CoA
1197	6	1.4	249	1	R3M56	ribosomal protein	1270	6	1.4	263	2	E70215	hypothenical prote

1417 6 1.4 289 2 T49154 DNA-binding WRKY-1
1418 6 1.4 289 2 G83029 hypothetical prote
1419 6 1.4 289 2 G64105 transferrin-bindin
1420 6 1.4 289 2 JC5938 thioedoxin-like p
1421 6 1.4 289 2 E86148 TING.12 protein -
1422 6 1.4 289 2 A98217 hemk protein homol
1423 6 1.4 289 2 A13069 protoporphyrihogen
1424 6 1.4 289 2 A84790 probable RNA-bindi
1425 6 1.4 290 2 D82233 conserved hypothet
1426 6 1.4 290 2 T21846 hypothetical prote
1427 6 1.4 290 2 T21198 hypothetical prote
1428 6 1.4 291 1 S31435 glycine-rich prote
1429 6 1.4 291 2 AH3074 short-chain dehydr
1430 6 1.4 291 2 A96212 probable short-cha
1431 6 1.4 291 2 B70337 aspartate carbamoy
1432 6 1.4 291 2 S73501 probable UTP-gluco
1433 6 1.4 291 2 F75172 hypothetical prote
1434 6 1.4 292 2 T06201 xyloglucan endo-1,
1435 6 1.4 292 2 T04514 xyloglucan endo-1,
1436 6 1.4 292 2 T34997 lysR-type transcri
1437 6 1.4 292 2 F98340 hypothetical prote
1438 6 1.4 292 2 AD2942 conserved hypothet
1439 6 1.4 292 2 AE0419 probable ABC trans
1440 6 1.4 293 1 WMBP11 gene 11 protein -
1441 6 1.4 293 1 WMBP09 succinyl-CoA synth
1442 6 1.4 293 2 AB2295 hypothetical prote
1443 6 1.4 293 2 F70724 lysR-family transc
1444 6 1.4 293 2 AF0475 hypothetical prote.
1445 6 1.4 293 2 B82988 hypothetical prote
1446 6 1.4 294 2 S72897 pyrroline-5-carbox
1447 6 1.4 294 2 G84949 hypothetical prote
1448 6 1.4 294 2 T46195 hypothetical prote
1449 6 1.4 294 2 D70525 probable beta-1 -
1450 6 1.4 294 2 T31946 hypothetical prote
1451 6 1.4 294 2 A55477 survival motor neu
1452 6 1.4 294 2 E81420 probable flagellar
1453 6 1.4 295 2 G70745 probable proc prot
1454 6 1.4 295 2 S49261 ornithine carbamoy
1455 6 1.4 295 2 B82109 kinase, GHMP famil
1456 6 1.4 295 2 T02575 adenylate kinase h
1457 6 1.4 295 2 A54962 hypothetical prote
1458 6 1.4 296 2 A36366 enhancer-binding p
1459 6 1.4 296 2 H83480 cytochrome o ubiq
1460 6 1.4 296 2 T48401 histone deacetylase
1461 6 1.4 296 2 AH1173 conserved hypothet
1462 6 1.4 297 2 A35914 transcription fact
1463 6 1.4 297 2 T51005 hypothetical prote
1464 6 1.4 298 2 A49934 hypothetical prote
1465 6 1.4 298 2 E87134 conserved hypothet
1466 6 1.4 298 2 C96690 unknown protein F2
1467 6 1.4 299 2 I46690 CD80 precursor - r
1468 6 1.4 299 2 E82116 flagellar biosynth
1469 6 1.4 299 2 AH0245 probable 4-diphosp
1470 6 1.4 299 2 F96554 hypothetical prote
1471 6 1.4 299 2 T47989 RAV-like protein -
1472 6 1.4 299 2 F97089 probable permease,
1473 6 1.4 300 1 WMLJB1 bel-1 protein - hu
1474 6 1.4 300 2 D83158 hypothetical prote
1475 6 1.4 300 2 S75558 cytochrome-c oxida
1476 6 1.4 300 2 A69351 heterodisulfide re
1477 6 1.4 301 1 QOEC3R transcription acti
1478 6 1.4 301 2 D82997 ribosomal protein
1479 6 1.4 301 2 B82096 ribosomal protein
1480 6 1.4 301 2 B85482 transcription acti
1481 6 1.4 301 2 B90631 transcription acti
1482 6 1.4 301 2 JQ1663 hybrid proline-ric
1483 6 1.4 301 2 A70787 hypothetical prote
1484 6 1.4 301 2 G85928 hypothetical prote
1485 6 1.4 302 1 S31818 myb-related protei
1486 6 1.4 302 2 S69188 probable flavonol
1487 6 1.4 302 2 F83492 conserved hypothet
1488 6 1.4 302 2 D83479 probable transcrip
1489 6 1.4 302 2 C84470 hypothetical prote

1490 6 1.4 303 2 B69160 mevalonate kinase
1491 6 1.4 303 2 A81215 transcription regu
1492 6 1.4 303 2 H81792 probable LysR-fami
1493 6 1.4 303 2 D83503 probable transcrip
1494 6 1.4 303 2 T29321 hypothetical prote
1495 6 1.4 303 2 B84744 hypothetical prote
1496 6 1.4 303 2 C69897 hypothetical prote
1497 6 1.4 303 2 T02606 hypothetical prote
1498 6 1.4 304 2 B96009 probable dihydroti
1499 6 1.4 304 2 E71823 DNA transfer prote
1500 6 1.4 304 2 E64697 conjugative transf

ALIGNMENTS

RESULT 1

T08852

lustrin A - California red abalone

C/Species: Halotis rufescens (California red abalone)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08852

R/Shen, X.; Belcher, A.M.; Hansma, P.K.; Stucky, G.D.; Morse, D.E.

J. Biol. Chem. 272, 32472-32481, 1997

A/Title: Molecular cloning and characterization of lustrin A, a matrix protein from shell

A/Reference number: Z16496; MUID:98070424; PMID:9405458

A/Accession: T08852

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1428 <SHE>

A/Cross-references: UNIPROT:O44341; EMBL:AF023459; NID:G2723361; PIDN:AAB95154.1; PID:G2:

A/Experimental source: tissue type mantle (shell and pearl nacre); cell type pallial

C/Keywords: extracellular matrix; extracellular protein

F/1382-1426/Domain: antileukoproteinase repeat homology <ALP>

Query Match 3.0%; Score 13; DB 2; Length 1428;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSSGSSSG 283

Db 1027 GSSSGSSSGSSSG 1039

RESULT 2

A82704

1,4-beta-cellobiosidase XPI267 [imported] - Xylella fastidiosa (strain 9a5c)

C/Species: Xylella fastidiosa

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C/Accession: A82704

R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; MUID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: A82704

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-683 <SIM>

A/Cross-references: UNIPROT:Q9PDW2; GB:AE003960; GB:AE003849; NID:g9106242; PIDN:AAP84076

A/Experimental source: strain 9a5c

R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carrato, D.M.; Carrer, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.B.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1267

Query Match 2.7%; Score 12; DB 2; Length 683;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 SSSGSSSSSGSSG 283
|||||
Db 557 SSSGSSSSSGSSG 568

RESULT 3
S39356
transcription factor btd - fruit fly (*Drosophila* sp.)
C;Species: *Drosophila* sp.
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
R;Wimmer, E.A.; Jaecckle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A;Title: A *Drosophila* homologue of human Sp1 is a head-specific segmentation gene.
A;Reference number: S39356; MUID:94081952; PMID:8259212
A;Accession: S39356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-644 <WIM>
A;Cross-references: EMBL:Z29361; NID:g441283; PID:g441284
C;Genetics:
A;Gene: FlyBase:btd
A;Cross-references: FlyBase:FBgn0000233
A;Introns: 245/2

Query Match 2.5%; Score 11; DB 2; Length 644;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GSSGSSSSSGSS 281
|||||
Db 107 GSSGSSSSSGSS 117

RESULT 4
S68178
mixed-lineage protein kinase 2 (EC 2.7.1.-) - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68178; I38044; S32468
R;Dorow, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Simpson, J.; Blochem. 234, 492-500, 1995
A;Title: Complete nucleotide sequence, expression, and chromosomal localisation of human mixed-lineage protein kinase 2.
A;Reference number: S68178; MUID:96128179; PMID:8536694
A;Accession: S68178
A;Molecule type: mRNA
A;Residues: 1-954 <DOR>
A;Cross-references: UNIPROT:Q02779; EMBL:X90846; NID:g971419; PIDN:CAA62351.1; PID:g971419
R;Katoh, M.; Hirai, M.; Sugimura, T.; Terada, M.
Oncogene 10, 1447-1451, 1995
A;Title: Cloning and characterization of MST, a novel (putative) serine/threonine kinase from *Mytilus*.
A;Reference number: I38044; MUID:95249256; PMID:7731697
A;Accession: I38044
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-461, 'A', 'V', '465-470, 'S', '472-806, 'R', '808-817, 'A', '819-954 <RES>
A;Cross-references: EMBL:Z48615; NID:g758592; PIDN:CAA88531.1; PID:g758593
R;Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kreter, T.
Eur. J. Biochem. 213, 701-710, 1993
A;Title: Identification of a new family of human epithelial protein kinases containing a conserved catalytic domain.
A;Reference number: S32467; MUID:93238756; PMID:8477742
A;Accession: S32468
A;Molecule type: mRNA
A;Residues: 244-464, 'AQAQRQHPQALWL' <DO2>

C;Genetics:
A;Gene: GDB:MLX2; GDB:MST
A;Cross-references: GDB:362654; GDB:624810; OMIM:600137
A;Map position: 19q13.1-19q13.2
C;Superfamily: mixed-lineage protein kinase 2; protein kinase homology; SH3 homology
C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein kinase

F;23-76/Domain: SH3 homology <SH3>
F;96-364/Domain: protein kinase homology <KIN>
F;104-112/Region: protein kinase ATP-binding motif
F;384-405/Region: leucine zipper motif
F;419-440/Region: leucine zipper motif
F;449-463/Region: basic
F;125,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 2.5%; Score 11; DB 1; Length 954;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GSSGSSSSSGSS 285
|||||
Db 525 GSSGSSSSSGSS 535

RESULT 5
T18272
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - slime mold (*Dictyostelium discoideum*)
C;Species: *Dictyostelium discoideum*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18272
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in *Dictyostelium discoideum*: Biochemical and molecular cloning of a novel member.
A;Reference number: Z06411
A;Accession: T18272
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1570 <ZHO>
A;Cross-references: UNIPROT:P54673; EMBL:U23476; NID:g733519; PID:g733520; PIDN:AAA85721.
C;Genetics:
A;Gene: PIK1
C;Keywords: phosphotransferase

Query Match 2.5%; Score 11; DB 2; Length 1570;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 275 GSSGSSSSSGSS 285
|||||
Db 171 GSSGSSSSSGSS 181

RESULT 6
G01758
transcription factor SOX11 - human
N;Alternate names: Aip-1
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G01758; J07156
R;Jay, P.
submitted to the EMBL Data Library, March 1995
A;Reference number: G08331
A;Accession: G01758
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-441 <JAY>
A;Cross-references: UNIPROT:P35716; EMBL:U23752; NID:g974247; PIDN:AA808518.1; PID:g974247
R;Azuma, T.; Ao, S.; Saito, Y.; Yano, K.; Seki, N.; Wakao, H.; Masuho, Y.; Muramatsu, M.
DNA Res. 6, 357-360, 1999
A;Title: Human SOX11, an upregulated gene during the neural differentiation, has a long 3' UTR.
A;Reference number: J07156; MUID:20039622; PMID:10574465
A;Accession: J07156
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-441 <AZU>
A;Cross-references: DDBJ:AB028641; NID:G6527111; PIDN:BAA88122.1; PID:G6527112
C;Genetics:
A;Gene: GDB:SOX11; SOX-11
A;Cross-references: GDB:677487; OMIM:600898
A;Map position: 2p25-2p25
C;Superfamily: HMG box homology
F;46-121/Domain: HMG box homology <HMG1>

Query Match 2.3%; Score 10; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 SSGSSSGSS 281
Db 345 SSGSSSGSS 354
|||||

RESULT 7
T37541
probable glycolipid anchored surface protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37541
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Submitted to the EMBL Data Library, August 1997
A;Reference number: Z21721
A;Accession: T37541
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-510 <MUR>
A;Cross-references: UNIPROT:O13692; EMBL:Z98595; PIDN:CAB11192.1; GSPDB:GN00066; SPDB:SF
A;Experimental source: strain 972h-; cosmid c11E3
C;Genetics:
A;Gene: SPDB:SPAC11E3.13c
A;Map position: 1
C;Superfamily: Glycophospholipid-anchored surface glycoprotein GAS1

Query Match 2.3%; Score 10; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 SSGSSSGSS 282
Db 473 SSGSSSGSS 482
|||||

RESULT 8
T06728
pectate lyase (EC 4.2.2.2) F28P10.100 - Arabidopsis thaliana
N;Alternate names: protein F28P10.100
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T06728
R;Quetier, F.; Choise, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artig
Submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15793
A;Accession: T06728
A;Molecule type: DNA
A;Residues: 1-542 <QUE>
A;Cross-references: EMBL:AL049655
A;Experimental source: cultivar Columbia; BAC clone F28P10
C;Genetics:
A;Map position: 3
A;Introns: 46/2; 346/3; 413/2; 480/2
A;Note: F28P10.100
C;Superfamily: pectate lyase LAT59
C;Keywords: carbon-oxygen lyase

Query Match 2.3%; Score 10; DB 2; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 GSGSSSGSSG 292
Db 433 GSGSSSGSSG 442
|||||

RESULT 9
KRH02
keratin 1, type II, cytoskeletal - human
N;Alternate names: 67K type II epidermal keratin; cytokeratin 1
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 22-Oct-1999 #text_change 10-Dec-1999
C;Accession: A22940; A02950; A43342
R;Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985
A;Reference number: A22940; MUID:85166239; PMID:2580302
A;Accession: A22940
A;Molecule type: DNA
A;Residues: 1-643 <JOH>
A;Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:G1843461
A;Note: translation of initiator Met is not shown
R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J. Biol. Chem. 260, 7142-7149, 1985
A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000
late filament subunits.
A;Reference number: A92535; MUID:85207740; PMID:2581964
A;Accession: A02950
A;Molecule type: mRNA
A;Residues: 151-183, 'K', 185-199, 'M', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 358-
'S', 638-643 <STE>
A;Cross-references: GB:M10938; NID:G186787; PIDN:AAA36153.1; PID:G386854
A;Experimental source: tissue neonatal foreskin
A;Note: the authors translated the codon CUG for residue 476 as Met
R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGiovanna, J.J.; Compton, J.G.; S
Cell 70, 821-828, 1992
A;Title: A leucine---proline mutation in the H1 subdomain of keratin 1 causes epidermol
A;Reference number: A43342; MUID:92386601; PMID:1381288
A;Accession: A43342
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>
A;Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:G1843461
A;Note: sequence extracted from NCBI backbone (NCBIP:112784)
C;Comment: The cytoskeletal and microfibrillar keratins are classified into two types, ty
atin IF protein subunit appears to be a heterotetramer of two type I and two type II prot
C;Comment: Keratin 1 is expressed in terminally differentiating epidermis.
C;Genetics:
A;Gene: GDB:KRT1
A;Cross-references: GDB:128198; OMIM:139350
A;Map position: 12q11-12q13
A;Note: defects in this gene may result in epidermolytic hyperkeratosis
C;Complex: heterotetramer of two type I, usually keratin 10 (see PIR:KRH00), and two type
C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; heterotetramer; intermediate filament
F;4-179/Domain: head <HED>
F;4-143/Region: E1 and V1 subdomains
F;14-179/Region: H1 subdomain
F;180-492/Domain: rod <ROD>
F;180-214/Region: coil 1A
F;215-226/Region: linker 1
F;227-327/Region: coil 1B
F;328-344/Region: linker 12
F;345-363/Region: coil 2A
F;364-371/Region: linker 2
F;372-492/Region: coil 2B
F;430/Region: stutter
F;493-643/Domain: tail <END>
F;493-512/Region: H2 subdomain
F;513-643/Region: V2 and E2 subdomains

Query Match 2.3%; Score 10; DB 1; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 GGSSGGSSGG 292
Db 605 GGSSGGSSGG 614

RESULT 10

outD protein - *Erwinia chrysanthemi*
 C:Species: *Erwinia chrysanthemi*
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C:Accession: S28014; S23986
 R:Condemine, G.; Dorel, C.; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.
 Mol. Microbiol. 6, 3199-3211, 1992
 A:Title: Some of the out genes involved in the secretion of pectate lyases in *Erwinia chrysanthemi*
 A:Reference number: S28011; MUID:93086427; PMID:1453958
 A:Accession: S28014
 A:Molecule type: DNA
 A:Residues: 1-710 <CON>
 A:Cross-references: UNIPROT:Q01565; EMBL:X65265; NID:g3152953; PIDN:CAA46370.1; PID:g501565
 C:Genetics:
 A:Gene: outD
 A:Start codon: GTG

Query Match	Best Local Similarity	Matches	10; Conservative
QY	273	SSGSSSGSSS	282
Pb	322	SSGSSSGSSS	331

RESULT 11

T09219
basal transcription factor SNAPc large chain SNAP190 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004
C:Accession: T09219
R:Wong, M.W.; Henry, R.W.; Ma, B.; Kobayashi, R.; Klages, N.; Matthias, P.; Strubin, M.;
Mol. Cell. Biol. 18, 368-377, 1998
A:Title: The large subunit of basal transcription factor SNAPc is a Myb domain protein that
A:Reference number: Z161616; MUID:98078693; PMID:9418884
A:Accession: T09219
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1469 -WON>
A:Cross-references: UNIPROT:Q9V6P7; EMBL:AF032387; NID:G2641556; PIDN:AAC02972.1; PID:G2641556
A:Experimental source: tissue type fetal cell teratocarcinoma
C:Genetics:
A:Gene: SNAP190

C;Function: transcription factor; required for transcription of snRNA genes
C;Description: myb DNA-binding repeat homology
C;Superfamily: myb DNA-binding repeat homology
C;Keywords: DNA binding; RNA biogenesis; transcription factor
F:396-447/Domain: myb DNA-binding repeat homology <MYB>

Query Match	Best Local Similarity	Matches	10; Conservativ
Qy	272	SSSGSSSGSS	281
Db	522	SSSGSSSGSS	531

RESULT 12

Tl3594
hypothetical protein pib - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C/Accession: Tl3594
R/Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
submitted to the EMBL Data Library. October 1998

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
 A;Reference number: Z17692
 A;Accession: F13594
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1891 <FER>
 A;Cross-references: UNIPROT:O77275; EMBL:AL031227; NID:e1330103; PID:e1316856
 C;Genetics:
 A;Gene: deb
 A;Cross-references: FlyBase:FBgn003053
 A;Introns: 289/3

Query Match	2.3%	Score 10;	DB 2;	Length 1891;
Best Local Similarity	100.0%;	Pred. No. 2;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	276	SSGSSSSGGGS	285	
Db	215	SSGSSSSGGGS	224	

RESULT 13

Tl13893
 gene hindsight protein - fruit fly *Drosophila melanogaster*
 C:Species: *Drosophila melanogaster*
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: Tl13893
 R:Yip, M.L.R.; Lamka, M.L.; Lipshitz, H.D.
 Development 124, 2129-2141, 1997
 A>Title: Control of germ-band retraction in *Drosophila* by the zinc-finger p
 A/Reference number: Z17807; MUID:97330681; PMID:19187140
 A/Accession: Tl13893
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type:mRNA
 A/Residues: 1-1920 <YIP>
 A/Cross-references: UNIPROT:O46205; EMBL:U86010; NID:g2769709; PID:g2769710
 C:Genetics:
 A/Gene: hindsight
 A/Cross-references: FlyBase:FBgn0003053
 C/Function:
 A/Description: probably function as a transcription factor
 C/Keywords: nucleus; zinc finger

Query Match	2.38;	Score 10;	DB 2;	Length 1920;
Best Local Similarity	100.0%;	Pred. No. 2;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	276	SSSGSSSGGS	285	
Db	215	SSSGSSSGGS	224	

RESULT 14

D87278
DNA-binding response regulator [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: D87278
R:Nierman, W.C.; DeBlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; H
B.; Laub, M.T.; DeBoy, R.J.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: B87249: MUID:21173698: PMID:11259647

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <SFO>
A:Cross-references: UNIPROT:Q9ABJ0; GB:AE005673; NID:gl3
C:Genetics:
A:Gene: CCQ237
C:Superfamily: ompR protein; response regulator homology

Query Match 2.0%; Score 9; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AGGAAGSKV 67
Db 129 AGGAAGSKV 137
|||||

RESULT 15
F84088
N-acetylmuramoyl-L-alanine amidase (sporulation mother cell wall hydrolase) BH3510 [impo
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84088
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84088
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <STO>
A;Cross-references: UNIPROT:Q9K763; GB:AF001519; GB:BA000004; NID:g10176109; PIDN:BA072
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3510

Query Match 2.0%; Score 9; DB 2; Length 275;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 SSGSGSGS 289
Db 184 SSGSGSGS 192
|||||

Search completed: April 7, 2005, 00:41:20
Job time : 62 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:23:07 ; Search time 178 Seconds
(without alignments)
1265.814 Million cell updates/sec

Title: US-10-063-561-52
Perfect score: 440
Sequence: 1 MKFGPLACLLALCLGSGE.....KLGFINDAINKQDRSRIP 440

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	440	100.0	440	2	Q6UXC7
2	178	40.5	476	2	Q6E0U4
3	25	5.7	137	2	Q6E0W8
4	16	3.6	182	2	Q9CR91
5	15	3.4	319	2	Q6C4B0
6	15	3.4	417	2	Q693B5
7	15	3.4	456	2	Q7UJ76
8	14	3.2	792	2	Q8PZV5
9	13	3.0	120	2	Q6ZUH6
10	13	3.0	199	2	Q94476
11	13	3.0	202	2	Q8WML4
12	13	3.0	282	2	Q8MYJ1
13	13	3.0	297	2	Q86HE5
14	13	3.0	375	2	Q8TI63
15	13	3.0	418	2	Q9GRU6
16	13	3.0	476	2	O18453
17	13	3.0	770	2	Q6BIY3
18	13	3.0	1428	2	O44341
19	12	2.7	283	2	Q6NZV7
20	12	2.7	283	2	Q6PG31
21	12	2.7	411	2	Q8LW55
22	12	2.7	484	2	Q75WB9
23	12	2.7	487	2	Q75WB8
24	12	2.7	683	2	Q9PDW2
25	12	2.7	708	2	Q8SX98
26	12	2.7	751	2	Q8MLU0
27	12	2.7	761	2	Q7KVL6
28	12	2.7	1690	2	Q76P31
29	11	2.5	90	2	Q7RWL2
30	11	2.5	158	2	Q9EWB3
31	11	2.5	161	1	TATB_STRCO

32	11	2.5	167	2	Q6EP11	Q6ep11 oryza sativ
33	11	2.5	202	1	SSBI_STRAW	Q82fg5 streptomyce
34	11	2.5	252	2	Q9WJ70	Q9w300 drosophila
35	11	2.5	270	1	CIT2_HUMAN	Q9967 homo sapien
36	11	2.5	315	2	Q8SX83	Q8ex33 drosophila
37	11	2.5	473	1	CHIA_MOUSE	Q9ix99 mus musculu
38	11	2.5	493	2	Q6SZJ9	Q6szj9 mus musculu
39	11	2.5	508	2	Q6P253	Q6p253 mus musculu
40	11	2.5	517	2	Q6E0U6	Q6e0u6 mus musculu
41	11	2.5	525	2	Q693B7	Q693b7 microbulbif
42	11	2.5	530	2	Q693B6	Q693b6 microbulbif
43	11	2.5	590	2	Q693B6	Q693b6 microbulbif
44	11	2.5	607	2	Q6BIY4	Q6biy4 debaryomyce
45	11	2.5	644	1	BTB_DROME	Q24266 drosophila
46	11	2.5	718	2	Q73619	Q73619 xenopus lae
47	11	2.5	766	2	Q6CV63	Q6cv63 kluyveromyc
48	11	2.5	954	1	M3KA_HUMAN	Q54779 homo sapien
49	10	2.3	1570	1	P3K1_DICDI	P54673 dictyosteli
50	10	2.3	100	2	Q964C3	Q964c3 encephalito
51	10	2.3	102	2	Q964C0	Q964c0 encephalito
52	10	2.3	117	2	Q964C2	Q964c2 encephalito
53	10	2.3	121	2	Q964C5	Q964c5 encephalito
54	10	2.3	125	2	Q964C1	Q964c1 encephalito
55	10	2.3	138	2	Q964C4	Q964c4 encephalito
56	10	2.3	185	2	Q827Z8	Q827z8 streptomyce
57	10	2.3	174	2	Q6BNH9	Q6bnh9 debaryomyce
58	10	2.3	230	2	Q8TCV1	Q8tcv1 plasmodium
59	10	2.3	232	2	Q8TCV2	Q8tcv2 plasmodium
60	10	2.3	251	2	Q9UVE7	Q9uve7 yarrowia li
61	10	2.3	273	2	Q898T3	Q898t3 clostridium
62	10	2.3	407	2	Q8C4L6	Q8c4l6 mus musculu
63	10	2.3	441	1	SL11_HUMAN	F35716 homo sapien
64	10	2.3	450	1	SWP1_ENCCU	Q9xv1 encephalito
65	10	2.3	454	2	Q7X8B6	Q7x8b6 oryza sativ
66	10	2.3	476	2	CHIA_HUMAN	Q9b26 homo sapien
67	10	2.3	480	2	Q80890	Q80890 herpesvirus
68	10	2.3	501	1	PL13_ARATH	Q8t215 dictyosteli
69	10	2.3	508	2	Q8DA23	Q8da23 arabidopsis
70	10	2.3	510	1	YDID_SCHPO	O13692 schizosacch
71	10	2.3	542	2	Q7MK56	Q7mk56 vibrio vuln
72	10	2.3	561	2	Q7TFC1	Q7tpc1 mus musculu
73	10	2.3	572	2	Q88NL2	Q88nl2 pseudomonas
74	10	2.3	641	1	GSQD_ERWCH	Q7pfh8 anopheles g
75	10	2.3	710	1	Q7RYT2	O1565 erwinia chr
76	10	2.3	732	2	Q9VAV0	Q9vav0 neuropept
77	10	2.3	952	2	Q9VAV0	Q9vav0 drosophila
78	10	2.3	1028	2	Q86P35	Q86p35 drosophila
79	10	2.3	1398	2	Q6E2N4	Q6e2n4 brachydanio
80	10	2.3	1398	2	Q6UV33	Q6uv33 brachydanio
81	10	2.3	1469	2	Q9Y6P7	Q9y6p7 homo sapien
82	10	2.3	1562	2	Q7YY78	Q7yy78 cryptospori
83	10	2.3	1891	2	Q72725	Q72725 drosophila
84	10	2.3	1893	2	Q9W4J1	Q9w4j1 drosophila
85	10	2.3	1920	2	O46205	O46205 drosophila
86	10	2.3	2090	2	Q8B3T9	Q8b3t9 citrus tris
87	10	2.3	3122	2	Q8B3T9	Q8b3t9 citrus tris
88	9	2.0	109	2	Q71D57	Q71d57 drosophila
89	9	2.0	152	2	Q8B571	Q8b571 pseudocowpo
90	9	2.0	167	2	Q9D428	Q9d428 mus musculu
91	9	2.0	197	2	Q9CRD9	Q9crd9 mus musculu
92	9	2.0	207	2	Q7Z4M7	Q7z4m7 homo sapien
93	9	2.0	208	2	Q7PFN9	Q7pf9 anopheles g
94	9	2.0	227	2	Q6ZBR3	Q6zbr3 oryza sativ
95	9	2.0	230	2	Q9N9X2	Q9n9x2 geodia cydo
96	9	2.0	235	2	Q9ABJ0	Q9abj0 caulobacter
97	9	2.0	260	2	Q86UT4	Q86ut4 dictyosteli
98	9	2.0	262	2	Q767M8	Q767m8 sus scrofa
99	9	2.0	275	2	Q9K763	Q9k763 bacillus ha
100	9	2.0	280	2	Q9VI07	Q9vi07 drosophila
101	9	2.0	322	2	Q8G4E5	Q8g4e5 bifidobacte
102	9	2.0	324	2	Q7X6C5	Q7x6c5 oryza sativ
103	9	2.0	326	2	Q9C9A0	Q9c9a0 arabidopsis
104	9	2.0	328	2	Q6BK18	Q6bk18 debaryomyce

105	9	2.0	343	2	Q7S729	Q7s729 neurospora	178	9	2.0	1427	2	Q9KGX8	Q9kgx8 mycoplasma
106	9	2.0	347	2	Q8C9F3	Q8c9f3 mus musculus	179	9	2.0	1436	2	Q8C523	Q8c523 bifidobacte
107	9	2.0	360	2	Q8MSN0	Q8msn0 drosophila	180	9	2.0	1478	2	Q8TLD5	Q8tld5 methanosarc
108	9	2.0	361	2	Q8C9Q5	Q8c9q5 mus musculus	181	9	2.0	1486	2	Q95RES	Q95res drosophila
109	9	2.0	388	2	Q8IR08	Q8ir08 drosophila	182	9	2.0	1486	2	Q967Y2	Q967y2 drosophila
110	9	2.0	389	2	Q7PT82	Q7pt82 anopheles g	183	9	2.0	1486	2	Q7KRP7	Q7krp7 drosophila
111	9	2.0	394	2	Q8TQ10	Q8tq10 methanosarc	184	9	2.0	1582	2	Q7KRP6	Q7krp6 drosophila
112	9	2.0	395	1	QX11_MOUSE	Qx11 mouse	185	9	2.0	1709	1	CHD1_HUMAN	Chd1 homo sapien
113	9	2.0	395	2	Q7M6Y2	Q7m6y2 mus musculus	186	9	2.0	1711	1	CHD1_MOUSE	Chd1 mus musculus
114	9	2.0	395	2	Q8OXF0	Q8oxf0 mus musculus	187	9	2.0	1786	2	Q7ZT34	Q7zt34 poephila gu
115	9	2.0	402	1	QPS4_CANAL	P46596 candida alb	188	9	2.0	1806	2	Q800S6	Q800s6 poephila gu
116	9	2.0	406	2	Q8YH69	Q8yh69 bradyrhizob	189	9	2.0	1808	2	Q42142	Q42142 gallus galli
117	9	2.0	417	2	Q7PS00	Q7ps00 anopheles g	190	9	2.0	1815	2	Q6CF66	Q6cf66 yarrowia li
118	9	2.0	420	2	Q82HS1	Q82hs1 streptomyc	191	9	2.0	1840	2	Q6PD15	Q6pd15 mus musculus
119	9	2.0	432	2	Q9BLJ0	Q9blj0 halocynthia	192	9	2.0	3099	2	Q6EB12	Q6eb12 dictyosteli
120	9	2.0	486	1	CDSN_HUMAN	Q15517 homo sapien	193	9	2.0	3409	2	Q6SSE6	Q6sse6 chlamydomon
121	9	2.0	499	2	Q9NRH4	Q9nrh4 homo sapien	194	8	1.8	67	1	YG26_STRRP6	Q8cyd7 streptococc
122	9	2.0	499	2	Q9NRH5	Q9nrh5 homo sapien	195	8	1.8	67	1	YI05_STRPN	Q97p39 streptococc
123	9	2.0	500	2	Q9NP52	Q9np52 homo sapien	196	8	1.8	78	2	Q6W067	Q6w067 mus musculus
124	9	2.0	500	2	Q9NP50	Q9np50 homo sapien	197	8	1.8	97	2	Q49407	Q4940 mycoplasma
125	9	2.0	500	2	Q9NPG5	Q9np55 homo sapien	198	8	1.8	99	2	Q9CD66	Q9cd66 mycobacteri
126	9	2.0	500	2	Q9NRH6	Q9nrh6 homo sapien	199	8	1.8	102	2	Q86EM7	Q86em7 schistosoma
127	9	2.0	500	2	Q9NRH7	Q9nrh7 homo sapien	200	8	1.8	114	2	Q9JG72	Q9jg72 tt virus. o
128	9	2.0	500	2	Q9NRH8	Q9nrh8 homo sapien	201	8	1.8	115	1	SER1_GALME	Q96614 galliera me
129	9	2.0	503	2	Q6FLN7	Q6fln7 candida gla	202	8	1.8	118	2	Q949R3	Q949r3 arabidopsis
130	9	2.0	513	2	Q95IF9	Q95if9 homo sapien	203	8	1.8	120	2	Q925G3	Q925g3 mycobacteri
131	9	2.0	517	1	Y652_HUMAN	Q75143 homo sapien	204	8	1.8	130	2	Q8S5Q1	Q8ssq1 oryza sativ
132	9	2.0	518	2	Q67WR0	Q67wr0 oryza sativ	205	8	1.8	133	2	Q9D731	Q9d731 mus musculus
133	9	2.0	528	2	Q8IZU5	Q8izu5 homo sapien	206	8	1.8	136	2	Q6W031	Q6w031 mus musculus
134	9	2.0	528	2	Q8IZU6	Q8izu6 homo sapien	207	8	1.8	137	2	Q8NN75	Q8nn75 corynebacte
135	9	2.0	528	2	Q8NSP3	Q8nsp3 homo sapien	208	8	1.8	137	2	Q9D149	Q9d149 mus musculus
136	9	2.0	529	2	Q43509	Q43509 homo sapien	209	8	1.8	139	2	Q9W2M0	Q9w2w0 drosophila
137	9	2.0	529	2	Q8IZU4	Q8izu4 homo sapien	210	8	1.8	139	2	Q9D0X3	Q9d0x3 mus musculus
138	9	2.0	529	2	Q7YR44	Q7yr44 pan troglod	211	8	1.8	139	2	Q9D195	Q9d195 mus musculus
139	9	2.0	535	2	Q24455	Q24455 drosophila	212	8	1.8	140	2	Q9D6R3	Q9d6r3 mus musculus
140	9	2.0	549	2	Q19318	Q19318 caenorhabdi	213	8	1.8	143	2	Q9CQH5	Q9cqh5 m mus muscu
141	9	2.0	595	2	Q7SFY1	Q7sfy1 neurospora	214	8	1.8	143	2	Q9D139	Q9d139 mus musculus
142	9	2.0	596	2	Q8MZ04	Q8mz04 drosophila	215	8	1.8	147	2	Q9D1C5	Q9dic5 mus musculus
143	9	2.0	596	2	Q9VB83	Q9vb83 drosophila	216	8	1.8	147	2	Q9D1I4	Q9di14 mus musculus
144	9	2.0	604	2	Q87XD4	Q87xd4 pseudomonas	217	8	1.8	149	2	Q9D1K4	Q9d1k4 mus musculus
145	9	2.0	610	2	Q7KTN9	Q7ktn9 drosophila	218	8	1.8	149	2	Q9D6P5	Q9d6p5 mus musculus
146	9	2.0	624	1	RN12_HUMAN	Q9nvw2 homo sapien	219	8	1.8	156	2	Q6W073	Q6w073 mus musculus
147	9	2.0	624	2	Q96D38	Q96d38 homo sapien	220	8	1.8	160	2	Q7XEK1	Q7xe1 oryza sativ
148	9	2.0	633	2	Q96GF2	Q96gf2 homo sapien	221	8	1.8	161	2	Q8W007	Q8w007 oryza sativ
149	9	2.0	660	2	Q75J88	Q75j88 dictyosteli	222	8	1.8	161	2	Q84Q77	Q84q77 oryza sativ
150	9	2.0	668	2	Q48297	Q48297 halobacteri	223	8	1.8	164	2	Q9NSJ2	Q9nsj2 homo sapien
151	9	2.0	668	2	Q9HQW7	Q9hqw7 halobacteri	224	8	1.8	164	2	Q7PN76	Q7pn76 anopheles g
152	9	2.0	668	2	Q9ZKJ0	Q9zkj0 helicobacte	225	8	1.8	179	2	Q9HQS3	Q9hqs3 halobacteri
153	9	2.0	675	1	HS7M_PHAVU	Q01899 phaseolus v	226	8	1.8	180	2	Q72GQ6	Q72gq6 thermus the
154	9	2.0	677	1	SP87_DICDI	P54643 dictyosteli	227	8	1.8	185	2	Q7XDV1	Q7xdv1 oryza sativ
155	9	2.0	712	1	GSPD_ERWCH	P31700 erwinia chr	228	8	1.8	185	2	Q9LVB5	Q9l1b5 arabidopsis
156	9	2.0	717	2	Q6MTA9	Q6mta9 mycoplasma	229	8	1.8	190	2	Q8LBE9	Q8lbe9 arabidopsis
157	9	2.0	718	2	Q94HG1	Q94hg1 oryza sativ	230	8	1.8	194	2	Q8LBE9	Q8lbe9 arabidopsis
158	9	2.0	729	2	Q18660	Q18660 drosophila	231	8	1.8	199	2	Q9SD84	Q9sd84 arabidopsis
159	9	2.0	729	2	Q9VMS4	Q9vms4 drosophila	232	8	1.8	202	2	Q9WA49	Q9wa49 porcine ade
160	9	2.0	768	2	Q7Q394	Q7q394 anopheles g	233	8	1.8	204	2	Q8MYL3	Q8myl3 drosophila
161	9	2.0	868	2	Q8SX72	Q8sx72 drosophila	234	8	1.8	211	1	PEN_RAT	Q6330 rattus norv
162	9	2.0	879	2	Q6CXL0	Q6cx10 kluyveromyc	235	8	1.8	214	2	Q922H8	Q922h8 mus musculus
163	9	2.0	923	2	Q8CTE9	Q8cte9 methanosarc	236	8	1.8	216	2	Q7OZ58	Q7o258 canis fami1
164	9	2.0	942	2	Q8CAH0	Q8cah0 mus musculus	237	8	1.8	216	2	Q7OZ60	Q7o260 canis fami1
165	9	2.0	973	2	Q6ZR04	Q6zr04 homo sapien	238	8	1.8	216	2	Q7OZ13	Q7o213 canis fami1
166	9	2.0	1046	2	Q7KQZ6	Q7kqz6 drosophila	239	8	1.8	217	2	Q8MYL2	Q8myl2 drosophila
167	9	2.0	1064	2	Q7KQZ5	Q7kqz5 drosophila	240	8	1.8	224	2	Q7FF45	Q7pf45 anopheles g
168	9	2.0	1065	2	Q9V5N1	Q9v5n1 drosophila	241	8	1.8	228	2	Q9NYG3	Q9nyg3 homo sapien
169	9	2.0	1081	2	Q8C7Q2	Q8c7q2 mus musculus	242	8	1.8	232	1	DJB8_HUMAN	Q8nhs0 homo sapien
170	9	2.0	1085	2	Q7JN04	Q7jno4 drosophila	243	8	1.8	239	2	Q69T79	Q69t79 oryza sativ
171	9	2.0	1097	1	CCT_DRONE	Q96433 drosophila	244	8	1.8	247	2	Q6ARC8	Q6arc8 desulfotale
172	9	2.0	1173	2	Q9VRC2	Q9vrc2 drosophila	245	8	1.8	251	2	Q92TZ5	Q92tz5 rhizobium m
173	9	2.0	1266	2	Q6BXJ1	Q6bxj1 debaryomyce	246	8	1.8	254	2	Q8BEN1	Q8ben1 callitrichi
174	9	2.0	1306	1	MSB2_YEAST	F32334 saccharomyc	247	8	1.8	260	2	Q7Q616	Q7q616 anopheles g
175	9	2.0	1333	2	Q70JAB	Q70jab butyrivibri	248	8	1.8	262	2	Q94115	Q94115 sorghum bic
176	9	2.0	1357	2	Q9W4M4	Q9w4m4 drosophila	249	8	1.8	273	2	Q9VY58	Q9vy58 drosophila
177	9	2.0	1410	2	Q9KGY0	Q9kgy0 mycoplasma	250	8	1.8	275	2	Q6C2G8	Q6c2g8 yarrowia li

251	8	1.8	276	1	SLEB_OCEIH	PS9105 oceanobacil	324	8	1.8	392	2	Q7U3X2	Q7u3x2 synechococc
252	8	1.8	276	2	Q9W5C7	Q9w5c7 drosophila	325	8	1.8	393	2	Q18880	Q18880 caenorhabdi
253	8	1.8	277	2	Q9AE60	Q9ae60 rhodococcus	326	8	1.8	393	2	Q6VYN1	Q6vyn1 drosophila
254	8	1.8	282	2	Q8WY42	Q8wy42 homo sapien	327	8	1.8	396	2	Q975D0	Q975d0 sulfolobus
255	8	1.8	288	2	Q9VRL6	Q9vrl6 drosophila	328	8	1.8	396	2	Q7R271	Q7r271 giardia lam
256	8	1.8	290	2	Q91P07	Q91p07 cynomolgus	329	8	1.8	396	2	Q65450	Q65450 arabidopsis
257	8	1.8	293	2	Q7EZ23	Q7ez23 oryza sativ	330	8	1.8	396	2	Q6YTH3	Q6yth3 oryza sativ
258	8	1.8	295	2	Q6ERH9	Q6erh9 oryza sativ	331	8	1.8	397	2	Q6CG83	Q6cg83 yarrowia li
259	8	1.8	296	2	Q6P9D8	Q6p9d8 homo sapien	332	8	1.8	398	2	Q9UXP2	Q9uxf2 sulfolobus
260	8	1.8	296	2	Q6LTX0	Q6ltx0 photobacter	333	8	1.8	399	2	Q82PG5	Q82pg5 streptomyce
261	8	1.8	305	2	Q75308	Q75308 homo sapien	334	8	1.8	406	2	Q8NAC5	Q8nac5 homo sapien
262	8	1.8	305	2	Q15287	Q15287 homo sapien	335	8	1.8	407	2	Q75DT6	Q75dt6 ashyba goes
263	8	1.8	305	2	Q15844	Q15844 leishmania	336	8	1.8	408	2	Q96WQ9	Q96wq9 aspergillus
264	8	1.8	305	2	Q6AYK1	Q6ayk1 rattus norv	337	8	1.8	410	2	Q7S340	Q7s340 neurospora
265	8	1.8	305	2	Q99M28	Q99m28 mus musculu	338	8	1.8	410	2	Q9W1W2	Q9w1w2 drosophila
266	8	1.8	309	2	Q8IMV1	Q8imv1 drosophila	339	8	1.8	414	2	Q876J8	Q876j8 saccharomyc
267	8	1.8	311	1	OSAN_HUMAN	Q8ang8 homo sapien	340	8	1.8	415	2	Q9VHX2	Q9vhx2 drosophila
268	8	1.8	311	2	Q6CA10	Q6ca40 yarrowia li	341	8	1.8	415	2	Q6AYD4	Q6ayd4 rattus norv
269	8	1.8	311	2	Q8RK77	Q8rkt7 pseudomonas	342	8	1.8	416	2	Q9DBF7	Q9dbf7 mus musculu
270	8	1.8	312	2	Q8VFW5	Q8vfv5 mus musculu	343	8	1.8	417	2	Q9KWC4	Q9kwc4 agrobacteri
271	8	1.8	312	2	Q8VFW6	Q8vfv6 mus musculu	344	8	1.8	418	2	Q7RL88	Q7rl88 plasmodium
272	8	1.8	312	2	Q8VFW8	Q8vfv8 mus musculu	345	8	1.8	421	2	Q7M984	Q7m984 wolinnella s
273	8	1.8	312	2	Q7TOR7	Q7tqr7 mus musculu	346	8	1.8	422	2	Q95YL3	Q95yl3 ciona savig
274	8	1.8	312	2	Q7TOR8	Q7tqr8 mus musculu	347	8	1.8	423	2	Q9ST79	Q9st79 oryza sativ
275	8	1.8	312	2	Q7TOR9	Q7tqr9 mus musculu	348	8	1.8	423	2	Q8DW34	Q8dw34 streptococc
276	8	1.8	314	2	Q7S8K9	Q7s8k9 neurospora	349	8	1.8	427	1	AROA_ABRSA	Q03321 aeromonas s
277	8	1.8	315	1	SOL2_YEAST	P37262 saccharomyc	350	8	1.8	430	1	PIF4_ARATH	Q8w2f3 arabidopsis
278	8	1.8	315	2	Q8VFW7	Q8vfv7 mus musculu	351	8	1.8	431	2	Q692G4	Q692g4 nephila cla
279	8	1.8	316	1	LORI_HUMAN	P23490 homo sapien	352	8	1.8	431	2	Q6L8K1	Q6l8k1 canis famli
280	8	1.8	316	2	Q6FHT3	Q6fhy3 homo sapien	353	8	1.8	434	2	Q87CW9	Q87cw9 xyiella fae
281	8	1.8	319	2	Q9NF33	Q9nf33 drosophila	354	8	1.8	435	2	Q65IH0	Q65ih0 bacillus li
282	8	1.8	319	2	Q9W5B4	Q9w5b4 drosophila	355	8	1.8	436	2	Q7QDL5	Q7qdl5 anopheles g
283	8	1.8	319	2	Q38926	Q38926 arabidopsis	356	8	1.8	441	2	Q9LX71	Q9lxt7 arabidopsis
284	8	1.8	325	2	Q6AXH2	Q6axh2 mus musculu	357	8	1.8	442	1	CYS4_DICDI	P54639 dictyosteli
285	8	1.8	326	2	Q62010	Q62010 ceratitidis c	358	8	1.8	442	1	UFO_ARATH	Q39090 arabidopsis
286	8	1.8	326	2	Q9NFX5	Q9nfx5 ceratitidis c	359	8	1.8	447	2	Q9SIA8	Q9sia8 arabidopsis
287	8	1.8	326	2	Q6GQX6	Q6gqx6 mus musculu	360	8	1.8	458	2	Q89VK4	Q89vk4 bradyrhizob
288	8	1.8	329	2	Q8SV52	Q8sv52 drosophila	361	8	1.8	459	2	Q89Q42	Q89q42 bradyrhizob
289	8	1.8	329	2	Q80ZE8	Q80ze8 rattus norv	362	8	1.8	460	2	Q72NI1	Q72ni1 leptospira
290	8	1.8	329	2	Q80ZK5	Q80zk5 mus musculu	363	8	1.8	460	2	Q9XD16	Q9xd16 leptospira
291	8	1.8	330	2	Q7PPX2	Q7ppx2 anopheles g	364	8	1.8	461	2	Q89I33	Q89i33 bradyrhizob
292	8	1.8	331	2	Q692G6	Q692g6 nephila cla	365	8	1.8	463	1	CD4_CANFA	F33705 canis famli
293	8	1.8	332	1	SIX3_HUMAN	Q95343 homo sapien	366	8	1.8	466	2	Q7PSE1	Q7pse1 anopheles g
294	8	1.8	332	2	Q6C1Z7	Q6clz7 yarrowia li	367	8	1.8	469	2	Q6DVF4	Q6dvf4 oryzias lat
295	8	1.8	333	1	AMR1_HUMAN	Q9y4x0 homo sapien	368	8	1.8	471	1	SIR2_SCHPO	Q94640 schistosacch
296	8	1.8	334	2	Q8N9L6	Q8n9l6 homo sapien	369	8	1.8	471	2	Q6P2R2	Q6p2r2 homo sapien
297	8	1.8	336	2	Q98321	Q98321 molluscum c	370	8	1.8	471	2	Q9ZWB3	Q9zbw3 arabidopsis
298	8	1.8	338	2	Q60354	Q60354 homo sapien	371	8	1.8	472	1	POU2_BRARE	Q90270 brachydanio
299	8	1.8	338	2	Q8VJ24	Q8vj24 mycobacteri	372	8	1.8	472	2	Q7ZU11	Q7zu11 brachydanio
300	8	1.8	340	2	Q9KY73	Q9ky73 streptomyce	373	8	1.8	473	1	CHIA_RAT	Q6ry07 rattus norv
301	8	1.8	344	1	AMR1_MOUSE	Q9jht5 mus musculu	374	8	1.8	475	2	Q9H8I3	Q6h8i3 s transcrip
302	8	1.8	347	2	Q8MT45	Q8mt45 drosophila	375	8	1.8	475	2	Q9P8U4	Q9p8u4 aspergillus
303	8	1.8	347	2	Q9V5I8	Q9v5i8 drosophila	376	8	1.8	475	2	Q88G07	Q88g07 pseudomonas
304	8	1.8	351	2	Q86M55	Q86m55 drosophila	377	8	1.8	475	2	Q89QAI	Q89qai bradyrhizob
305	8	1.8	355	2	Q9VCW9	Q9vcw9 drosophila	378	8	1.8	476	2	Q8W0Z0	Q8w0z0 arabidopsis
306	8	1.8	356	2	Q8T0P0	Q8t0p0 drosophila	379	8	1.8	476	2	Q9FFH8	Q9ffh8 arabidopsis
307	8	1.8	356	2	Q670B2	Q67qb2 symbiobacte	380	8	1.8	476	2	Q6N5K0	Q6n5k0 rhodopseudo
308	8	1.8	359	2	Q6ZUZ0	Q6zuz0 homo sapien	381	8	1.8	477	2	Q9PPU5	Q9ppu5 ureaplasma
309	8	1.8	360	2	P77853	P77853 dictyoglomu	382	8	1.8	482	1	GATA_SYNEL	Q8dk65 synechococc
310	8	1.8	361	2	Q52375	Q52375 caldicellul	383	8	1.8	482	2	Q8RYL5	Q8ryl5 oryza sativ
311	8	1.8	369	2	Q9AV13	Q9av13 oryza sativ	384	8	1.8	484	2	Q6MWY1	Q6mwy1 mycobacteri
312	8	1.8	370	2	Q6CVD1	Q6cvd1 kluyveromyc	385	8	1.8	486	1	LORI_MOUSE	P18165 mus musculu
313	8	1.8	371	2	Q8QC02	Q8qc02 methanoearc	386	8	1.8	486	2	Q7Q3X8	Q7q3x8 anopheles g
314	8	1.8	371	2	Q8MKV0	Q8mkv0 drosophila	387	8	1.8	490	2	Q89CA1	Q89ca1 bradyrhizob
315	8	1.8	380	2	Q9HKR5	Q9hkr5 thermoplas	388	8	1.8	492	2	Q6IA44	Q6ia44 homo sapien
316	8	1.8	380	2	Q9VHI7	Q9vhi7 drosophila	389	8	1.8	492	2	Q9GZU3	Q9gzuz3 homo sapien
317	8	1.8	381	2	Q8NFJ8	Q8nfj8 homo sapien	390	8	1.8	496	2	Q62MR4	Q62mr4 burkholderi
318	8	1.8	382	2	Q6LKC2	Q6lkc2 photobacter	391	8	1.8	496	2	Q63YJ9	Q63yj9 burkholderi
319	8	1.8	384	2	Q6BU29	Q6bu29 debaryomyc	392	8	1.8	498	2	Q6PUU6	Q6puu6 methanoearc
320	8	1.8	386	2	Q62003	Q62003 branchiost	393	8	1.8	500	2	Q6N950	Q6n950 rhodopseudo
321	8	1.8	387	2	Q692G3	Q692g3 nephila cla	394	8	1.8	505	1	AMID_PSECL	P27765 pseudomonas
322	8	1.8	389	2	Q8BKH6	Q8bkh6 mus musculu	395	8	1.8	506	1	GATA_TREPA	Q83983 treponema p
323	8	1.8	392	1	HME1_HUMAN	Q05925 homo sapien	396	8	1.8	508	2	Q9LLF2	Q9llf2 lycopersico

397	8	1.8	512	2	Q95KP5	Q95KP5 canis famil	470	8	1.8	671	2	Q7ZXV4	Q7zxv4 xenopus lae
398	8	1.8	521	2	Q8TS45	Q8ts45 methanosarc	471	8	1.8	672	2	Q6FK03	Q6fk03 candida gla
399	8	1.8	521	2	Q9ABN0	Q9abn0 caulobacter	472	8	1.8	673	2	Q7PPD2	Q7ppd2 anopheles g
400	8	1.8	522	2	Q9P9G7	Q9p9g7 methanococc	473	8	1.8	673	2	Q81179	Q81179 drosophila
401	8	1.8	523	2	Q8C774	Q8c774 mus musculus	474	8	1.8	677	2	Q7VEL0	Q7vel0 drosophila
402	8	1.8	527	2	Q01894	Q01894 caenorhabdi	475	8	1.8	689	2	Q70UR5	Q70ur5 mus musculus
403	8	1.8	527	2	Q95Q27	Q95q27 caenorhabdi	476	8	1.8	694	1	FR22_DROME	Q9vvx3 drosophila
404	8	1.8	527	2	Q95Q28	Q95q28 caenorhabdi	477	8	1.8	695	2	Q8N568	Q8n568 homo sapien
405	8	1.8	529	2	Q95Q29	Q95q29 caenorhabdi	478	8	1.8	703	2	Q7S2G5	Q7s2g5 neurospora
406	8	1.8	535	2	Q8UZG3	Q8uzg3 cercopitheci	479	8	1.8	707	2	Q9ASH4	Q9ash4 cryza sativ
407	8	1.8	536	2	Q9UVS8	Q9uv88 aspergillus	480	8	1.8	710	2	Q7CTV9	Q7ctv9 agrobacteri
408	8	1.8	544	2	Q46171	Q46171 nephila cla	481	8	1.8	716	2	Q8U8R8	Q8u8r8 agrobacteri
409	8	1.8	547	2	Q8TFP9	Q8tf99 schizosacch	482	8	1.8	718	2	Q9NKS6	Q9nks6 leishmania
410	8	1.8	548	1	ERF_HUMAN	P50548 homo sapien	483	8	1.8	721	2	Q7QLG4	Q7qlg4 anopheles g
411	8	1.8	549	1	AMDY_YEAST	P22580 saccharomyc	484	8	1.8	727	1	BRCL_DROME	Q01r95 drosophila
412	8	1.8	550	2	Q6F379	Q6f379 oryza sativ	485	8	1.8	728	2	Q8QZ68	Q8qz68 tomato mild
413	8	1.8	551	1	ERF_MOUSE	P70459 mus musculus	486	8	1.8	730	1	CCT2_HUMAN	Q60583 homo sapien
414	8	1.8	551	2	Q6P544	Q6p544 mus musculus	487	8	1.8	733	2	Q6AWZ0	Q6awz0 homo sapien
415	8	1.8	552	2	Q6CA43	Q6ca43 yarrowia li	488	8	1.8	747	1	SPD1_NEPCL	P19837 nephila cla
416	8	1.8	552	2	Q6IFZ8	Q6ifz8 mus musculus	489	8	1.8	749	2	Q8LPD9	Q8lpd9 chlamydomon
417	8	1.8	553	2	Q8HXE2	Q8hxe2 macaca fasc	490	8	1.8	750	2	Q8LPE0	Q8lep0 chlamydomon
418	8	1.8	556	2	Q8LM88	Q8lm88 photobacter	491	8	1.8	750	2	Q9C6W1	Q9c6w1 mus musculus
419	8	1.8	558	2	Q8JKR4	Q8jkr4 heliothis z	492	8	1.8	756	2	Q68DC2	Q68dc2 homo sapien
420	8	1.8	561	2	Q6C873	Q6c873 yarrowia li	493	8	1.8	756	2	Q8JG32	Q8jg32 gallus gall
421	8	1.8	562	2	Q80WS6	Q80ws6 mus musculus	494	8	1.8	763	1	DYRA_HUMAN	Q13627 homo sapien
422	8	1.8	570	2	Q8IQC5	Q8iqc5 drosophila	495	8	1.8	763	1	DYRA_MOUSE	Q61214 mus musculus
423	8	1.8	570	2	Q95TF7	Q95tf7 drosophila	496	8	1.8	763	1	DYRA_RAT	Q63470 rattus norv
424	8	1.8	570	2	Q95665	Q95665 cellvibrio	497	8	1.8	766	2	Q9DW77	Q9dwf7 rat cytoMeg
425	8	1.8	575	2	Q6BVD6	Q6bvd6 debaryomyce	498	8	1.8	772	2	Q21492	Q21492 caenorhabdi
426	8	1.8	579	2	Q16901	Q16901 caenorhabdi	499	8	1.8	773	2	P79149	P79149 canis famil
427	8	1.8	581	2	Q18349	Q18349 drosophila	500	8	1.8	774	2	Q868B4	Q868b4 caenorhabdi
428	8	1.8	582	2	Q9VUH2	Q9vuh2 drosophila	501	8	1.8	775	2	Q21493	Q21493 caenorhabdi
429	8	1.8	584	2	Q68DB8	Q68db8 homo sapien	502	8	1.8	777	2	Q8MQ04	Q8mq04 caenorhabdi
430	8	1.8	588	2	Q9IPQ8	Q9ipq8 cytomoligus	503	8	1.8	778	1	PG46_MYCTU	P71333 mycobacteri
431	8	1.8	589	1	DYR_MOUSE	Q9zi88 mus musculus	504	8	1.8	786	2	O18740	O18740 canis famil
432	8	1.8	589	2	Q7TSJ1	Q7tsj1 mus musculus	505	8	1.8	791	2	Q9GRX2	Q9grx2 drosophila
433	8	1.8	590	2	Q7Y214	Q7y214 arabidopsis	506	8	1.8	791	2	Q9NFS1	Q9nfs1 drosophila
434	8	1.8	592	2	Q7V676	Q7v676 prochloroco	507	8	1.8	791	2	Q9VSY7	Q9vsy7 drosophila
435	8	1.8	593	2	Q8K006	Q8k006 mus musculus	508	8	1.8	805	1	E2F_DROME	Q27368 drosophila
436	8	1.8	594	2	Q9A796	Q9a796 caulobacter	509	8	1.8	805	2	Q8XUS1	Q8xus1 ralstonia s
437	8	1.8	595	2	Q8FRP9	Q8frp9 corynebacte	510	8	1.8	806	2	Q7K9G4	Q7k9g4 drosophila
438	8	1.8	599	2	Q8PEM1	Q8pem1 xanthomonas	511	8	1.8	815	2	Q96JS2	Q96js2 homo sapien
439	8	1.8	600	2	Q8TJW3	Q8tjw3 methanosarc	512	8	1.8	816	1	NEL2_HUMAN	Q99435 homo sapien
440	8	1.8	600	2	Q75RY3	Q75ry3 oleomonas s	513	8	1.8	821	2	Q9W1J9	Q9w1j9 drosophila
441	8	1.8	600	2	Q6D599	Q6d599 erwinia car	514	8	1.8	831	2	Q7RWM6	Q7rwm6 neurospora
442	8	1.8	601	2	Q887D5	Q887d5 pseudomonas	515	8	1.8	833	2	Q9UZS8	Q9uzs8 caenorhabdi
443	8	1.8	603	2	Q897G7	Q897g7 clostridium	516	8	1.8	838	2	Q9Y0C9	Q9y0c9 dictyosteli
444	8	1.8	604	2	Q9ALV2	Q9alv2 enterobacte	517	8	1.8	847	2	Q9GN13	Q9gn13 homo sapien
445	8	1.8	605	2	Q936X2	Q936x2 pseudomonas	518	8	1.8	849	2	Q8GCE4	Q8gce4 mus musculus
446	8	1.8	607	2	Q7QJ60	Q7qj60 anopheles g	519	8	1.8	858	2	Q9UA70	Q9ua70 dictyosteli
447	8	1.8	608	1	SAV_DROME	Q9vcr6 drosophila	520	8	1.8	858	2	Q9XXV8	Q9xxv8 dictyosteli
448	8	1.8	609	2	Q96E25	Q96e25 homo sapien	521	8	1.8	859	2	Q7PRJ1	Q7prj1 anopheles g
449	8	1.8	614	2	Q80220	Q80220 brachydanio	522	8	1.8	866	2	Q962I0	Q962i0 drosophila
450	8	1.8	617	2	Q46172	Q46172 nephila cla	523	8	1.8	867	2	Q7ZVU1	Q7zvu1 brachydanio
451	8	1.8	618	2	Q6CB69	Q6cb69 yarrowia li	524	8	1.8	877	2	Q9UE51	Q9uf51 homo sapien
452	8	1.8	619	2	Q9IPQ9	Q9ipq9 cytomoligus	525	8	1.8	881	2	Q9NE42	Q9ne42 leishmania
453	8	1.8	629	1	DYR_HUMAN	Q9y463 homo sapien	526	8	1.8	883	2	Q8TTT9	Q8ttt9 methanosarc
454	8	1.8	629	2	Q9EPM2	Q9epm2 mus musculus	527	8	1.8	890	1	BCN5_CLOPE	P08596 clostridium
455	8	1.8	633	2	Q9ZKQ8	Q9zq88 arabidopsis	528	8	1.8	893	2	Q7XNW2	Q7xmw2 oryza sativ
456	8	1.8	638	2	Q8EAU4	Q8eau4 shewanella	529	8	1.8	894	2	Q9GYB4	Q9gyb4 leishmania
457	8	1.8	643	2	Q9LSL2	Q9lsl2 arabidopsis	530	8	1.8	903	2	Q8TLY6	Q8tly6 methanosarc
458	8	1.8	643	2	Q87B00	Q87e00 xylolla fas	531	8	1.8	908	2	Q8GJ00	Q8g100 dictyosteli
459	8	1.8	644	2	Q8WSW4	Q8ws44 nephila cla	532	8	1.8	913	2	Q6C979	Q6c979 yarrowia li
460	8	1.8	644	2	Q8BKB2	Q8bkb2 mus musculus	533	8	1.8	918	2	Q7SGE4	Q7sged4 neurospora
461	8	1.8	645	2	Q84965	Q84965 anaplagma p	534	8	1.8	918	2	Q8ML49	Q8ml49 drosophila
462	8	1.8	645	2	Q6PG69	Q6pg69 mus musculus	535	8	1.8	918	2	Q8GNR8	Q8gnr8 drosophila
463	8	1.8	646	2	Q96F45	Q96f45 homo sapien	536	8	1.8	927	2	Q7QBA4	Q7qba4 anopheles g
464	8	1.8	650	2	Q9N013	Q9n013 macaca fasc	537	8	1.8	934	1	IP3L_RAT	P42335 rattus norv
465	8	1.8	656	1	UL25_HCMVA	P16761 human cytom	538	8	1.8	937	1	HYR1_CANAL	P46591 candida alb
466	8	1.8	656	2	Q7MQ68	Q7mq68 human cytom	539	8	1.8	948	2	Q8T065	Q8t065 drosophila
467	8	1.8	660	2	Q23832	Q23832 cryptospori	540	8	1.8	950	2	Q9ULL2	Q9ull2 homo sapien
468	8	1.8	661	2	Q59674	Q59674 cellvibrio	541	8	1.8	957	2	Q8TR89	Q8tr89 methanosarc
469	8	1.8	663	2	Q8CHT4	Q8cht4 mus musculus	542	8	1.8	965	2	Q66665	Q66665 equid herpe

543	8	1.8	968	2	Q9VKL0	Q9vkl0 drosophila	616	8	1.8	2761	2	Q18447	Q18447 caenorhabdi
544	8	1.8	970	2	Q6MTA8	Q6mta8 mycoplasma	617	8	1.8	2850	1	HORN HUMAN	Q86y23 homo sapien
545	8	1.8	973	2	Q7PMX5	Q7pmx5 anopheles g	618	8	1.8	3080	2	Q9V602	Q9v602 drosophila
546	8	1.8	977	1	KFMS MOUSE	P09581 mus musculus	619	8	1.8	3109	2	Q9BMQ0	Q9bmq0 drosophila
547	8	1.8	977	1	Q6NXV8	Q6nxv8 mus musculus	620	8	1.8	3446	2	Q86AC8	Q86ac8 dictyosteli
548	8	1.8	978	1	KFMS RAT	Q00495 rattus norv	621	8	1.8	3726	1	TRX_DROME	P20659 drosophila
549	8	1.8	1007	2	Q8C8T6	Q8c8t6 mus musculus	622	8	1.8	3726	2	Q9VFL1	Q9vfl1 drosophila
550	8	1.8	1009	2	Q8PM63	Q8pm63 xanthomonas	623	8	1.8	10	2	Q8BHN2	Q8bhn2 mus musculus
551	8	1.8	1024	1	U203 ARATH	Q9m2q4 arabidopsis	624	7	1.6	14	2	Q8CJA8	Q8cja8 mus musculus
552	8	1.8	1029	1	RIP3 RAT	Q9ere6 rattus norv	625	7	1.6	15	2	Q8CJA9	Q8cja9 mus musculus
553	8	1.8	1031	2	Q7SRN6	Q7srn6 neurospora	626	7	1.6	16	2	Q86UF7	Q86uf7 homo sapien
554	8	1.8	1033	2	Q8D6V3	Q8d6v3 vibrio vuln	627	7	1.6	38	2	Q96850	Q96850 bombyx mori
555	8	1.8	1037	2	Q6P559	Q6p559 mus musculus	628	7	1.6	38	2	Q96851	Q96851 bombyx mori
556	8	1.8	1040	2	Q7MDU0	Q7mdu0 vibrio vuln	629	7	1.6	46	2	Q8MQF7	Q8mqf4 bdellovibri
557	8	1.8	1052	2	Q8Q0S0	Q8q0s0 methanosarc	630	7	1.6	51	2	Q8CIW7	Q8ciw7 mus musculus
558	8	1.8	1087	2	Q7UUE7	Q7uu67 rhodopirell	631	7	1.6	52	2	Q67U08	Q67u08 oryza sativ
559	8	1.8	1108	2	Q7YU81	Q7yu81 drosophila	632	7	1.6	54	2	Q85513	Q85513 feline earc
560	8	1.8	1108	2	Q9V788	Q9v788 drosophila	633	7	1.6	57	2	Q6YRP3	Q6yrp3 oryza sativ
561	8	1.8	1119	2	Q6ZQ66	Q6zq66 mus musculus	634	7	1.6	57	2	Q92K72	Q92k72 rhizobium m
562	8	1.8	1141	1	SRE2 HUMAN	Q12772 homo sapien	635	7	1.6	61	2	Q65285	Q65285 african swi
563	8	1.8	1193	2	Q86V36	Q86v36 homo sapien	636	7	1.6	62	1	PA2S AUSSU	P59067 austrelaps
564	8	1.8	1198	2	Q7PKP4	Q7pkp4 anopheles g	637	7	1.6	62	2	Q6X1B8	Q6xib8 drosophila
565	8	1.8	1229	2	Q68H99	Q68h99 sus scrofa	638	7	1.6	63	2	Q25832	Q25832 plasmodium
566	8	1.8	1230	1	ST20 CANAL	Q92212 candida alb	639	7	1.6	65	2	Q9ZRS4	Q9ztz4 zea mays (m
567	8	1.8	1230	2	Q13431	Q13431 candida alb	640	7	1.6	66	1	PER_DROSA	Q04536 drosophila
568	8	1.8	1233	1	M4K4 MOUSE	P97820 mus musculus	641	7	1.6	66	2	Q9XZQ8	Q9xxz8 caenorhabdi
569	8	1.8	1235	2	Q8T250	Q8t250 dictyosteli	642	7	1.6	69	2	Q86JP8	Q86jp8 dictyosteli
570	8	1.8	1239	1	M4K4 HUMAN	Q95819 homo sapien	643	7	1.6	71	2	Q8H442	Q8h442 oryza sativ
571	8	1.8	1255	2	Q6ZQ68	Q6zq68 mus musculus	644	7	1.6	72	2	Q7YTK1	Q7ytk1 caenorhabdi
572	8	1.8	1258	2	Q8R457	Q8r457 mus musculus	645	7	1.6	72	2	Q6Z4A6	Q6z4a6 oryza sativ
573	8	1.8	1258	2	Q8R458	Q8r458 rattus norv	646	7	1.6	72	2	Q8H7A9	Q8h7a9 arabidopsis
574	8	1.8	1263	2	Q7R1D0	Q7r1d0 giardia lam	647	7	1.6	72	2	Q8UUQ2	Q8uuq2 oncorhynch
575	8	1.8	1265	2	Q8EV72	Q8ev72 mycoplasma	648	7	1.6	73	2	Q64M28	Q64m28 bacteroides
576	8	1.8	1266	2	Q800D9	Q800d9 gallus gall	649	7	1.6	74	2	Q6TLV4	Q6tlv4 macaca fasc
577	8	1.8	1278	2	Q9AV65	Q9av65 oryza sativ	650	7	1.6	74	2	Q6L549	Q6l549 oryza sativ
578	8	1.8	1281	2	Q82KW0	Q82kw0 streptomyc	651	7	1.6	75	2	Q6YMA4	Q6yma4 oryza sativ
579	8	1.8	1287	2	Q68DW9	Q68dw9 homo sapien	652	7	1.6	77	2	Q7SEB9	Q7seb9 neurospora
580	8	1.8	1317	1	GAP CAEEL	P34288 caenorhabdi	653	7	1.6	78	2	Q63082	Q63082 rattus norv
581	8	1.8	1349	2	Q9B272	Q9b272 homo sapien	654	7	1.6	79	2	Q6YTA1	Q6yta1 oryza sativ
582	8	1.8	1359	2	Q9P271	Q9p271 homo sapien	655	7	1.6	80	2	Q6ASQ3	Q6asq3 oryza sativ
583	8	1.8	1359	2	Q8CHH0	Q8chh0 mus musculus	656	7	1.6	82	2	Q9FYR0	Q9fyro arabidopsis
584	8	1.8	1404	2	Q86180	Q86180 dictyosteli	657	7	1.6	84	2	Q7X182	Q7x182 oryza sativ
585	8	1.8	1422	2	Q95KU4	Q95ku4 canis famli	658	7	1.6	86	2	Q8CJA5	Q8cja5 mus musculus
586	8	1.8	1456	2	Q6PDJ8	Q6pdj8 mus musculus	659	7	1.6	87	2	Q9GC22	Q9gc22 oceanodroma
587	8	1.8	1474	2	Q86G87	Q86g87 pseudoplusi	660	7	1.6	87	2	Q9DUC6	Q9duc6 tt virus. o
588	8	1.8	1476	2	Q8ST66	Q8st66 dictyosteli	661	7	1.6	88	2	Q84MS9	Q84ms9 oryza sativ
589	8	1.8	1476	2	Q965D3	Q965d3 dictyosteli	662	7	1.6	90	2	Q8HAN9	Q8han9 oryza sativ
590	8	1.8	1479	2	Q7Q1C2	Q7q1c2 anopheles g	663	7	1.6	90	2	Q6NTS2	Q6ntc2 xenopus lae
591	8	1.8	1490	1	CRK7 HUMAN	Q9nyv4 homo sapien	664	7	1.6	91	2	Q92G67	Q92g67 rickettsia
592	8	1.8	1523	2	Q86L99	Q86l99 dictyosteli	665	7	1.6	91	2	Q8XBR6	Q8xb6 escherichia
593	8	1.8	1583	2	Q6C398	Q6c398 yarrowia li	666	7	1.6	94	2	Q68AY8	Q68ay8 canis famli
594	8	1.8	1606	2	Q924A2	Q924a2 mus musculus	667	7	1.6	95	2	Q6DGJ3	Q6dgt3 brachydanio
595	8	1.8	1693	2	Q86J17	Q86j17 dictyosteli	668	7	1.6	96	2	Q88DT1	Q88dt1 pseudomonas
596	8	1.8	1723	1	FW20 CHLPN	Q9z812 chlamydia p	669	7	1.6	97	2	Q8AGE5	Q8ages leifsonia x
597	8	1.8	1751	2	Q6C3G1	Q6c3g1 yarrowia li	670	7	1.6	99	2	Q8C9S1	Q8c9s1 mus musculus
598	8	1.8	1796	2	Q6NNW7	Q6nnw7 drosophila	671	7	1.6	99	2	Q9SP64	Q9sp64 penaeus van
599	8	1.8	1851	2	Q7KV98	Q7kv98 drosophila	672	7	1.6	99	2	Q8PLF4	Q8plf4 xanthomonas
600	8	1.8	1889	2	Q7Q138	Q7q138 anopheles g	673	7	1.6	100	2	Q6NZ39	Q6nz39 homo sapien
601	8	1.8	1934	2	Q7QDG9	Q7qdg9 anopheles g	674	7	1.6	100	2	Q8QGB6	Q8qgb6 oncorhynch
602	8	1.8	1960	1	TF20 HUMAN	Q9ugu0 homo sapien	675	7	1.6	100	2	Q8QGB7	Q8qgb7 oncorhynch
603	8	1.8	1960	2	Q7R4L8	Q7r4l8 giardia lam	676	7	1.6	100	2	Q710Q6	Q710q6 oncorhynch
604	8	1.8	2142	1	B4634	B4634 homo sapien	677	7	1.6	102	1	MIH PENVA	P55322 penaeus van
605	8	1.8	2148	2	Q8IR53	Q8ir53 drosophila	678	7	1.6	102	2	Q816N5	Q8i6n5 penaeus van
606	8	1.8	2157	2	Q95875	Q95875 homo sapien	679	7	1.6	102	2	Q817Y6	Q8i7y6 penaeus van
607	8	1.8	2157	2	Q96QC6	Q96qc6 homo sapien	680	7	1.6	103	2	Q810H5	Q8i0h5 penaeus van
608	8	1.8	2157	2	Q6P9P7	Q6p9p7 homo sapien	681	7	1.6	105	2	Q9FW42	Q9fw42 oryza sativ
609	8	1.8	2167	1	SHK1 RAT	Q9wv48 rattus norv	682	7	1.6	106	2	Q9NR52	Q9nr52 homo sapien
610	8	1.8	2196	2	Q9VY40	Q9vy40 drosophila	683	7	1.6	107	2	Q52119	Q52119 plasmid psw
611	8	1.8	2197	2	Q9W016	Q9w016 drosophila	684	7	1.6	109	2	Q9VTF2	Q9vtf2 drosophila
612	8	1.8	2223	2	Q7Q1V0	Q7qv0 anopheles g	685	7	1.6	110	2	Q24333	Q24333 drosophila
613	8	1.8	2228	2	Q9VN58	Q9vn58 drosophila	686	7	1.6	110	2	Q9KTV8	Q9kyv8 streptomyc
614	8	1.8	2254	2	Q75JU5	Q75ju5 dictyosteli	687	7	1.6	111	2	Q9VEJ1	Q9vej1 drosophila
615	8	1.8	2517	2	Q7QL19	Q7ql19 anopheles g	688	7	1.6	113	2	Q82H68	Q82h68 streptomyc

689	7	1.6	114	2	Q9LB87	Q9LB87 helicobacte	762	7	1.6	157	2	Q8CJA7	Q8CJA7 mus musculu
690	7	1.6	116	2	Q9LB77	Q9LB77 helicobacte	763	7	1.6	158	2	Q6X757	Q6X757 neurospora
691	7	1.6	118	1	CRYP_CRYPA	F52753 cryptonectr	764	7	1.6	159	2	Q6X752	Q6X752 neurospora
692	7	1.6	118	1	NLTI_ARATH	Q42589 arabidopsis	765	7	1.6	159	2	Q7QK59	Q7QK59 anopheles g
693	7	1.6	118	2	Q6IKB2	Q6IKB2 drosophila	766	7	1.6	159	2	Q87BU9	Q87BU9 xylella fas
694	7	1.6	118	2	Q9S1B5	Q9S1B5 arthrobacte	767	7	1.6	159	2	Q8JIL5	Q8JIL5 astatotilap
695	7	1.6	119	2	Q99865	Q99865 cynoscion a	768	7	1.6	159	2	Q8JIL6	Q8JIL6 astatoreoch
696	7	1.6	119	2	Q8B8C1	Q8B8C1 mus musculu	769	7	1.6	159	2	Q8JIL7	Q8JIL7 tropheus du
697	7	1.6	120	2	Q648Z3	Q648Z3 uncultured	770	7	1.6	159	2	Q8JIL8	Q8JIL8 labidochrom
698	7	1.6	120	2	Q82HT6	Q82HT6 streptomyc	771	7	1.6	160	2	Q8UKJ6	Q8UKJ6 heliothis z
699	7	1.6	121	2	Q9LB62	Q9LB62 helicobacte	772	7	1.6	161	2	Q6X751	Q6X751 neurospora
700	7	1.6	124	2	Q9VQ84	Q9VQ84 drosophila	773	7	1.6	161	2	Q6X754	Q6X754 neurospora
701	7	1.6	125	2	Q8LP38	Q8LP38 pueraria lo	774	7	1.6	161	2	Q6X755	Q6X755 neurospora
702	7	1.6	125	2	Q655T4	Q655T4 oryza sativ	775	7	1.6	161	2	Q43472	Q43472 hordeum vul
703	7	1.6	125	2	Q73282	Q73282 human immun	776	7	1.6	161	2	Q8ZCP1	Q8ZCP1 yersinia pe
704	7	1.6	128	2	Q6MWK9	Q6MWK9 oryza sativ	777	7	1.6	162	2	Q8RMH6	Q8RMH6 chloroflexu
705	7	1.6	129	2	Q9LB75	Q9LB75 helicobacte	778	7	1.6	163	2	Q6X749	Q6X749 neurospora
706	7	1.6	129	2	Q9LB87	Q9LB87 helicobacte	779	7	1.6	163	2	Q8IQW8	Q8IQW8 drosophila
707	7	1.6	129	2	Q8JAH6	Q8JAH6 chimpanzee	780	7	1.6	163	2	Q7XM11	Q7XM11 oryza sativ
708	7	1.6	131	2	Q8TW52	Q8TW52 methanopyru	781	7	1.6	164	2	Q6X763	Q6X763 neurospora
709	7	1.6	131	2	Q84N67	Q84N67 swartzia jo	782	7	1.6	164	2	Q6XQF0	Q6XQF0 enterobacte
710	7	1.6	132	2	Q7Y7S2	Q7Y7S2 caenorhabdi	783	7	1.6	165	2	Q6X759	Q6X759 neurospora
711	7	1.6	132	2	Q9LBB9	Q9LBB9 helicobacte	784	7	1.6	166	2	Q8GQX0	Q8GQX0 plasmodium
712	7	1.6	133	1	VEGH_OREN2	P52584 orf virus (785	7	1.6	166	2	Q8RYF2	Q8RYF2 avena strig
713	7	1.6	133	2	Q8DA19	Q8DA19 vibrio vuln	786	7	1.6	167	2	Q6X753	Q6X753 neurospora
714	7	1.6	133	2	Q8FMP5	Q8FMP5 corynebacte	787	7	1.6	167	2	Q7X683	Q7X683 oryza sativ
715	7	1.6	134	2	Q7MFX0	Q7MFX0 vibrio vuln	788	7	1.6	167	2	Q7P7Z4	Q7P7Z4 fusobacteri
716	7	1.6	136	2	Q6BKU5	Q6BKU5 debaryomyc	789	7	1.6	167	2	Q9UKT9	Q9UKT9 neisseria m
717	7	1.6	136	2	Q8CIU7	Q8CIU7 mus musculu	790	7	1.6	167	2	Q63115	Q63115 rattus norv
718	7	1.6	137	2	Q7RAW9	Q7RAW9 plasmodium	791	7	1.6	168	2	Q711H0	Q711H0 lactobacill
719	7	1.6	138	2	Q8AXY1	Q8AXY1 bothrops ja	792	7	1.6	169	2	Q7KR54	Q7KR54 drosophila
720	7	1.6	139	2	Q7QZK6	Q7QZK6 anopheles g	793	7	1.6	170	2	Q43539	Q43539 lilium long
721	7	1.6	139	2	Q9V556	Q9V556 drosophila	794	7	1.6	172	2	Q8LJQ4	Q8LJQ4 prunus pers
722	7	1.6	139	2	Q9MA77	Q9MA77 arabidopsis	795	7	1.6	172	2	Q8B0S5	Q8B0S5 mus musculu
723	7	1.6	140	1	EXB1_XANCP	Q34259 xanthomonas	796	7	1.6	173	2	Q876E9	Q876E9 saccharomyc
724	7	1.6	140	2	Q9LB71	Q9LB71 helicobacte	797	7	1.6	173	2	Q6Z7U4	Q6Z7U4 oryza sativ
725	7	1.6	140	2	Q8PRF3	Q8PRF3 xanthomonas	798	7	1.6	173	2	Q7N8T0	Q7N8T0 photorhabdu
726	7	1.6	143	2	Q6IKU8	Q6IKU8 drosophila	799	7	1.6	173	2	Q7N8T1	Q7N8T1 photorhabdu
727	7	1.6	143	2	Q61L10	Q61L10 drosophila	800	7	1.6	175	2	Q7KLE9	Q7KLE9 drosophila
728	7	1.6	143	2	Q9QZD3	Q9QZD3 rattus ever	801	7	1.6	175	2	Q8GWW9	Q8GWW9 arabidopsis
729	7	1.6	144	2	Q7M4U6	Q7M4U6 pleurotus c	802	7	1.6	175	2	Q9LSN6	Q9LSN6 arabidopsis
730	7	1.6	145	1	HB2_XENBO	P07433 xenopus bor	803	7	1.6	175	2	Q9M1T6	Q9M1T6 arabidopsis
731	7	1.6	145	2	Q23606	Q23606 caenorhabdi	804	7	1.6	175	2	Q66639	Q66639 aquifex aeo
732	7	1.6	146	2	Q9NWA0	Q9NWA0 homo sapien	805	7	1.6	175	2	Q8FS08	Q8FS08 corynebacte
733	7	1.6	146	2	Q6ZLH9	Q6ZLH9 oryza sativ	806	7	1.6	175	2	Q9JW30	Q9JW30 neisseria m
734	7	1.6	146	2	Q6DXM5	Q6DXM5 xenopus lae	807	7	1.6	175	2	Q6AZH4	Q6AZH4 xenopus lae
735	7	1.6	147	2	Q7LHH0	Q7LHH0 saccharomyc	808	7	1.6	177	2	Q6C8X6	Q6C8X6 yarrowia li
736	7	1.6	148	2	Q6X748	Q6X748 neurospora	809	7	1.6	177	2	Q6CBT3	Q6CBT3 yarrowia li
737	7	1.6	148	2	Q7Q8C1	Q7Q8C1 anopheles g	810	7	1.6	177	2	Q6CFK5	Q6CFK5 yarrowia li
738	7	1.6	148	2	Q9UB93	Q9UB93 helicoverpa	811	7	1.6	177	2	Q85KF6	Q85KF6 macodon an
739	7	1.6	149	2	Q6X747	Q6X747 neurospora	812	7	1.6	177	2	Q9M9H3	Q9M9H3 arabidopsis
740	7	1.6	149	2	Q6X758	Q6X758 neurospora	813	7	1.6	177	2	Q63HA4	Q63HA4 bacillus ce
741	7	1.6	150	2	Q8O490	Q8O490 arabidopsis	814	7	1.6	177	2	Q92F29	Q92F29 listeria ce
742	7	1.6	150	2	Q8RYF3	Q8RYF3 avena strig	815	7	1.6	177	2	Q73FB0	Q73FB0 bacillus ce
743	7	1.6	151	2	Q6X756	Q6X756 neurospora	816	7	1.6	177	2	Q81J54	Q81J54 bacillus ce
744	7	1.6	151	2	Q7QHH5	Q7QHH5 anopheles g	817	7	1.6	177	2	Q81VU4	Q81VU4 bacillus an
745	7	1.6	151	2	Q9LB65	Q9LB65 helicobacte	818	7	1.6	177	2	Q6HPS2	Q6HPS2 bacillus th
746	7	1.6	151	2	Q8B0V5	Q8B0V5 mus musculu	819	7	1.6	177	2	Q6KYJ3	Q6KYJ3 bacillus an
747	7	1.6	152	2	Q86BL6	Q86BL6 schistosoma	820	7	1.6	178	2	Q9C7W1	Q9C7W1 arabidopsis
748	7	1.6	152	2	Q73VH4	Q73VH4 mycobacteri	821	7	1.6	179	2	Q7R2J4	Q7R2J4 giardia lam
749	7	1.6	153	2	Q6K8J6	Q6K8J6 oryza sativ	822	7	1.6	180	2	Q9LR35	Q9LR35 arabidopsis
750	7	1.6	153	2	Q8K064	Q8K064 mus musculu	823	7	1.6	181	2	Q61KG1	Q61KG1 drosophila
751	7	1.6	154	2	Q6X750	Q6X750 neurospora	824	7	1.6	181	2	Q864S4	Q864S4 ovis aries
752	7	1.6	154	2	Q6X761	Q6X761 neurospora	825	7	1.6	181	2	Q69QAS	Q69QAS oryza sativ
753	7	1.6	154	2	Q6B877	Q6B877 ixodes paci	826	7	1.6	181	2	Q82K97	Q82K97 streptomyc
754	7	1.6	154	2	Q79FQ8	Q79FQ8 mycobacteri	827	7	1.6	181	2	Q8EKA9	Q8EKA9 shewanella
755	7	1.6	154	2	Q7U0C8	Q7U0C8 saccharomyc	828	7	1.6	182	1	K2C3_BOVIN	P04261 bos taurus
756	7	1.6	155	1	YFH3_YEAST	P43587 saccharomyc	829	7	1.6	182	1	K2C4_BOVIN	P04260 bos taurus
757	7	1.6	155	2	Q8SV08	Q8SV08 encephalito	830	7	1.6	182	2	Q6ZP96	Q6ZP96 homo sapien
758	7	1.6	155	2	Q6XHY3	Q6XHY3 drosophila	831	7	1.6	182	2	Q86MQ9	Q86MQ9 drosophila
759	7	1.6	157	2	Q6X760	Q6X760 neurospora	832	7	1.6	182	2	Q948F5	Q948F5 oryza sativ
760	7	1.6	157	2	Q6X762	Q6X762 neurospora	833	7	1.6	182	2	Q6K846	Q6K846 oryza sativ
761	7	1.6	157	2	Q96DN7	Q96DN7 homo sapien	834	7	1.6	183	2	Q86QX1	Q86QX1 plasmodium

835	7	1.6	183	2	Q69886	Q69886	Oryza sativ	908	7	1.6	218	2	Q6K5T4	Q6K5T4	Oryza sativ
836	7	1.6	183	2	Q6Y7H2	Q6Y7H2	anaplasma p	909	7	1.6	218	2	Q8UVD4	Q8UVD4	Gallus gall
837	7	1.6	183	2	Q8P912	Q8P912	xanthomonas	910	7	1.6	219	2	Q7SEB3	Q7SEB3	neurospora
838	7	1.6	183	2	Q8BSF8	Q8BSF8	mus musculus	911	7	1.6	219	2	Q9NG66	Q9NG66	speleonecete
839	7	1.6	184	2	Q8C2X0	Q8C2X0	cladosporiu	912	7	1.6	219	2	Q8VK50	Q8VK50	mycobacteri
840	7	1.6	184	2	Q83FU1	Q83FU1	tropheryma	913	7	1.6	219	2	Q7VW56	Q7VW56	bordetella
841	7	1.6	185	2	Q9NAB4	Q9NAB4	caenorhabdi	914	7	1.6	220	2	Q8MVP0	Q8MVP0	bolitenia vi
842	7	1.6	185	2	Q8L8M5	Q8L8M5	arabidopsis	915	7	1.6	220	2	Q7PVU8	Q7PVU8	anopheles g
843	7	1.6	185	2	Q705U8	Q705U8	avena strig	916	7	1.6	220	2	Q6ZGC4	Q6ZGC4	Oryza sativ
844	7	1.6	185	2	Q8H2M5	Q8H2M5	Oryza sativ	917	7	1.6	220	2	Q6NF64	Q6NF64	Corynebacte
845	7	1.6	185	2	Q8C5Y9	Q8C5Y9	mus musculus	918	7	1.6	221	2	Q7RYB1	Q7RYB1	neurospora
846	7	1.6	186	2	Q7QT36	Q7QT36	giardia lam	919	7	1.6	221	2	Q6SEW8	Q6SEW8	bacillus li
847	7	1.6	186	2	Q85KG5	Q85KG5	macrododon an	920	7	1.6	221	2	Q8YXH1	Q8YXH1	anabaena sp
848	7	1.6	186	2	Q705U9	Q705U9	avena strig	921	7	1.6	221	2	Q6WF72	Q6WF72	bdellovibri
849	7	1.6	188	2	Q9VVD8	Q9VVD8	drosofila	922	7	1.6	222	2	Q867E3	Q867E3	drosofila
850	7	1.6	188	2	Q72NE3	Q72NE3	leptospi	923	7	1.6	222	2	Q868B5	Q868B5	drosofila
851	7	1.6	188	2	Q8F844	Q8F844	leptospi	924	7	1.6	222	2	Q86ML2	Q86ML2	drosofila
852	7	1.6	189	2	Q668S3	Q668S3	yersinia ps	925	7	1.6	222	2	Q7YRX1	Q7YRX1	procyon loc
853	7	1.6	189	2	Q8CLE0	Q8CLE0	yersinia pe	926	7	1.6	222	2	Q69K36	Q69K36	Oryza sativ
854	7	1.6	190	2	Q9BX21	Q9BX21	homo sapien	927	7	1.6	222	2	Q7W5L3	Q7W5L3	bordetella
855	7	1.6	191	2	Q46029	Q46029	chironomus	928	7	1.6	222	2	Q7WD49	Q7WD49	bordetella
856	7	1.6	191	2	Q93JB5	Q93JB5	streptomyc	929	7	1.6	222	2	Q82RK8	Q82RK8	streptomyc
857	7	1.6	192	2	Q7YV80	Q7YV80	cryptospori	930	7	1.6	223	1	COAT_TRVCA	COAT_TRVCA	tobacco rat
858	7	1.6	192	2	Q7XDT3	Q7XDT3	Oryza sativ	931	7	1.6	224	2	Q17668	Q17668	caenorhabdi
859	7	1.6	192	2	Q8DYK7	Q8DYK7	streptococc	932	7	1.6	224	2	Q6ZIG9	Q6ZIG9	Oryza sativ
860	7	1.6	192	2	Q8E463	Q8E463	streptococc	933	7	1.6	225	2	Q866V9	Q866V9	macrotus ca
861	7	1.6	193	1	CIT1_HUMAN	CIT1_HUMAN	homo sapien	934	7	1.6	225	2	Q75HQ2	Q75HQ2	Oryza sativ
862	7	1.6	193	2	Q66250	Q66250	mycobacteri	935	7	1.6	225	2	Q90XZ3	Q90XZ3	erpetoichth
863	7	1.6	193	2	Q8NRP9	Q8NRP9	corynebacte	936	7	1.6	226	2	Q7QCJ2	Q7QCJ2	anopheles g
864	7	1.6	193	2	Q88PF9	Q88PF9	pseudomonas	937	7	1.6	226	2	Q22684	Q22684	arabidopsis
865	7	1.6	195	2	Q7PUD3	Q7PUD3	anopheles g	938	7	1.6	226	2	Q9LK95	Q9LK95	arabidopsis
866	7	1.6	196	2	Q6L4V1	Q6L4V1	Oryza sativ	939	7	1.6	227	2	Q84W21	Q84W21	arabidopsis
867	7	1.6	196	2	Q9A726	Q9A726	caulobacter	940	7	1.6	228	2	Q6YW05	Q6YW05	Oryza sativ
868	7	1.6	197	2	Q93103	Q93103	aedes aegyp	941	7	1.6	230	2	Q9HLZ9	Q9HLZ9	thermoplasm
869	7	1.6	197	2	Q9WM61	Q9WM61	streptococc	942	7	1.6	230	2	Q69GY7	Q69GY7	solanum tub
870	7	1.6	198	2	Q9CRS6	Q9CRS6	mus musculus	943	7	1.6	231	1	YC9G_SCHPO	YC9G_SCHPO	schizosacch
871	7	1.6	199	2	Q8T1B2	Q8T1B2	dictyosteli	944	7	1.6	231	2	Q94F39	Q94F39	arabidopsis
872	7	1.6	199	2	Q82GT5	Q82GT5	streptomyc	945	7	1.6	233	2	Q9NZ86	Q9NZ86	homo sapien
873	7	1.6	200	1	SP24_BOVIN	SP24_BOVIN	bos taurus	946	7	1.6	233	2	Q9BIT6	Q9BIT6	nephila ina
874	7	1.6	200	2	Q7TTE1	Q7TTE1	bordetella	947	7	1.6	233	2	Q9XUQ2	Q9XUQ2	caenorhabdi
875	7	1.6	200	2	Q72087	Q72087	human immun	948	7	1.6	234	2	Q9XRE4	Q9XRE4	brachydanio
876	7	1.6	201	2	Q8WSQ6	Q8WSQ6	penaeus jap	949	7	1.6	234	2	Q76KU9	Q76KU9	pisum sativ
877	7	1.6	202	2	Q754L2	Q754L2	ashbya goss	950	7	1.6	234	2	Q03538	Q03538	plasmid rp4
878	7	1.6	202	2	Q9SII2	Q9SII2	arabidopsis	951	7	1.6	234	2	Q62IB0	Q62IB0	burkholderi
879	7	1.6	202	2	Q7WMF1	Q7WMF1	bordetella	952	7	1.6	234	2	Q6DHH2	Q6DHH2	brachydanio
880	7	1.6	202	2	Q9AG99	Q9AG99	caulobacter	953	7	1.6	234	2	Q8AXN7	Q8AXN7	cyprinus ca
881	7	1.6	203	2	Q70TH4	Q70TH4	ovis aries	954	7	1.6	235	2	Q8IGN6	Q8IGN6	drosofila
882	7	1.6	203	2	Q6GX94	Q6GX94	streptococc	955	7	1.6	236	2	Q6GLZ6	Q6GLZ6	xenopus lae
883	7	1.6	204	2	Q84US8	Q84US8	arabidopsis	956	7	1.6	236	2	Q9W6H2	Q9W6H2	xenopus lae
884	7	1.6	204	2	Q9AV63	Q9AV63	Oryza sativ	957	7	1.6	237	2	Q38004	Q38004	bacterioph
885	7	1.6	204	2	Q9AXJ0	Q9AXJ0	Oryza sativ	958	7	1.6	237	2	Q7XLA1	Q7XLA1	Oryza sativ
886	7	1.6	204	2	Q9SHJ9	Q9SHJ9	arabidopsis	959	7	1.6	237	2	Q674Y1	Q674Y1	gymnarchus
887	7	1.6	204	2	Q6QWB0	Q6QWB0	azospirillu	960	7	1.6	237	2	Q9PUT2	Q9PUT2	brachydanio
888	7	1.6	204	2	Q7V6G4	Q7V6G4	prochloroco	961	7	1.6	238	2	Q63WG5	Q63WG5	burkholderi
889	7	1.6	205	2	Q8LCZ7	Q8LCZ7	arabidopsis	962	7	1.6	239	2	Q6ZJE7	Q6ZJE7	Oryza sativ
890	7	1.6	205	2	Q7XUD3	Q7XUD3	Oryza sativ	963	7	1.6	239	2	Q8G6R1	Q8G6R1	bifidobacte
891	7	1.6	207	2	Q8WYX6	Q8WYX6	homo sapien	964	7	1.6	240	2	Q6BNL7	Q6BNL7	debaromyce
892	7	1.6	208	2	Q9W2Z9	Q9W2Z9	drosofila	965	7	1.6	240	2	Q6B8G7	Q6B8G7	ixodes paci
893	7	1.6	208	2	Q70614	Q70614	rattus sp.	966	7	1.6	240	2	Q8RU62	Q8RU62	Oryza sativ
894	7	1.6	208	2	Q9QYQ9	Q9QYQ9	rattus exul	967	7	1.6	240	2	Q6UUL3	Q6UUL3	Oryza sativ
895	7	1.6	209	2	Q7X7I0	Q7X7I0	Oryza sativ	968	7	1.6	240	2	Q87YL4	Q87YL4	pseudomonas
896	7	1.6	209	2	Q83UE0	Q83UE0	cloning vec	969	7	1.6	241	2	Q8LM66	Q8LM66	Oryza sativ
897	7	1.6	210	2	Q8XTQ7	Q8XTQ7	ralstonia s	970	7	1.6	243	2	Q67WQ9	Q67WQ9	Oryza sativ
898	7	1.6	211	1	ZEP5_ARATH	ZEP5_ARATH	arabidopsis	971	7	1.6	245	2	Q863J4	Q863J4	ovis aries
899	7	1.6	211	2	Q8H5E5	Q8H5E5	Oryza sativ	972	7	1.6	245	2	Q849T3	Q849T3	haemophilus
900	7	1.6	213	2	Q7VDU5	Q7VDU5	prochloroco	973	7	1.6	246	2	Q8XGK1	Q8XGK1	salmonella
901	7	1.6	214	2	Q8JFN4	Q8JFN4	oncorhynch	974	7	1.6	246	2	Q7CQX7	Q7CQX7	salmonella
902	7	1.6	216	1	FLGH_AQUAE	FLGH_AQUAE	aquifex aeo	975	7	1.6	247	2	Q41616	Q41616	trifolium r
903	7	1.6	216	2	Q7XW20	Q7XW20	Oryza sativ	976	7	1.6	247	2	Q89LL9	Q89LL9	bradyrhizob
904	7	1.6	216	2	Q67QM3	Q67QM3	symbiobacte	977	7	1.6	247	2	Q8K116	Q8K116	mus musculu
905	7	1.6	216	2	Q7WAY7	Q7WAY7	bordetella	978	7	1.6	248	1	ATPD_TOBAC	ATPD_TOBAC	nicotiana t
906	7	1.6	217	1	RIT2_MOUSE	RIT2_MOUSE	mus musculu	979	7	1.6	248	2	Q9USS9	Q9USS9	schizosacch
907	7	1.6	218	2	Q759N0	Q759N0	ashbya goss	980	7	1.6	248	2	Q9FH54	Q9FH54	arabidopsis

981	7	1.6	248	2	O6GMF7	O6gmf7 brachydanio	1054	7	1.6	267	2	O6I417	O6i417 bacillus an
982	7	1.6	249	2	O6GUG5	O6gug5 pterocarpus	1055	7	1.6	267	2	O8UYU8	O8uyy8 sugarcane m
983	7	1.6	249	2	O8GTR8	O8gtr8 arabisopsis	1056	7	1.6	267	2	O8UYU9	O8uyy9 sugarcane m
984	7	1.6	249	2	O8XV4	O8xv4 ralstonia s	1057	7	1.6	267	2	O8UYV0	O8uyv0 sugarcane m
985	7	1.6	250	2	O84PD9	O84pd9 oryza sativ	1058	7	1.6	267	2	O8UYV1	O8uyv1 sugarcane m
986	7	1.6	250	2	O84K25	O84k25 mus musculu	1059	7	1.6	267	2	O8UYV2	O8uyv2 sugarcane m
987	7	1.6	250	2	O7SZT0	O7szt0 xenopus lae	1060	7	1.6	267	2	O8UYV3	O8uyv3 sugarcane m
988	7	1.6	250	2	O9PUY6	O9puy6 anguilla sp	1061	7	1.6	267	2	O8UYV4	O8uyv4 sugarcane m
989	7	1.6	251	2	O9LWR2	O9lwr2 oryza sativ	1062	7	1.6	267	2	O8UYV5	O8uyv5 sugarcane m
990	7	1.6	251	2	O8COC5	O8coc5 m mus muscu	1063	7	1.6	267	2	O8UYV6	O8uyv6 sugarcane m
991	7	1.6	251	2	O9DW88	O9dwr88 rat cytomeg	1064	7	1.6	267	2	O8UYV7	O8uyv7 sugarcane m
992	7	1.6	252	2	O7ST55	O7st55 prunus pers	1065	7	1.6	267	2	O7T3J3	O7t3j3 oreochromis
993	7	1.6	252	2	O9ATL3	O9atl3 zea mays (m	1066	7	1.6	268	1	PSB4 DROME	O9vna5 drosophila
994	7	1.6	252	2	O67E15	O67e15 zenopsis co	1067	7	1.6	268	2	O8IW10	O8iw10 homo sapien
995	7	1.6	253	2	O7SBQ0	O7sbq0 neurospora	1068	7	1.6	268	2	O96JC9	O96jc9 homo sapien
996	7	1.6	253	2	O9BIT4	O9bit4 nephila sen	1069	7	1.6	268	2	O6ZN62	O6zn62 homo sapien
997	7	1.6	253	2	O49388	O49388 arabisopsis	1070	7	1.6	268	2	O7FNQ5	O7fnq5 anopheles g
998	7	1.6	253	2	O6IQD2	O6iqd2 brachydanio	1071	7	1.6	268	2	O8NKZ1	O8nkz1 xanthomonas
999	7	1.6	254	1	PRIO_SIGHI	O9zot3 sigmodon hi	1072	7	1.6	268	2	O8PJ80	O8pj80 xanthomonas
1000	7	1.6	254	2	O05777	O05777 saccharomyc	1073	7	1.6	268	2	O9D4C5	O9d4c5 m mus muscu
1001	7	1.6	254	2	O18434	O18434 helicoverpa	1074	7	1.6	269	2	O7OHS8	O7ohs8 leishmania
1002	7	1.6	254	2	O18436	O18436 helicoverpa	1075	7	1.6	269	2	O8SKF1	O8skf1 macrodon an
1003	7	1.6	254	2	O6YJN7	O6ynj7 oryza sativ	1076	7	1.6	269	2	O8SKF2	O8skf2 macrodon an
1004	7	1.6	254	2	O6ZFM9	O6zfm9 oryza sativ	1077	7	1.6	269	2	O8SKF3	O8skf3 macrodon an
1005	7	1.6	254	2	O84N51	O84n51 oryza sativ	1078	7	1.6	269	2	O8SKG2	O8skg2 macrodon an
1006	7	1.6	254	2	O9ZOT4	O9zot4 sigmodon fu	1079	7	1.6	270	1	PLJN RAT	O8k4i4 rattus norv
1007	7	1.6	254	2	O9COC5	O9coc5 m mus muscu	1080	7	1.6	270	2	O8SAZ7	O8sa27 macrodon an
1008	7	1.6	254	2	O9PUY4	O9puy4 chanos chan	1081	7	1.6	270	2	O8SB79	O8sb79 macrodon an
1009	7	1.6	255	2	O7S567	O7s567 neurospora	1082	7	1.6	270	2	O8SBU3	O8sbu3 macrodon an
1010	7	1.6	255	2	O692G5	O692g5 nephila cia	1083	7	1.6	270	2	O8SBW7	O8sbw7 macrodon an
1011	7	1.6	255	2	O8LPS7	O8lps7 arabisopsis	1084	7	1.6	270	2	O8SBW8	O8sbw8 macrodon an
1012	7	1.6	255	2	O9ASV3	O9asv3 arabisopsis	1085	7	1.6	270	2	O8SKB9	O8ske9 macrodon an
1013	7	1.6	255	2	O9SJW8	O9sjw8 arabisopsis	1086	7	1.6	270	2	O8SKF0	O8skf0 macrodon an
1014	7	1.6	256	2	O9XUQ3	O9xug3 caenorhabdi	1087	7	1.6	270	2	O8SKF4	O8skf4 macrodon an
1015	7	1.6	256	2	O24568	O24568 zea mays (m	1088	7	1.6	270	2	O8SKF5	O8skf5 macrodon an
1016	7	1.6	256	2	O82F25	O82f25 streptomyce	1089	7	1.6	270	2	O8SKF8	O8skf8 macrodon an
1017	7	1.6	256	2	O82F25	O82f25 human immun	1090	7	1.6	270	2	O8SKF9	O8skf9 macrodon an
1018	7	1.6	256	2	O7ZGM1	O7zgm1 human immun	1091	7	1.6	270	2	O8SKG0	O8skg0 macrodon an
1019	7	1.6	257	2	O6YX12	O6yx12 oryza sativ	1092	7	1.6	270	2	O8SKG1	O8skg1 macrodon an
1020	7	1.6	257	2	O9XIL1	O9xil1 arabisopsis	1093	7	1.6	270	2	O8SKG3	O8skg3 macrodon an
1021	7	1.6	257	2	O81275	O81275 bacillus an	1094	7	1.6	270	2	O8SKG4	O8skg4 macrodon an
1022	7	1.6	258	2	O49284	O49284 arabisopsis	1095	7	1.6	270	2	O8SKG6	O8skg6 macrodon an
1023	7	1.6	258	2	O9M0J2	O9m0j2 arabisopsis	1096	7	1.6	270	2	O9R8B0	O9r8b0 mycobacteri
1024	7	1.6	258	2	O83VA1	O83va1 western x p	1097	7	1.6	270	2	O61764	O61764 mus musculu
1025	7	1.6	259	2	O9C8P8	O9c8p8 arabisopsis	1098	7	1.6	271	2	O81793	O81793 arabisopsis
1026	7	1.6	260	2	O6IHY8	O6ihy8 drosophila	1099	7	1.6	271	2	Q8PNK6	Q8pnk6 xanthomonas
1027	7	1.6	260	2	O8GS50	O8gs50 pterocarpus	1100	7	1.6	272	1	YD66 MYCPN	P75415 mycoplasma
1028	7	1.6	260	2	O8GSD2	O8gsd2 pterocarpus	1101	7	1.6	272	2	O7QG03	O7qgu3 anopheles g
1029	7	1.6	260	2	O8GU50	O8gu50 pterocarpus	1102	7	1.6	272	2	O69SG3	O69sg3 oryza sativ
1030	7	1.6	261	2	O6C0J1	O6c0j1 yarrowia li	1103	7	1.6	272	2	O6YT06	O6yt06 oryza sativ
1031	7	1.6	261	2	O8NGL9	O8ngl9 homo sapien	1104	7	1.6	272	2	O8GRS1	O8grs1 pterocarpus
1032	7	1.6	261	2	O9LH16	O9lh16 arabisopsis	1105	7	1.6	272	2	O97M20	O97m20 clostridium
1033	7	1.6	261	2	O78279	O78279 human immun	1106	7	1.6	273	2	O04032	O04032 arabisopsis
1034	7	1.6	262	2	O9SRV2	O9srv2 drosophila	1107	7	1.6	273	2	O75135	O75135 oryza sativ
1035	7	1.6	262	2	O95289	O95289 leishmania	1108	7	1.6	273	2	O8PQG6	O8pgg6 xanthomonas
1036	7	1.6	262	2	O9VIX5	O9vix5 drosophila	1109	7	1.6	274	2	O871T9	O871t9 neurospora
1037	7	1.6	262	2	O8W2Q2	O8w2q2 oryza sativ	1110	7	1.6	274	2	O8PDH9	O8pdh9 xanthomonas
1038	7	1.6	262	2	O9M3C1	O9m3c1 arabisopsis	1111	7	1.6	275	1	Z339 HUMAN	O8pfp0 homo sapien
1039	7	1.6	262	2	O9F945	O9f945 rhodobacter	1112	7	1.6	275	2	O9B850	O9b850 aspergillus
1040	7	1.6	263	2	O9TH24	O9th24 aspergillus	1113	7	1.6	275	2	O9XLX5	O9xlx5 aspergillus
1041	7	1.6	263	2	O8RXV5	O8rxv5 arabisopsis	1114	7	1.6	276	2	O8TUR9	O8tur9 methanopyru
1042	7	1.6	263	2	O9LY29	O9ly29 arabisopsis	1115	7	1.6	276	2	O9KAX8	O9kax8 bacillus ha
1043	7	1.6	263	2	O67KZ5	O67kz5 symbiobacte	1116	7	1.6	276	2	O9DAU1	O9dau1 m mus muscu
1044	7	1.6	264	2	O8SKF7	O8skf7 macrodon an	1117	7	1.6	277	2	O17376	O17376 caenorhabdi
1045	7	1.6	264	2	O8BQT2	O8bqt2 mus musculu	1118	7	1.6	277	2	O61297	O61297 haemaphysal
1046	7	1.6	265	2	O7SSK4	O7ssk4 neurospora	1119	7	1.6	277	2	O6H500	O6h500 oryza sativ
1047	7	1.6	265	2	O69PC6	O69pc6 oryza sativ	1120	7	1.6	277	2	O90Z61	O90z61 scophthalmu
1048	7	1.6	265	2	O97L09	O97l09 clostridium	1121	7	1.6	278	2	O6FSF5	O6fsf5 candida gla
1049	7	1.6	265	2	O6ML35	O6ml35 bdellovibri	1122	7	1.6	278	2	O8JFN5	O8jfn5 oncorhynch
1050	7	1.6	266	2	O72C40	O72c40 desulfovibr	1123	7	1.6	278	2	O9AVD0	O9avd0 oryza sativ
1051	7	1.6	266	2	O86G55	O86g55 glomeris ma	1124	7	1.6	278	2	O7UNE9	O7une9 rhodopirell
1052	7	1.6	267	1	COLI_PIG	P01192 s corticotr	1125	7	1.6	279	2	O861Z8	O861z8 dictyosteli
1053	7	1.6	267	1	PANB_SULTO	O974y0 sulfolobus	1126	7	1.6	280	2	O6JBP9	O6jbp9 zea mays (s

1127	7	1.6	280	2	Q6R7B4	Q6r7p4 streptomyce	1200	7	1.6	302	2	Q9VQH5	Q9vqh5 drosophila
1128	7	1.6	281	2	Q6C8B5	Q6c8e5 yarrowia li	1201	7	1.6	302	2	Q7Y4N4	Q7y4n4 bacterioph
1129	7	1.6	282	2	Q71TA4	Q71ta4 bacterioph	1202	7	1.6	302	2	Q93Y00	Q93y00 arabidopsi
1130	7	1.6	283	2	Q6JBR1	Q6jbr1 zea mays (s	1203	7	1.6	303	2	Q8NC24	Q8nc24 homo sapien
1131	7	1.6	284	2	Q6JBR1	Q6jbr1 zea mays (s	1204	7	1.6	303	2	Q9HA60	Q9ha60 homo sapien
1132	7	1.6	285	2	Q8MGG1	Q8mvg1 drosophila	1205	7	1.6	303	2	Q8W5G1	Q8w5g1 oryza sativ
1133	7	1.6	286	2	Q7SPQ1	Q7spq1 neurospora	1206	7	1.6	303	2	Q8BRJ3	Q8brj3 mus musculu
1134	7	1.6	287	2	Q9P331	Q9p331 sus scrofa	1207	7	1.6	304	2	Q631F9	Q631f9 burkholderi
1135	7	1.6	288	2	Q8L9D1	Q8l9d1 arabidopsi	1208	7	1.6	304	2	Q8A394	Q8a394 bacteroides
1136	7	1.6	289	2	Q69MN1	Q69mn1 oryza sativ	1209	7	1.6	305	1	PYRD_LACPL	P77887 lactobacill
1137	7	1.6	290	2	Q9BSD6	Q9bsd6 homo sapien	1210	7	1.6	305	2	Q7PRF9	Q7prf9 anopheles g
1138	7	1.6	291	2	Q9BVF4	Q9bvf4 homo sapien	1211	7	1.6	305	2	Q7QEB6	Q7qeb6 anopheles g
1139	7	1.6	292	2	Q9NWF5	Q9nwf5 homo sapien	1212	7	1.6	305	2	Q8PDN7	Q8pdn7 xanthomonas
1140	7	1.6	293	2	Q9NEF0	Q9nef0 leishmania	1213	7	1.6	305	2	Q8QND6	Q8qnd6 ectocarpus
1141	7	1.6	294	2	Q8GUN3	Q8gun3 arabidopsi	1214	7	1.6	306	2	Q8W0D0	Q8w0d0 oryza sativ
1142	7	1.6	295	2	Q7KNB1	Q7knb1 drosophila	1215	7	1.6	307	1	DF54_ARATH	Q81d10 arabidopsi
1143	7	1.6	296	2	Q9LVU0	Q9lvu0 arabidopsi	1216	7	1.6	307	2	Q6AVL6	Q6avl6 oryza sativ
1144	7	1.6	297	1	CAP2_DICD1	P34122 dictyosteli	1217	7	1.6	307	2	Q6K5Q4	Q6k5q4 oryza sativ
1145	7	1.6	298	2	Q8N358	Q8n358 homo sapien	1218	7	1.6	308	2	Q76762	Q76762 anopheles g
1146	7	1.6	299	2	Q9VIX6	Q9vix6 drosophila	1219	7	1.6	308	2	Q8BPI5	Q8bp15 mus musculu
1147	7	1.6	300	2	Q8RUI9	Q8rui9 oryza sativ	1220	7	1.6	309	2	Q95PQ4	Q95pq4 oikopleura
1148	7	1.6	301	2	Q69PU4	Q69pu4 oryza sativ	1221	7	1.6	310	2	Q8NIY9	Q8niy9 neurospora
1149	7	1.6	302	2	Q8PBU3	Q8pbu3 xanthomonas	1222	7	1.6	310	2	Q817E6	Q817e6 bacillus ce
1150	7	1.6	303	2	Q846S8	Q846s8 myxococcus	1223	7	1.6	310	2	Q88198	Q88198 sugarcane m
1151	7	1.6	304	2	Q21155	Q21155 caenorhabdi	1224	7	1.6	311	2	Q6CL53	Q6cl53 kluyveromyc
1152	7	1.6	305	2	Q7SAF2	Q7saf2 neurospora	1225	7	1.6	312	1	RALY_MOUSE	Q94012 mus musculu
1153	7	1.6	306	2	Q8IG11	Q8ig11 drosophila	1226	7	1.6	312	2	Q9XZ15	Q9xz15 drosophila
1154	7	1.6	307	2	Q7PP09	Q7pp09 anopheles g	1227	7	1.6	312	2	Q82HK0	Q82hk0 streptomyce
1155	7	1.6	308	2	Q8E164	Q8e164 streptococc	1228	7	1.6	312	2	Q82HR2	Q82hr2 streptomyce
1156	7	1.6	309	2	Q8E6L9	Q8e6l9 streptococc	1229	7	1.6	312	2	Q9RX31	Q9rx31 deinococcus
1157	7	1.6	310	2	Q9FK36	Q9fk36 arabidopsi	1230	7	1.6	312	2	Q8VF59	Q8vf59 mus musculu
1158	7	1.6	311	2	Q75MR7	Q75mr7 homo sapien	1231	7	1.6	313	1	KRE1_YEAST	P17260 saccharomyc
1159	7	1.6	312	2	Q23620	Q23620 arabidopsi	1232	7	1.6	313	2	Q8RVW3	Q8rvw3 lycopersico
1160	7	1.6	313	2	Q94H41	Q94h41 oryza sativ	1233	7	1.6	313	2	Q9RGW7	Q9rgw7 streptomyce
1161	7	1.6	314	2	Q9D4F2	Q9d4f2 mus musculu	1234	7	1.6	313	2	Q80PW8	Q80pw8 sugarcane m
1162	7	1.6	315	1	VHED_BPT2	P09035 bacterioph	1235	7	1.6	313	2	Q88194	Q88194 sugarcane m
1163	7	1.6	316	1	VHED_BPT6	P09797 bacterioph	1236	7	1.6	313	2	Q88195	Q88195 sugarcane m
1164	7	1.6	317	2	Q7S3Z7	Q7s3z7 neurospora	1237	7	1.6	313	2	Q88197	Q88197 sugarcane m
1165	7	1.6	318	2	Q7Q3D6	Q7q3d6 anopheles g	1238	7	1.6	313	2	Q88199	Q88199 sugarcane m
1166	7	1.6	319	2	Q87973	Q87973 mycobacteri	1239	7	1.6	314	2	Q9VVP2	Q9vvp2 drosophila
1167	7	1.6	320	2	Q9R3P7	Q9r3p7 mycobacteri	1240	7	1.6	314	2	Q7XXC8	Q7xxc8 oryza sativ
1168	7	1.6	321	2	Q6NCM5	Q6ncm5 rhodospseudo	1241	7	1.6	315	1	SLX12_HUMAN	Q15370 homo sapien
1169	7	1.6	322	2	Q66H88	Q66h88 rattus norv	1242	7	1.6	315	2	Q8BKE4	Q8bke4 mus musculu
1170	7	1.6	323	2	Q90Y65	Q90y65 paralichthy	1243	7	1.6	316	1	CC12_CABEL	P20630 caenorhabdi
1171	7	1.6	324	2	Q6GND1	Q6gnd1 xenopus lae	1244	7	1.6	316	1	CC13_CABEL	P20631 caenorhabdi
1172	7	1.6	325	2	Q8N144	Q8n144 homo sapien	1245	7	1.6	316	2	Q9VOB3	Q9vob3 drosophila
1173	7	1.6	326	2	Q8YB41	Q8yb41 brucella me	1246	7	1.6	316	2	Q87972	Q87972 streptococ
1174	7	1.6	327	2	Q6MGT3	Q6mgt3 bdellovibri	1247	7	1.6	316	2	Q829C9	Q829c9 streptomyce
1175	7	1.6	328	2	Q8FEG9	Q8feg9 escherichia	1248	7	1.6	316	2	Q9FJK6	Q9fjk6 streptomyce
1176	7	1.6	329	2	Q8CFT0	Q8cft0 mus musculu	1249	7	1.6	317	1	V35K_RCNMV	P10838 red clover
1177	7	1.6	330	2	Q6ZUM6	Q6zum6 homo sapien	1250	7	1.6	317	2	Q9WLK3	Q9wlk3 drosophila
1178	7	1.6	331	2	Q76407	Q76407 caenorhabdi	1251	7	1.6	318	2	Q9V8Z9	Q9v8z9 drosophila
1179	7	1.6	332	2	Q9VNN2	Q9vnn2 drosophila	1252	7	1.6	318	2	Q6KAR2	Q6kar2 mus musculu
1180	7	1.6	333	2	Q94GG7	Q94gg7 oryza sativ	1253	7	1.6	319	2	Q75EP9	Q75ep9 ashbya goss
1181	7	1.6	334	2	Q7XGA2	Q7xga2 oryza sativ	1254	7	1.6	319	2	Q8LJL5	Q8lj15 oryza sativ
1182	7	1.6	335	2	Q95PQ3	Q95pq3 oikopleura	1255	7	1.6	319	2	Q82HH3	Q82hh3 streptomyce
1183	7	1.6	336	2	Q94CN4	Q94cn4 oryza sativ	1256	7	1.6	320	2	Q692U7	Q692u7 ixodes scap
1184	7	1.6	337	2	Q9ADH8	Q9adh8 ehrlichia c	1257	7	1.6	320	2	Q7QDP2	Q7qdp2 anopheles g
1185	7	1.6	338	2	Q982J9	Q982j9 thizobium l	1258	7	1.6	320	2	Q8V6R9	Q8v6r9 halovirus h
1186	7	1.6	339	2	Q9SA66	Q9sa66 arabidopsi	1259	7	1.6	320	2	Q68YW0	Q68yw0 maize dwarf
1187	7	1.6	340	2	Q9HY18	Q9hy18 pseudomonas	1260	7	1.6	320	2	Q7TDX8	Q7tdx8 halovirus h
1188	7	1.6	341	2	Q61061	Q61061 plasmodium	1261	7	1.6	321	2	Q92MP7	Q92mp7 rhizobium m
1189	7	1.6	342	2	Q85944	Q85944 sphingomona	1262	7	1.6	321	2	Q7NGB4	Q7ngb4 gloeobacter
1190	7	1.6	343	2	Q67P11	Q67p11 symbiobacte	1263	7	1.6	321	2	Q9KDA6	Q9kda6 bacillus ha
1191	7	1.6	344	2	Q9Y4N3	Q9y4n3 homo sapien	1264	7	1.6	322	2	Q8WQK5	Q8wqk5 calliphora
1192	7	1.6	345	2	Q98JQ4	Q98jq4 thizobium l	1265	7	1.6	322	2	Q69P59	Q69p59 oryza sativ
1193	7	1.6	346	2	Q87RR5	Q87rr5 vibrio para	1266	7	1.6	323	1	KLFE_HUMAN	Q8td94 homo sapien
1194	7	1.6	347	2	Q7PTF4	Q7ptf4 anopheles g	1267	7	1.6	323	2	Q6LX22	Q6lx22 methanococ
1195	7	1.6	348	2	Q8RXG4	Q8rxg4 arabidopsi	1268	7	1.6	323	2	Q6CDB8	Q6cdb8 yarrowia li
1196	7	1.6	349	2	Q8J111	Q8j111 brachydanio	1269	7	1.6	323	2	Q6BC34	Q6bc34 patinopecte
1197	7	1.6	350	1	Q9P6P8	Q9p6p8 homo sapien	1270	7	1.6	323	2	Q7Q197	Q7q197 anopheles g
1198	7	1.6	351	1	VHED_BPT4	P03695 bacterioph	1271	7	1.6	324	1	HME2_MOUSE	P09066 mus musculu
1199	7	1.6	352	2	Q9VND7	Q9vnd7 drosophila	1272	7	1.6	324	2	Q7SDB1	Q7sdb1 neurospora

1273	7	1.6	324	2	Q873A5	O873a5 neurospora	1346	7	1.6	350	2	Q692Q4	O692q4 citrus tris
1274	7	1.6	324	2	Q7QH82	Q7qh82 anopheles g	1347	7	1.6	351	1	RSH1_MAIZE	Q41853 zea mays (m
1275	7	1.6	324	2	Q7XR2	Q7xr2 oryza sativ	1348	7	1.6	352	2	Q8T089	O8t089 drosophila
1276	7	1.6	325	2	Q8MR03	Q8mr03 drosophila	1349	7	1.6	352	2	Q84DD2	Q84dd2 uncultured
1277	7	1.6	325	2	Q7QH81	Q7qh81 anopheles g	1350	7	1.6	352	2	Q7NF17	Q7nf17 gloebacter
1278	7	1.6	326	2	Q7Y1K8	Q7y1k8 oryza sativ	1351	7	1.6	353	1	ROD_RAT	Q9j154 rattus norv
1279	7	1.6	328	2	Q757X0	Q757x0 ashbya goss	1352	7	1.6	353	2	Q8MRN0	Q8mrn0 drosophila
1280	7	1.6	328	2	Q89MW9	Q89mw9 bradyrhizob	1353	7	1.6	353	2	Q61KW2	Q61kw2 drosophila
1281	7	1.6	329	2	Q9M2K4	Q9m2k4 arabisdopsis	1354	7	1.6	353	2	Q7F0Q2	Q7f0q2 oryza sativ
1282	7	1.6	330	2	Q652X5	Q652x5 oryza sativ	1355	7	1.6	353	2	Q8B4G1	Q8b4g1 hepaticis b
1283	7	1.6	330	2	Q921Q4	Q921q4 rhizobium m	1356	7	1.6	353	2	Q7SXL1	Q7sxl1 brachydanio
1284	7	1.6	330	2	Q899Q3	Q899q3 murid herpe	1357	7	1.6	354	2	Q7XUH5	Q7xuh5 oryza sativ
1285	7	1.6	331	2	Q7XFD0	Q7xfdo oryza sativ	1358	7	1.6	354	2	Q9LEN4	Q9len4 cicera ariet
1286	7	1.6	331	2	Q9AUN4	Q9aun4 oryza sativ	1359	7	1.6	354	2	Q9LRY5	Q9lry5 arabisdopsis
1287	7	1.6	331	2	Q89W98	Q89w98 bradyrhizob	1360	7	1.6	354	2	Q6P898	Q6p898 xenopus tro
1288	7	1.6	331	2	Q6DGL6	Q6dgl6 brachydanio	1361	7	1.6	356	1	APTX_FUGRU	P61800 fugu rubrip
1289	7	1.6	332	1	HBPB_WHEAT	P23923 triticum ae	1362	7	1.6	356	2	Q6C2J9	Q6c2j9 yarrowia li
1290	7	1.6	332	1	Q7WPH0	Q7wph0 bordetella	1363	7	1.6	356	2	Q8R8B5	O8rb85 thermoanaer
1291	7	1.6	333	2	Q8S9P2	Q8sp2 oryza sativ	1364	7	1.6	357	2	Q8INJ1	Q8inj1 drosophila
1292	7	1.6	335	2	Q8T3W1	Q8t3w1 drosophila	1365	7	1.6	357	2	Q65034	Q65034 oryza sativ
1293	7	1.6	335	2	Q8W048	Q8w048 oryza sativ	1366	7	1.6	357	2	Q932I9	Q93i9 arabisdopsis
1294	7	1.6	336	2	Q8PP26	Q8pp26 xanthomonas	1367	7	1.6	357	2	Q6K8S6	Q6k8s6 oryza sativ
1295	7	1.6	336	2	Q745J7	Q745j7 mycobacteri	1368	7	1.6	357	2	Q8BLH9	Q8blh9 mus musculu
1296	7	1.6	337	2	Q62022	Q62022 caenorhabdi	1369	7	1.6	358	2	Q9HFZ2	Q9hfz2 candida alb
1297	7	1.6	337	2	Q6N314	Q6n314 rhodopeudo	1370	7	1.6	358	2	Q8WRT8	Q8wrt8 bicyclus an
1298	7	1.6	337	2	Q91708	Q91708 xenopus lae	1371	7	1.6	358	2	Q69XD4	Q69xd4 oryza sativ
1299	7	1.6	338	2	Q8L6T5	Q8l6t5 arabisdopsis	1372	7	1.6	358	2	Q89K27	Q89k27 bradyrhizob
1300	7	1.6	339	1	DJBI_MOUSE	Q9qy73 mus musculu	1373	7	1.6	358	2	Q9C248	Q9c248 mus musculu
1301	7	1.6	339	2	Q6CA18	Q6cal8 yarrowia li	1374	7	1.6	358	2	Q702R6	Q702r6 xenopus tro
1302	7	1.6	339	2	Q75028	Q75028 ashbya goss	1375	7	1.6	359	2	Q97Y95	Q97y95 sulfolobus
1303	7	1.6	339	2	Q8INR1	Q8inr1 drosophila	1376	7	1.6	359	2	Q96153	Q96153 homo sapien
1304	7	1.6	339	2	Q98S17	Q98s17 xenopus lae	1377	7	1.6	359	2	Q7PF57	Q7pf57 anopheles g
1305	7	1.6	340	2	Q94816	Q94816 trichinella	1378	7	1.6	359	2	Q7XZ87	Q7xz87 lycopersico
1306	7	1.6	340	2	Q63G11	Q63g11 bacillus ce	1379	7	1.6	359	2	Q9QXFP6	Q9qx16 mesocricetu
1307	7	1.6	340	2	Q98P78	Q98p78 rhizobium l	1380	7	1.6	360	2	Q70D55	Q70d55 xenopus lae
1308	7	1.6	340	2	Q86893	Q86893 maize dwarf	1381	7	1.6	361	2	Q9LZQ3	Q9lzk3 arabisdopsis
1309	7	1.6	341	2	Q7NGU1	Q7ngu1 gloebacter	1382	7	1.6	361	2	Q73JX2	Q73jx2 treponema d
1310	7	1.6	341	2	Q82C28	Q82c28 streptomyc	1383	7	1.6	361	2	Q82JY4	Q82jy4 streptomyc
1311	7	1.6	341	2	Q88284	Q88284 mus musculu	1384	7	1.6	362	2	Q786D8	Q786d8 neurospora
1312	7	1.6	342	2	Q8S259	Q8s259 drosophila	1385	7	1.6	362	2	Q6W492	Q6w492 drosophila
1313	7	1.6	342	2	Q9W2U5	Q9w2u5 drosophila	1386	7	1.6	362	2	Q6W493	Q6w493 drosophila
1314	7	1.6	342	2	Q8RYX7	Q8ryx7 oryza sativ	1387	7	1.6	362	2	Q6W494	Q6w494 drosophila
1315	7	1.6	342	2	Q41240	Q41240 solanum tub	1388	7	1.6	362	2	Q6W495	Q6w495 drosophila
1316	7	1.6	342	2	Q9M324	Q9m324 cicera ariet	1389	7	1.6	362	2	Q6W4A6	Q6w4a6 drosophila
1317	7	1.6	342	2	Q6HNZ6	Q6hnz6 bacillus th	1390	7	1.6	362	2	Q6W4B4	Q6w4b4 drosophila
1318	7	1.6	343	2	Q7R748	Q7r748 plasmodium	1391	7	1.6	362	2	Q6H849	Q6h849 oryza sativ
1319	7	1.6	343	2	Q917J4	Q917j4 drosophila	1392	7	1.6	362	2	Q9SXX6	Q9sxx6 oryza sativ
1320	7	1.6	343	2	Q9XXU0	Q9xxu0 caenorhabdi	1393	7	1.6	362	2	Q8JJX2	Q8jjx2 sugarcane m
1321	7	1.6	343	2	Q81761	Q81761 arabisdopsis	1394	7	1.6	362	2	Q8UYU4	Q8uyu4 sugarcane m
1322	7	1.6	343	2	Q94CS1	Q94cs1 oryza sativ	1395	7	1.6	362	2	Q8UYU5	Q8uyu5 sugarcane m
1323	7	1.6	345	2	Q7XT06	Q7xt06 oryza sativ	1396	7	1.6	362	2	Q8UYU6	Q8uyu6 sugarcane m
1324	7	1.6	345	2	Q87VX1	Q87vx1 pseudomonas	1397	7	1.6	363	2	Q86DR2	Q86dr2 drosophila
1325	7	1.6	345	2	Q88DM9	Q88dm9 pseudomonas	1398	7	1.6	363	2	Q86DR3	Q86dr3 drosophila
1326	7	1.6	345	2	Q9HX31	Q9hx31 pseudomonas	1399	7	1.6	363	2	Q86DR4	Q86dr4 drosophila
1327	7	1.6	345	2	Q9DW86	Q9dw86 rat cytomeg	1400	7	1.6	363	2	Q86DR5	Q86dr5 drosophila
1328	7	1.6	346	2	Q6VW58	Q6vw58 acanthisatt	1401	7	1.6	363	2	Q86DR6	Q86dr6 drosophila
1329	7	1.6	347	2	Q6KY25	Q6ky25 picophilus	1402	7	1.6	363	2	Q86DR7	Q86dr7 drosophila
1330	7	1.6	348	1	DJB5_MOUSE	Q89114 mus musculu	1403	7	1.6	363	2	Q86DR8	Q86dr8 drosophila
1331	7	1.6	348	2	Q6BQB0	Q6bqb0 debaryomyce	1404	7	1.6	363	2	Q86DR9	Q86dr9 drosophila
1332	7	1.6	348	2	Q75CJ3	Q75cj3 ashbya goss	1405	7	1.6	363	2	Q86DS0	Q86ds0 drosophila
1333	7	1.6	348	2	Q94H66	Q94h66 oryza sativ	1406	7	1.6	363	2	Q86DS1	Q86ds1 drosophila
1334	7	1.6	348	2	Q6MQ17	Q6mq17 bdellovibri	1407	7	1.6	363	2	Q86DS2	Q86ds2 drosophila
1335	7	1.6	348	2	Q74DF1	Q74df1 geobacter s	1408	7	1.6	363	2	Q86DS3	Q86ds3 drosophila
1336	7	1.6	348	2	Q9F220	Q9f220 streptomyc	1409	7	1.6	363	2	Q86DS4	Q86ds4 drosophila
1337	7	1.6	349	2	Q6C605	Q6c605 yarrowia li	1410	7	1.6	363	2	Q86DS5	Q86ds5 drosophila
1338	7	1.6	349	2	Q6W489	Q6w489 drosophila	1411	7	1.6	363	2	Q9ZS11	Q9za11 arabisdopsis
1339	7	1.6	349	2	Q6W490	Q6w490 drosophila	1412	7	1.6	364	2	Q7S222	Q7s222 neurospora
1340	7	1.6	350	2	Q6H511	Q6h511 oryza sativ	1413	7	1.6	365	2	Q9HL12	Q9hl12 thermoplasma
1341	7	1.6	350	2	Q692A7	Q692p7 citrus tris	1414	7	1.6	365	2	Q7KWL1	Q7kwl1 dictyosteli
1342	7	1.6	350	2	Q692P9	Q692p9 citrus tris	1415	7	1.6	366	2	Q961C8	Q961c8 drosophila
1343	7	1.6	350	2	Q692Q1	Q692q1 citrus tris	1416	7	1.6	366	2	Q964C6	Q964c6 musca domes
1344	7	1.6	350	2	Q692Q2	Q692q2 citrus tris	1417	7	1.6	368	2	Q77297	Q77297 echinococcu
1345	7	1.6	350	2	Q692Q3	Q692q3 citrus tris	1418	7	1.6	368	2	Q81BZ2	Q81bz2 plasmodium


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QY 361 MREISKEGNRLGSGDNYRGSSWGSAGGDAVGGVNTVNTSETSPGMENFDTFWKNFKS 420
DB 361 MREISKEGNRLGSGDNYRGSSWGSAGGDAVGGVNTVNTSETSPGMENFDTFWKNFKS 420
QY 421 KLGFINWDINKDORSRIP 440
DB 421 KLGFINWDINKDORSRIP 440

RESULT 2
Q6E0U4 ID Q6E0U4 PRELIMINARY; PRT; 476 AA.
AC Q6E0U4; 2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dermokine-beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayaishi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Inai T., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RT complex on human chromosome 19q13.1.";
RL Genomics 84:384-397(2004).
DR EMBL; AY622965; AAT68269.1; -.
SQ SEQUENCE 476 AA; 47010 MW; E2206CC864AC4992 CRC64;

Query Match 40.5%; Score 178; DB 2; Length 476;
Best Local Similarity 99.6%; Pred. No. 4.9e-153;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFGPLACLLALCLGSGAGPLQSGESTGTNIGALGHGLDALSSEGVAIGKEAG 60
DB 1 MKFGPLACLLALCLGSGAGPLQSGESTGTNIGALGHGLDALSSEGVAIGKEAG 60
QY 61 GAAGSKVSEALGGTREAAGTGVQVQFCAADALGNRVGEAAHALGNTGHEIGRAEDV 120
DB 61 GAAGSKVSEALGGTREAAGTGVQVQFCAADALGNRVGEAAHALGNTGHEIGRAEDV 120
QY 121 IRHGADAVRGSWGQVPGHSGAWETSGGHGIFGSGGLGGQGGQGNPGGLGTPWVHGYPGNS 180
DB 121 IRHGADAVRGSWGQVPGHSGAWETSGGHGIFGSGGLGGQGGQGNPGGLGTPWVHGYPGNS 180
QY 181 AGSFGMNPQAPWGQGGNGGPPHFGTNTQGAVAQPGYGSVRASNGEGCTNPPPSGGG 240
DB 181 AGSFGMNPQAPWGQGGNGGPPHFGTNTQGAVAQPGYGSVRASNGEGCTNPPPSGGG 240
QY 241 SSNSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 279
DB 241 SSNSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 279

RESULT 3
Q96EW8 ID Q96EW8 PRELIMINARY; PRT; 137 AA.
AC Q96EW8; Q9BSY6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ZD52F10 protein.
GN Name=ZD52F10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011886; AAH11886.1; -.
DR EMBL; BC004493; AAH04493.2; -.
SQ SEQUENCE 137 AA; 15484 MW; 5830C737DA329566 CRC64;

Query Match 5.7%; Score 25; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 MFNFDTFWKFNFKSLGFINWDINK 432
DB 1 MFNFDTFWKFNFKSLGFINWDINK 25

RESULT 4
Q9CR91 ID Q9CR91 PRELIMINARY; PRT; 182 AA.
AC Q9CR91;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:4833420N21 product:weakly similar to EPIDERMAL
DE DIFFERENTIATION COMPLEX PROTEIN LIKE PROTEIN (Mus musculus 18-day
DE embryo whole body cDNA, RIKEN full-length enriched library,
DE clone:1110019L16 product:weakly similar to EPIDERMAL DIFFERENTIATION
DE COMPLEX PROTEIN LIKE PROTEIN) (Mus musculus 18-day embryo whole body
DE cDNA, RIKEN full-length enriched library, clone:1110059L13
DE product:weakly similar to EPIDERMAL DIFFERENTIATION COMPLEX PROTEIN
DE LIKE PROTEIN).
GN Name=Spr110;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaishizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
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OC Alteromonadaceae; Microbulbifer.
OX NCBI_TaxID=48074;
RN [1]
RP SEQUENCE FROM N.A.
RA Howard M.B., Ekborg N.A., Taylor L.E. Jr., Weiner R.M.,
RA Hutcheson S.W.;
RT "Complex polysaccharide metabolic profiles of Microbulbifer sp. and
RT analysis of chitinases and other degradative enzymes of Microbulbifer
RT hydrolyticus.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
DR EMBL; AY646089; AAT81215.1; -.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL HYDROL F11.1; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 417 AA; 43830 MW; 76B5B56035323CB1 CRC64;

Query Match 3.4%; Score 15; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 SSGSGSGSGSGSGSG 295
Db [1]
387 SSGSGSGSGSGSGSG 401

RESULT 7
Q7UJ76 PRELIMINARY; PRT; 456 AA.
AC Q7UJ76;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Keratin.
GN OrderedLocusNames=RB12076;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294154; CAD77382.1; -.
KW Complete proteome.
SQ SEQUENCE 456 AA; 46867 MW; 0F68B67323907F53 CRC64;

Query Match 3.4%; Score 15; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 SSGSGSGSGSGSGSG 295
Db 106 SSGSGSGSGSGSGSG 120

RESULT 8
Q8PZV5 PRELIMINARY; PRT; 792 AA.
AC Q8PZV5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein.
GN OrderedLocusNames=MM0384;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartesch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wieser A., Baeumer S., Jacobi C.,
RA Bruggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
DR EMBL; AE013263; AAM30080.1; -.
DR InterPro; IPR006626; Pbh1.
DR InterPro; IPR011050; Pectin_lyas_like.
DR Pfam; PF00801; PKD; 2.
DR SMART; SM00710; Pbh1; 6.
DR SMART; SM00089; PKD; 2.
DR PROSITE; PS50093; PKD; 2.
KW Complete proteome.
SQ SEQUENCE 792 AA; 84670 MW; 64EC06653D0CF3BA CRC64;

Query Match 3.2%; Score 14; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 GSSSGSGSGSGSGSG 279
Db [1]
546 GSSSGSGSGSGSGSG 559

RESULT 9
Q6ZUH6 PRELIMINARY; PRT; 120 AA.
AC Q6ZUH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43707.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Esophageal;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuna M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isegai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK125695; BAC86249.1; -.
SQ SEQUENCE 120 AA; 13768 MW; A1CBA83310422C1B CRC64;

Query Match 3.0%; Score 13; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 350 QGFRGGVSSNMR 362
Db 104 QGFRGGVSSNMR 116

RESULT 10

Q94476 ID Q94476 PRELIMINARY; PRT; 199 AA.
AC Q94476
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORFvigil13 (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Loomis W.F.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U6523; AAB06786.1; -.
DR HSSP; P11376; 2EQL.
DR DictyBase; DB0185118; rc8BB.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR001916; Glyco_hydro_22.
DR SMART; SM00263; LY21; 1.
FT NON TER 1
SQ SEQUENCE 199 AA; 19335 MW; DBE0D17B1BC81A3A CRC64;

Query Match 3.0%; Score 13; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSSGSSSG 283
Db 145 GSSSGSSSGSSSG 157

RESULT 11

Q8MML4 ID Q8MML4 PRELIMINARY; PRT; 202 AA.
AC Q8MML4; Q8T171;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HypoPutative Glycosidase (Similar to Dictyostelium discoideum (Slime mold). ORFvigil13).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC123513; AAM4373.1; -.
DR EMBL; AC117070; AAM09345.2; -.
DR HSSP; P11376; 2EQL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001916; Glyco_hydro_22.
DR SMART; SM00263; LY21; 1.
KW Glycosidase.
SQ SEQUENCE 202 AA; 19375 MW; 3905406541395584 CRC64;

Query Match 3.0%; Score 13; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSSGSSSG 283
Db 148 GSSSGSSSGSSSG 160

RESULT 12

Q8MYJ1 ID Q8MYJ1 PRELIMINARY; PRT; 262 AA.
AC Q8MYJ1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Halotia rufescens (California red abalone). LUSTRIN
DE A.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116979; AAM34319.3; -.
DR InterPro; IPR007112; Expan_endogl.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ SEQUENCE 262 AA; 24798 MW; F8241CAA153D622B CRC64;

Query Match 3.0%; Score 13; DB 2; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 GSSSGSSSGSSSG 283
Db 98 GSSSGSSSGSSSG 110

RESULT 13

Q86HE5 ID Q86HE5 PRELIMINARY; PRT; 297 AA.
AC Q86HE5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Component of the counting factor complex.
GN Name=cf45-1;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22793726; PubMed=12912898; DOI=10.1128/EC.2.4.788-797.2003;
RA Brock D.A., Hutton R.D., Giurgutiu D.V., Scott B., Jang W.,
RA Ammann R., Comer R.H.;
RT "CF45-1, a secreted protein which participates in Dictyostelium group
RT size regulation.";
RL Eukaryotic Cell 21:788-797(2003).
DR EMBL; AY212268; AA052749.1; -.
DR DictyBase; DDB0191161; CF45-1.
DR GO; GO:0003796; F:lysozyme activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002053; Glyco_hydro_25.
DR ProDom; PD04620; Glyco_hydro_25; 1.
SQ SEQUENCE 297 AA; 29304 MW; A77398C396A3BCB CRC64;

Query Match 3.0%; Score 13; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GSSSGSSSGSSSG 283
Db 234 GSSSGSSSGSSSG 246
|||||
|||||

RESULT 14
Q8TI63 PRELIMINARY; PRT; 375 AA.
AC Q8TI63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MA4293.
GN OrderedLocuNames=MA4293;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Scange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011143; AAM07637.1; -.
DR InterPro; IPR008962; PapD-like.
KW Complete proteome.
SQ SEQUENCE 375 AA; 40367 MW; DAE26D2B548FD621 CRC64;

Query Match 3.0%; Score 13; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 GSSSGSSSGSSSG 290
Db 134 GSSSGSSSGSSSG 146
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RESULT 15
Q9GRU6 PRELIMINARY; PRT; 418 AA.
ID Q9GRU6
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AC Q9GRU6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-1,4-endoglucanase 1 (Fragment).
GN Name=engl;
OS Heterodera schachtii.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX NCBI_TaxID=97005;
RN [1]
RP SEQUENCE FROM N.A.
RA De Meutter J., Tytgat T., Gheysen G.D.C., Coomans A., Gheysen G.D.R.;
RT "Biochemical characterisation of pharyngeal secretions from Heterodera
RT schachtii stage 2 juveniles.";
RL Eur. J. Biochem. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA De Meutter J.J.;
RL Submitted (JCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ299386; CAC12958.1; -.
DR HSSP; P07103; IEG2.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001919; Bac_cellose-bind.
DR InterPro; IPR008965; Cellul bind.
DR InterPro; IPR001547; Glyco_Hydro_5.
DR Pfam; PF00150; Cellulase; 1.
DR SMART; SM00637; CBD_II; 1.
FT NON TER 1
SQ SEQUENCE 418 AA; 43739 MW; EAA16B402EDCSA9C CRC64;

Query Match 3.0%; Score 13; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GSSSGSSSGSSSG 283
Db 275 GSSSGSSSGSSSG 287
|||||
|||||

Search completed: April 7, 2005, 00:39:56
Job time : 212 secs
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OM protein - protein search, using sw model
 Run on: April 7, 2005, 00:02:45 ; Search time 75 Seconds
 (without alignments)
 2268.994 Million cell updates/sec

Title: US-10-063-561-52
 Perfect score: 2363
 Sequence: 1 MKFGQPLACLLALCLGSGE.....KLGFINWDINKDQSSRIP 440
 Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2105692
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : A_Geneseq_16Dec04:*
 1: Geneseqp1980s:*
 2: Geneseqp1990s:*
 3: Geneseqp2000s:*
 4: Geneseqp2001s:*
 5: Geneseqp2002s:*
 6: Geneseqp2003as:*
 7: Geneseqp2003bs:*
 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA99354	standard; protein; 440 AA.				
DE	Human PRO1411 (UNQ729) amino acid sequence	SEQ ID NO:52.				
PN	WO200012708-A2.					
PD	03-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 3;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 2						
ID	AA866103	standard; protein; 440 AA.				
DE	Protein of the invention #15.					
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 4;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 3						
ID	AA831205	standard; protein; 440 AA.				
DE	Amino acid sequence of human polypeptide PRO1411.					
PN	WO200077037-A2.					
PD	21-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 4;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 4						
ID	AAU29124	standard; protein; 440 AA.				
DE	Human PRO polypeptide sequence #101.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 4;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 5						
ID	AA87551	standard; protein; 440 AA.				
DE	Human PRO1411.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 2363;	DB 4;	Length 440;		
Best Local Similarity	100.0%;	Pred. No. 2.4e-137;				
RESULT 6						
ID	AAU83669	standard; protein; 440 AA.				

DE Human PRO protein, Seq ID No 156.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2363; DB 5; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 7
 ID ABG95876 standard; protein; 440 AA.
 DE Human secreted/transmembrane protein PRO1411.
 PN US2002119130-A1.
 PD 29-AUG-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2363; DB 5; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 8
 ID ABB84891 standard; protein; 440 AA.
 DE Human PRO1411 protein sequence SEQ ID NO:150.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2363; DB 5; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 9
 ID ABB95497 standard; protein; 440 AA.
 DE Human angiogenesis related protein PRO1411 SEQ ID NO: 150.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODO/) GODDARD A.
 PA (GODD/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J P.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 2363; DB 5; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 10
 ID ABUS8500 standard; protein; 440 AA.
 DE Human PRO polypeptide #101.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2363; DB 6; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 11
 ID ABUS8048 standard; protein; 440 AA.
 DE Novel human secreted and transmembrane protein PRO1411.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2363; DB 6; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 12
 ID ABUS4363 standard; protein; 440 AA.
 DE Human secreted/transmembrane protein (PRO) #101.
 PN US2003032112-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2363; DB 6; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 13
 ID ABR66237 standard; protein; 440 AA.
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2363; DB 6; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 14
ID ABR65627 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 15
ID ABU99567 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 16
ID ABR2806 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 17
ID ABU9927 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 18
ID ABR68176 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 19
ID ASU96229 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 20
ID ASU92660 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 21
ID ABU08016 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 22
ID ABO08737 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 23
ID ABO02789 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 24
ID ABR74943 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 25
ID ABR94705 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 26
ID ABO5176 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO141.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 27
ID ABO33782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 28
ID ABU85678 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 29
ID ABU98838 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 30
ID ABU98053 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 31
ID ABU91759 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 32
ID ABU89452 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 33
ID ABU86293 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 34

ID ABU67506 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 35
ID ABU80534 standard; protein; 440 AA.
DE Human PRO protein #101.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 36
ID ABU90901 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 37
ID ABO33960 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO411.
PN US200309013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 38
ID ABR99452 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 39
ID ABR98842 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 40
ID ABO16365 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 41
ID ABR92265 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 42
ID ABO18906 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 43
ID ABR78327 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 44
ID ABU71977 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 45
ID ABU85063 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 46
ID ABO00202 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 47
ID ABO11534 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 48
ID ABO02179 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 49
ID ABU8753 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 50
ID ABU67294 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 51
ID ABU83448 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 52
ID ABO06249 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 53
ID ABR59285 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

```
RESULT 54
ID ABO09347 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 55
ID ABO19211 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 56
ID ABO11229 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 57
ID ABR66847 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 58
ID ABO16060 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 59
ID ABO13766 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 60
ID ABO71531 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 61
ID ABO65669 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 202.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 62
ID ABO07517 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 63
ID ABO03704 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 64
ID ABR67152 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027286-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 65
ID ABO15755 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 66
ID ABUS6036 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO1411.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 67
ID ABU72312 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 68
ID ABUS6364 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032182-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 69
ID ABUS9309 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 70
ID ABU71212 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 71
ID ABO07822 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 72
ID ABR70063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 73
ID ABR69396 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
Pred. No. 2.4e-137;
RESULT 74
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ID ABO01537 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 75
ID ABU81339 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 76
ID ABR60136 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 77
ID ASU90985 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 78
ID ABR67871 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 79
ID ABR65259 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 80
ID ABR69481 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 81
ID ABR71893 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 82
ID ABU85373 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 83
ID ABU89063 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 84
ID ABO01537 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 85
ID ABU94999 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 86
ID ABU90547 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 87
ID ABU84058 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 88
ID ASU93709 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 89
ID ABR64954 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 90
ID ABR68786 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 91
ID ABO06602 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 92
ID ABR99147 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 93
ID ABUS7031 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 94
ID ABU72062 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.

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PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 95
ID ASU85983 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 96
ID ASU82270 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 97
ID ASU87281 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 98
ID ASU67163 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 99
ID ASU83753 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 100
ID ASO08127 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 101
ID ASU92501 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 102
ID ASU81838 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 103
ID ASU66002 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 104
ID ASU81171 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2002027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 105
ID ABR59831 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 106
ID ABU94019 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 107
ID ABU99872 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 108
ID ABU82125 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 109
ID ABR66542 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 110
ID ABR90960 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 111
ID ABO53286 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 112
ID ABU94387 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 113
ID ABU79269 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 114
ID ABU86598 standard; protein; 440 AA.
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DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 115
ID ABU86903 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 116
ID ABU94692 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 117
ID ABO04619 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 118
ID ABR70368 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 119
ID ARU98533 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 120
ID ABR65932 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 121
ID ABR64649 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 122
ID ABU79574 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 123
ID ABU92965 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 124
ID ABU95924 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036145-A1.

PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 125
ID ABU91144 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 126
ID ABU90237 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 127
ID ABO09652 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 128
ID ABO10924 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 129
ID ABR70978 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 130
ID ABU98288 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 131
ID ABU87586 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 132
ID ABU91454 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 133
ID ABU92993 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 134
ID ABU84668 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032116-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 135
ID ABR69758 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 136
ID ABU80135 standard; protein; 440 AA.
DE Human PRO protein #101.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 137
ID ABU82500 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 138
ID ABU93404 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 139
ID ABO09957 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 140
ID ABO09042 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 141
ID ABU96464 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003027993-A1.
PD 08-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 142
ID ABU10610 standard; protein; 440 AA.
DE Human secreted/transmembrane protein #101.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 143
ID ABU72134 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 144
ID ABU95619 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032115-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 145
ID ABU79805 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 146
ID ABU96828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 147
ID ABR70673 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 148
ID ABO05024 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 149
ID ABO08432 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 150
ID ABO05639 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 151
ID ABR74028 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 152
ID ABR95620 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 153
ID ABR80917 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 154
ID ABR81222 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 155
ID ABO00918 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 156
ID ABR88520 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 157
ID ABR77341 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 158
ID ABO28825 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 159
ID ABO31570 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 160
ID ABO7987 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 161
ID ABO40467 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 162
ID ABO35892 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 163
ID ABO44031 standard; protein; 440 AA.
DE Human PRO polypeptide #101.

PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 164
ID ADA77954 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 165
ID ABM24826 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 166
ID ABO03094 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 167
ID ABR90350 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 168
ID ABM17264 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 169
ID ABR95010 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 170
ID ABR95315 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 171
ID ABJ72305 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 172
ID ADB17109 standard; protein; 440 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 173
ID ABO21553 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 174
ID ABR97817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 175
ID ABR87605 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 176
ID ABR77646 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 177
ID ABR27876 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 178
ID ABR06157 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 179
ID ABR03663 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 180
ID ABR35114 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 181
ID ABR26351 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 182
ID ABO48133 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 183
ID ABR92875 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 184
ID ABO24636 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 185
ID ABR11647 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 186
ID ABR02748 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 187
ID ABR16044 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 188
ID ABO27605 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 189
ID ABR29096 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 190
ID ABR07072 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 191
ID ABR21166 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 192
ID ABO48133 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 192
ID ABO09512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 193
ID ABO41382 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 194
ID ABO36197 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 195
ID ABO43726 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 196
ID ABO76426 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 197
ID ABO76122 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 198
ID ABO25741 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 199
ID ABO26046 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 200
ID ABO03399 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;

RESULT 201
ID ABO02484 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 202
ID ABO44264 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 1411.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 203
ID ABR90655 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 204
ID ABR73723 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 205
ID ABO16975 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 206
ID ABR94400 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 207
ID ABR75907 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 208
ID ABR71283 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 209
ID ABR93180 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 210
ID ABR93485 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054478-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 211
ID ABR87910 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 212
ID ABO33596 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 213
ID ABO27910 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 214
ID ABO30045 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 215
ID ABO33254 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 216
ID ABO4942 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 217
ID ABO8902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 218
ID ABO36502 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 219
ID ABO3587 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 220
ID ABO39552 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 221
ID ABM10427 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 222
ID ABM1952 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 223
ID ABO52098 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 224
ID ABO52403 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 225
ID ADA19914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 226
ID ABO23721 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 227
ID ADB17297 standard; protein; 440 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 228
ID ABR97207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 229
ID ABR86995 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 230
ID ABR11037 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 231
ID ABR28181 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 232
ID ABO32180 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 233
ID ABR15307 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 234
ID ABR08462 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 235
ID ABR04273 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 236
ID ABR22386 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 237
ID ABR07682 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 238
ID ABR97512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

ID ABO40772 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 239
ID ABR35419 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 240
ID ABR33182 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 241
ID ABO52708 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 242
ID ABO50268 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 243
ID ABR99262 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 244
ID ABO04314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 245
ID ABO05944 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 246
ID ABR18484 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 247
ID ABR97512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 248
ID ABR80612 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 249
ID ABR01223 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 250
ID ABR88825 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 251
ID ABR13477 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 252
ID ABR20861 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 253
ID ABO41992 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 254
ID ABO42602 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 255
ID ABR010122 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 256
ID ABO38637 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 257
ID ABR32877 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 258
ID ABR22691 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 259
ID ABR74902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 260
ID ADA79746 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 261
ID ABR96292 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 262
ID ABR02443 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 263
ID ABR86385 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 264
ID ABR86690 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 265
ID ABR16654 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003084448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 266
ID ABR29706 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064456-A1.
PD 03-APR-2003.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 305
ID ABO47828 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 306
ID ABO30350 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 307
ID ABO30350 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 308
ID ABO3968 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 309
ID ABO37112 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 310
ID ABO41687 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 311
ID ABO35282 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 312
ID ABO25131 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 313
ID ABO47523 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 314
ID ABO47828 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 315
ID ABO48438 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 316
ID ABO51488 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 317
ID ABO51793 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 318
ID ABO50573 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 319
ID ABR79697 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 320
ID ABM16959 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 321
ID ABO17991 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 322
ID ABO20943 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 323
ID ABR96902 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US200304462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 324
ID ABM12257 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 325
ID ABM16349 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 326
ID ABM24216 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 327
ID ABM14697 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 328
ID ABM04578 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 329
ID ABM06767 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 330
ID ABM09207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 331
ID ABO39247 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 332
ID ABM75512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 333
ID ABM25436 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 334
ID ABM19946 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 335
ID ABO46852 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 336
ID ABO47157 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 337
ID ADA83271 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 338
ID ABR71588 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 339
ID ABR72198 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 340
ID ABR98537 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 341
ID ABO06907 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 342
ID ABR84860 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 343
ID ABR73418 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 344
ID ABR76512 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 345
ID ABR73113 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 346
ID ABJ72433 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 347
ID ARM18179 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 348
ID ABO20638 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 349
ID ABO25381 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 350
ID ABO25686 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 351
ID ABR94095 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 352
ID ABR80002 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 353
ID ABM11342 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 354
ID ABO32949 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 355
ID ABO30655 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 356
ID ABO30960 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 357
ID ABM27266 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 358
ID ABM30011 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 359
ID ABM05547 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 360
ID ABM15612 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 361
ID ABM08597 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 362
ID ABO42297 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 363
ID ABO38027 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 364
ID ABO45937 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 365
ID ABO66740 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 366
ID ADB20314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 367
ID AEM19641 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 368
ID ABO49353 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 369
ID ABO49658 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 370
ID ADA78566 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003073181-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 371
ID ABO34328 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 1411.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 372
ID ABR8215 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003086720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 373
ID ADA00383 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO 411.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 374
ID ABM26961 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 375
ID ABM03358 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003086763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 376
ID ABO39857 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 377
ID ABO49963 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 378
ID ABO50878 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 379
ID ABO5334 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036126-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 380
ID ABR74638 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 381
ID ABO44449 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 382
ID ABR77117 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 383
ID ABM17874 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 384
ID ABR5925 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 385
ID ABO21858 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 386
ID ABO20028 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 387
ID ABO24331 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 388
ID ABR86080 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 389
ID ABM10732 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064455-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 390
ID ABM76731 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 391
ID ABR89435 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 392
ID ABM12562 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 393
ID ABM05852 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 394
ID ABO34977 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 395
ID ABM03053 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 396
ID ABM19031 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 397
ID ABM19336 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 398
ID ABO46547 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 399
ID ABO49048 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 400
ID ABR69091 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 401
ID ABR89130 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 402
ID ABR7503 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 403
ID ABR74333 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 404
ID ABO18601 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044921-A1.
PD 08-MAR-2003.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 405
ID ABR80307 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 406
ID ABO1528 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 407
ID ABO2138 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 408
ID ABR87300 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 409
ID ABO12867 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 410
ID ABO30621 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 411
ID ABO24521 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 412
ID ABO29435 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 413
ID ABO31265 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 414
ID ABO14392 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 415
ID ABO09817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 416
ID ABO38942 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 417
ID ABO34707 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104538-A1.
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PD 05-JUN-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 418
ID ABO51183 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 419
ID ABO04009 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 420
ID ABO10479 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 421
ID ABR77722 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 422
ID ABR78932 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 423
ID ABO24026 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 424
ID ABR93790 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 425
ID ABO1833 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 426
ID ABR78256 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 427
ID ABO33473 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 428
ID ABR90045 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 429
ID ABM27571 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 430
ID ABM13172 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 431
ID ABO31875 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 432
ID ABM14087 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 433
ID ABM08292 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 434
ID ABO40162 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 435
ID ABM74597 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 436
ID ABM33792 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003096358-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 437
ID ABM20251 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 438
ID ABO48743 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 439
ID ABR72808 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 440
ID ABO15450 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 441
ID ABR85165 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 442
ID ABO15145 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 443
ID ABO17280 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 444
ID ABO19663 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 445
ID ABR17569 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 446
ID ABR72135 standard; protein; 440 AA.
DE Human membrane bound receptor/protein PRO1411 amino acid sequence.

PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 447
ID ABR85470 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 448
ID ABM77036 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 449
ID ABO28215 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 450
ID ABM22996 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 451
ID ABM30316 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 452
ID ABM21776 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 453
ID ABM21471 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 454
ID ABM15002 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 455
ID ABO41077 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068694-A1.


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Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 474
ID ADB87195 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 475
ID ADB84777 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 476
ID ADB68304 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 477
ID ADB68111 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 478
ID ADB31536 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 479
ID ADB30926 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 480
ID ADB83092 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 481
ID ADB73047 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 482
ID ADB90928 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 483
ID ADC07008 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 484
ID ADC17921 standard; protein; 440 AA.
DE Human PRO polypeptide #15.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 485
ID ADC17187 standard; protein; 440 AA.
DE Mammalian PRO polypeptide (SeqID 52).
PN US2003055143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 486
ID ADC14885 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 487
ID ADC36885 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 488
ID ADC52380 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 489
ID ADC21875 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 490
ID ADC49906 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 491
ID ADC49105 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 492
ID ADC49105 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
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ID ADC49622 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 493
ID ADC47483 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 494
ID ADC47228 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 495
ID ADC78103 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 496
ID ADD06338 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 497
ID ADD05675 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 498
ID ADD10439 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 499
ID ADC77857 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 500
ID ADD11399 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 501
ID ADD50820 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 502
ID ADD51066 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 503
ID ADD70567 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 504
ID ADD39644 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 505
ID ADD70090 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 506
ID ADD37192 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 507
ID ADD36056 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 508
ID ADD38211 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 509
ID ADD39167 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 510
ID ADD50547 standard; protein; 440 AA.
DE Human PRO polypeptide #78.

PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 511
ID ADD50301 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 512
ID ADD38690 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 513
ID ADD40121 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 514
ID ADD51312 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 515
ID ADE50342 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 516
ID ADE19954 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 517
ID ADE49865 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 518
ID ADE21423 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 519
ID ADF29848 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003204053-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 520
ID ADF5741 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 521
ID ADG01057 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 522
ID ADG08610 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 523
ID ADG02670 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 524
ID ADG01377 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 525
ID ADF95552 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 526
ID ADF95231 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 527
ID ADG12367 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 528
ID ADH24084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 529
ID ADH34110 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 530
ID ADH29943 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 531
ID ADH23914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 532
ID ADH09027 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 533
ID ADG83318 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 534
ID ADH24594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 535
ID ADH37450 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO411.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 536
ID ADH02039 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 537
ID ADH37620 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO411.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 538
ID ADG85658 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 539
ID ADH24254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 540
ID ADH38548 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 541
ID ADG63787 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 542
ID ADG83669 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 543
ID ADH29477 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 544
ID ADH27593 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 545
ID ADH37790 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO1411.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 546
ID ADH37967 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO411.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

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RESULT 547
ID ADH57387 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 548
ID ADH53529 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 549
ID ADH53699 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 550
ID ADH52035 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 551
ID ADH49890 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 552
ID ADI25400 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 553
ID ADH90193 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 554
ID ADI25570 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 555
ID ADH97744 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 556
ID ADH98084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 557
ID ADH99245 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003085142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 558
ID ADI11949 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 559
ID ADH90023 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 560
ID ADH98424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 561
ID ADI11099 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 562
ID ADI11609 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 563
ID ADH98254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 564
ID ADH98594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 565
ID ADH98084 standard; protein; 440 AA.
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DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 566
ID ADI05072 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 567
ID ADI03422 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO411.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 568
ID ADI04817 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 569
ID ADH78271 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 570
ID ADI19615 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 571
ID ADH90363 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 572
ID ADI03082 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 573
ID ADH77931 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 574
ID ADH97914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.

PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 575
ID ADI01299 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 576
ID ADI01994 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 577
ID ADI03252 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 578
ID ADI11439 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 579
ID ADI02341 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 580
ID ADI11779 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 581
ID ADI05416 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 582
ID ADH79488 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 583
ID ADI19445 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181675-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 584
ID ADI05246 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 585
ID ADH79658 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 586
ID ADI01484 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 587
ID ADI01654 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 588
ID ADI01824 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 589
ID ADH79828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 590
ID ADI04646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 591
ID ADI02782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 592
ID ADH78101 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181667-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 593
ID ADI25740 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 594
ID ADI25910 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 595
ID ADK5422 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 596
ID ADH98764 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 597
ID ADH80005 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 598
ID ADM30342 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 599
ID ADL93736 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 600
ID ADC48859 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 601
ID ADC52190 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 602
ID ADE21030 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 603
ID ADE05874 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 604
ID ADD75103 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 605
ID ADD75849 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 606
ID ADD85081 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 607
ID ADD86907 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 608
ID ADE20784 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 609
ID ADE39081 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 610
ID ADE05628 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 611
ID ADD73613 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 612
ID ADD78453 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 613
ID ADE41400 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 614
ID ADE74339 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 615
ID ADE21276 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 616
ID ADD77391 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 617
ID ADE20538 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 618
ID ADD75603 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 619
ID ADD74119 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 620
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
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ID ADD74365 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 621
ID ADD76095 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 622
ID ADD85587 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 623
ID ADD85136 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 624
ID ADD75349 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 625
ID ADD76893 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 626
ID ADD86661 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 627
ID ADE41201 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 628
ID ADD78129 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 629
ID ADE74951 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100724-A1.

DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 630
ID ADD77637 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 631
ID ADD77893 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 632
ID ADD85341 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 633
ID ADD73873 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 634
ID ADD74611 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 635
ID ADD77139 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 636
ID ADD85833 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 637
ID ADE05382 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 638
ID ADD74857 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100724-A1.

PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 639
ID ADE96425 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 640
ID ADF25736 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 641
ID ADF24635 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 642
ID ADF29371 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 643
ID ADE96902 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 644
ID ADG05669 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 645
ID ADG27223 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 646
ID ADF96164 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 647
ID ADG11286 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 648
ID ADG04435 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 649
ID ADG12065 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 650
ID ADG00595 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 651
ID ADF94622 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 652
ID ADG06718 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 653
ID ADH06622 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 654
ID ADH06452 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 655
ID ADG68873 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 656
ID ADH27763 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 657
ID ADH27763 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 657
ID ADH25104 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 658
ID ADH33736 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 659
ID ADG82851 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 660
ID ADH02940 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 661
ID ADH02379 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 662
ID ADH07986 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 663
ID ADG69383 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 664
ID ADH39204 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 665
ID ADH03894 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 666
ID ADH03417 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 667
ID ADH26132 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 668
ID ADG83944 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 669
ID ADH39062 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 670
ID ADG85488 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 671
ID ADG63636 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 672
ID ADH06282 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 673
ID ADH30112 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 674
ID ADH24424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 675
ID ADH03894 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
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ID ADH33101 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 676
ID ADG69553 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 677
ID ADH07816 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 678
ID ADG69528 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 679
ID ADH39374 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 680
ID ADH33566 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 681
ID ADH33906 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 682
ID ADH01116 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 683
ID ADG69723 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 684
ID ADH02209 standard; protein; 440 AA.

DE Human PRO polypeptide #26.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 685
ID ADG69213 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 686
ID ADG85998 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 687
ID ADH24934 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 688
ID ADH39551 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 689
ID ADH02549 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 690
ID ADG69043 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 691
ID ADH07646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 692
ID ADG86168 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 693
ID ADH24764 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.

PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 694
ID ADH25812 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 695
ID ADH38378 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 696
ID ADH57217 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 697
ID ADH43583 standard; protein; 440 AA.
DE Human PRO polypeptide #75.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 698
ID ADH52323 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 699
ID ADG34152 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 700
ID ADH04371 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 701
ID ADH49571 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 702
ID ADH90533 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181700-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 703
ID ADI11269 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 704
ID ADH98934 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 705
ID ADI33622 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 706
ID ADI02164 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 707
ID ADH69716 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 708
ID ADH61372 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 709
ID ADH90703 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 710
ID ADI29877 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 711
ID ADJ54840 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2004023321-A1.
PD 05-FEB-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 712
ID ADJ98578 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 713
ID ADJ98748 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 714
ID ADH78907 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 715
ID ADJ99141 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 716
ID ADJ99111 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 717
ID ADJ98929 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 718
ID ADH79077 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 719
ID ADK00937 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 720
ID ADK14458 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 721
ID ADM27274 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 722
ID ADK82928 standard; protein; 440 AA.
DE Human PRO polypeptide #75.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 723
ID ADJ64611 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 724
ID ADK66632 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 725
ID ADM31507 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 726
ID ADM36554 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 727
ID ADM40359 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 728
ID ADM80907 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 729
ID ADL94571 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 730
ID AON37967 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 731
ID ADL32808 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 99.7%; Score 2357; DB 7; Length 440;
Best Local Similarity 99.8%; Pred. No. 5.5e-137;
RESULT 732
ID AAB38324 standard; protein; 387 AA.
DE Human secreted protein encoded by gene 4 clone HKAJK47.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 85.9%; Score 2030; DB 3; Length 387;
Best Local Similarity 87.5%; Pred. No. 6e-117;
RESULT 733
ID AAY50941 standard; protein; 479 AA.
DE Human adult skin cDNA clone vd4_1 derived protein.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 95.1%; Score 2010.5; DB 3; Length 479;
Best Local Similarity 87.6%; Pred. No. 1.2e-115;
RESULT 734
ID ABO27306 standard; protein; 372 AA.
DE Human secreted/transmembrane polypeptide PRO411.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 83.1%; Score 1963; DB 6; Length 372;
Best Local Similarity 84.5%; Pred. No. 7.5e-113;
RESULT 735
ID ABO34192 standard; protein; 372 AA.
DE Human secreted/transmembrane polypeptide PRO 1411.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 83.1%; Score 1963; DB 6; Length 372;
Best Local Similarity 84.5%; Pred. No. 7.5e-113;
RESULT 736
ID AAY50940 standard; protein; 369 AA.
DE Human adult skin cDNA clone vd3_1 derived protein #2.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 81.5%; Score 1925.5; DB 3; Length 369;
Best Local Similarity 83.4%; Pred. No. 1.5e-110;
RESULT 737
ID AAY50939 standard; protein; 358 AA.
DE Human adult skin cDNA clone vd3_1 derived protein #1.
PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 71.6%; Score 1692; DB 3; Length 358;
Best Local Similarity 95.8%; Pred. No. 3.2e-96;
RESULT 738
ID ADP07783 standard; protein; 186 AA.
DE Human secreted protein, seq id 266.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 37.1%; Score 875.5; DB 8; Length 186;
Best Local Similarity 92.3%; Pred. No. 2.5e-46;

RESULT 739
ID AAY60056 standard; protein; 230 AA.
DE Human endometrium tumour EST encoded protein 116.
PN DE19817948-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 28.3%; Score 669; DB 2; Length 230;
Best Local Similarity 98.4%; Pred. No. 1.5e-33;
RESULT 740
ID ABO23519 standard; protein; 1079 AA.
DE Mycobacterium tuberculosis outlier protein #3.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match 19.1%; Score 450.5; DB 7; Length 1079;
Best Local Similarity 30.5%; Pred. No. 1.7e-19;
RESULT 741
ID ABU36481 standard; protein; 1306 AA.
DE Protein encoded by Prokaryotic essential gene #22008.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 18.6%; Score 439.5; DB 6; Length 1306;
Best Local Similarity 30.9%; Pred. No. 9.6e-19;
RESULT 742
ID AAO16495 standard; protein; 400 AA.
DE Kukulcania hibernalis spider silk protein #2.
PN WO200299082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Query Match 18.4%; Score 434; DB 6; Length 400;
Best Local Similarity 33.4%; Pred. No. 6.8e-19;
RESULT 743
ID ABU36971 standard; protein; 1381 AA.
DE Protein encoded by Prokaryotic essential gene #22498.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 17.6%; Score 415.5; DB 6; Length 1381;
Best Local Similarity 29.9%; Pred. No. 3e-17;
RESULT 744
ID ABM15873 standard; protein; 484 AA.
DE Mycobacterium tuberculosis mycobacterial antigen protein SEQ ID NO:111.
PN WO2003033530-A2.
PD 24-APR-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 17.5%; Score 412.5; DB 6; Length 484;
Best Local Similarity 33.6%; Pred. No. 1.7e-17;
RESULT 745
ID ABU36943 standard; protein; 484 AA.
DE Protein encoded by Prokaryotic essential gene #22470.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 17.5%; Score 412.5; DB 6; Length 484;
Best Local Similarity 33.6%; Pred. No. 1.7e-17;
RESULT 746
ID ABO23518 standard; protein; 484 AA.
DE Mycobacterium tuberculosis outlier protein #2..
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match 17.5%; Score 412.5; DB 7; Length 484;
Best Local Similarity 33.6%; Pred. No. 1.7e-17;
RESULT 747
ID AAM16105 standard; protein; 357 AA.
DE Peptide #2539 encoded by probe for measuring cervical gene expression.

PN W0200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 748
ID AB35090 standard; peptide; 357 AA.
DE Peptide #2596 encoded by human foetal liver single exon probe.
PN W0200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 749
ID AM28596 standard; protein; 357 AA.
DE Peptide #2633 encoded by probe for measuring placental gene expression.
PN W0200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 750
ID AB29912 standard; peptide; 357 AA.
DE Peptide #2563 encoded by breast cell single exon nucleic acid probe.
PN W0200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 751
ID AB20509 standard; protein; 357 AA.
DE Protein #2508 encoded by probe for measuring heart cell gene expression.
PN W0200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 752
ID AM68282 standard; protein; 357 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28588.
PN W0200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 753
ID AM55912 standard; protein; 357 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28017.
PN W0200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 754
ID ABG49940 standard; peptide; 357 AA.
DE Human liver peptide, SEQ ID NO 28588.
PN W0200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 755
ID AM03832 standard; protein; 357 AA.
DE Peptide #2514 encoded by probe for measuring breast gene expression.
PN W0200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 4; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 756
ID AG37823 standard; peptide; 357 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27488.
PN W0200186003-A2.

PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 17.2%; Score 406.5; DB 5; Length 357;
Best Local Similarity 31.6%; Pred. No. 3e-17;
RESULT 757
ID ABU36734 standard; protein; 532 AA.
DE Protein encoded by Prokaryotic essential gene #22261.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 17.1%; Score 404.5; DB 6; Length 532;
Best Local Similarity 32.2%; Pred. No. 5.8e-17;
RESULT 758
ID AAP80940 standard; protein; 1177 AA.
DE SLPIII protein comprising the gagags of silk fibroin.
PN W08003533-A.
PD 19-MAY-1988.
PA (SYTR) SYNTRO CORP.
Query Match 17.0%; Score 402.5; DB 1; Length 1177;
Best Local Similarity 30.4%; Pred. No. 1.6e-16;
RESULT 759
ID AAR05307 standard; protein; 1177 AA.
DE SLP III (Silk-fibroin like protein).
PN W09005177-A.
PD 17-MAY-1990.
PA (SYTR) SYNTRO CORP.
Query Match 17.0%; Score 402.5; DB 2; Length 1177;
Best Local Similarity 30.4%; Pred. No. 1.6e-16;
RESULT 760
ID AAR95105 standard; protein; 1177 AA.
DE Silk like protein (SLP)III.
PN US5514581-A.
PD 07-MAY-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 17.0%; Score 402.5; DB 2; Length 1177;
Best Local Similarity 30.4%; Pred. No. 1.6e-16;
RESULT 761
ID AAW26342 standard; protein; 1177 AA.
DE Silk-like protein slpIII.
PN US5641648-A.
PD 24-JUN-1997.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 17.0%; Score 402.5; DB 2; Length 1177;
Best Local Similarity 30.4%; Pred. No. 1.6e-16;
RESULT 762
ID AAV78277 standard; peptide; 1177 AA.
DE SLPIII amino acid sequence SEQ ID NO:64.
PN US6018030-A.
PD 25-JAN-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 17.0%; Score 402.5; DB 3; Length 1177;
Best Local Similarity 30.4%; Pred. No. 1.6e-16;
RESULT 763
ID AAB63995 standard; protein; 1177 AA.
DE SLPIII protein sequence SEQ ID 31.
PN US6140072-A.
PD 31-OCT-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 17.0%; Score 402.5; DB 4; Length 1177;
Best Local Similarity 30.4%; Pred. No. 1.6e-16;
RESULT 764
ID AAB72725 standard; protein; 1177 AA.
DE Repetitive protein polymer protein sequence #25.
PN US6184348-B1.
PD 06-FEB-2001.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 17.0%; Score 402.5; DB 4; Length 1177;
Best Local Similarity 30.4%; Pred. No. 1.6e-16;
RESULT 765
ID ABG69267 standard; protein; 1177 AA.
DE Silk-like protein SLPIII.
PN US6355776-B1.
PD 12-MAR-2002.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 17.0%; Score 402.5; DB 5; Length 1177;
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;
 RESULT 766
 ID ADE44959 standard; protein; 1177 AA.
 DE Silk fibroin protein repeating peptide related protein seq id 64.
 PN US2003083464-A1.
 PD 01-MAY-2003.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 17.0%; Score 402.5; DB 7; Length 1177;
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;
 RESULT 767
 ID AAR41007 standard; protein; 1178 AA.
 DE Silk-like protein Slp-III multimer.
 PN US5243038-A.
 PD 07-SEP-1993.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 17.0%; Score 402.5; DB 2; Length 1178;
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;
 RESULT 768
 ID AAW53518 standard; protein; 1178 AA.
 DE Amino acid sequence of the synthetic SlpIII protein.
 PN WO9810063-A1.
 PD 12-MAR-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 17.0%; Score 402.5; DB 2; Length 1178;
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;
 RESULT 769
 ID AAP82962 standard; protein; 1059 AA.
 DE SLP4 protein comprising gagags of silk fibroin.
 PN WO8803533-A.
 PD 19-MAY-1988.
 PA (SYTR) SYNTRO CORP.
 Query Match 17.0%; Score 401; DB 1; Length 1059;
 Best Local Similarity 30.4%; Pred. No. 1.8e-16;
 RESULT 770
 ID AAW53524 standard; protein; 1023 AA.
 DE Amino acid sequence of the SLP4 protein.
 PN WO9810063-A1.
 PD 12-MAR-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 16.9%; Score 399; DB 2; Length 1023;
 Best Local Similarity 30.4%; Pred. No. 2.3e-16;
 RESULT 771
 ID AAR41013 standard; protein; 1059 AA.
 DE SLP4 multimeric protein.
 PN US5243038-A.
 PD 07-SEP-1993.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 16.9%; Score 399; DB 2; Length 1059;
 Best Local Similarity 30.4%; Pred. No. 2.4e-16;
 RESULT 772
 ID AAW26348 standard; protein; 1059 AA.
 DE SLP4 synthetic protein.
 PN US5641648-A.
 PD 24-JUN-1997.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 16.9%; Score 399; DB 2; Length 1059;
 Best Local Similarity 30.4%; Pred. No. 2.4e-16;
 RESULT 773
 ID AAV78283 standard; protein; 1101 AA.
 DE SLP4 amino acid sequence SEQ ID NO:83.
 PN US6018030-A.
 PD 25-JAN-2000.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 16.9%; Score 399; DB 3; Length 1101;
 Best Local Similarity 30.4%; Pred. No. 2.5e-16;
 RESULT 774
 ID ABG69273 standard; protein; 1101 AA.
 DE Silk/Elastin-like protein SLP4.
 PN US6355776-B1.
 PD 12-MAR-2002.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 16.9%; Score 399; DB 5; Length 1101;
 Best Local Similarity 30.4%; Pred. No. 2.5e-16;
 RESULT 775
 ID ADE44978 standard; protein; 1101 AA.
 DE Recombinant structural protein SLP4 protein seq id 83.
 PN US2003083464-A1.
 PD 01-MAY-2003.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 16.9%; Score 399; DB 7; Length 1101;
 Best Local Similarity 30.4%; Pred. No. 2.5e-16;
 RESULT 776
 ID ABU36550 standard; protein; 923 AA.
 DE Protein encoded by Prokaryotic essential gene #22077.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 16.6%; Score 392.5; DB 6; Length 923;
 Best Local Similarity 27.7%; Pred. No. 5.3e-16;
 RESULT 777
 ID ABP53453 standard; protein; 1062 AA.
 DE Pre-gelled protein Polymer SLP3 related amino acid sequence #2.
 PN US2002045567-A1.
 PD 18-APR-2002.
 PA (CAPF/) CAPPELLO J.
 PA (STED/) STEDRONSKY E R.
 Query Match 16.4%; Score 386.5; DB 5; Length 1062;
 Best Local Similarity 31.5%; Pred. No. 1.4e-15;
 RESULT 778
 ID ABU36827 standard; protein; 778 AA.
 DE Protein encoded by Prokaryotic essential gene #22354.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 16.3%; Score 386; DB 6; Length 778;
 Best Local Similarity 31.2%; Pred. No. 1.1e-15;
 RESULT 779
 ID AAY28843 standard; protein; 641 AA.
 DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1).
 PN WO9947647-A1.
 PD 23-SEP-1999.
 PA (PHAR-) PHARMACOEPIA INC.
 Query Match 16.2%; Score 383; DB 2; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 780
 ID AAY95856 standard; protein; 641 AA.
 DE Epstein Barr virus nuclear antigen 1 protein (EBNA1).
 PN WO200047778-A1.
 PD 17-AUG-2000.
 PA (PHAR-) PHARMACOEPIA INC.
 Query Match 16.2%; Score 383; DB 3; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 781
 ID AAB62332 standard; protein; 641 AA.
 DE EBV tethering protein EBNA1.
 PN WO200125484-A2.
 PD 12-APR-2001.
 PA (UNMI) UNIV MICHIGAN.
 Query Match 16.2%; Score 383; DB 4; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 782
 ID ABP72663 standard; protein; 641 AA.
 DE Epstein-Barr virus nuclear antigen 1.
 PN WO2003018754-A2.
 PD 06-MAR-2003.
 PA (NEUR-) NEURONZ LTD.
 PA (NEUR-) NEURONZ BIOSCIENCES INC.
 Query Match 16.2%; Score 383; DB 6; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 783
 ID AAE34812 standard; protein; 641 AA.
 DE Epstein-barr virus nuclear antigen 1 (EBNA1).
 PN WO200290558-A1.
 PD 14-NOV-2002.

PA (FITB-) FIT BIOTECH OYJ PLC.
 Query Match 16.2%; Score 383; DB 6; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 784
 ID ADK65581 standard; protein; 641 AA.
 DE Human herpesvirus 4 nuclear antigen-1 protein.
 PN DE10207135-A1.
 PD 11-SEP-2003.
 PA (EURO-) EUROIMMUN GMBH.
 Query Match 16.2%; Score 383; DB 7; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 785
 ID ADJ57052 standard; protein; 641 AA.
 DE Epstein-Barr virus nuclear antigen 1.
 PN WO2004007536-A2.
 PD 22-JAN-2004.
 PA (AFFI-) AFFINIUM PHARM INC.
 Query Match 16.2%; Score 383; DB 8; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 786
 ID ADP12515 standard; protein; 641 AA.
 DE Protein encoded by mRNA of the invention #125.
 PN WO2004042346-A2.
 PD 21-MAY-2004.
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 Query Match 16.2%; Score 383; DB 8; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 787
 ID ADQ94586 standard; protein; 641 AA.
 DE Epstein-Barr virus EBNA1 protein.
 PN US2004141995-A1.
 PD 22-JUL-2004.
 PA (WANG/) WANG R.
 PA (VOOK/) VOOK K.
 Query Match 16.2%; Score 383; DB 8; Length 641;
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;
 RESULT 788
 ID ABU36438 standard; protein; 837 AA.
 DE Protein encoded by Prokaryotic essential gene #21965.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 16.1%; Score 380.5; DB 6; Length 837;
 Best Local Similarity 30.5%; Pred. No. 2.7e-15;
 RESULT 789
 ID ABP53456 standard; protein; 996 AA.
 DE Pre-gelated protein polymer SLP4 related amino acid sequence #2.
 PN US2002045567-A1.
 PD 18-APR-2002.
 PA (CAPP/) CAPPELLO J.
 PA (STED/) STEDRONSKY E R.
 Query Match 16.0%; Score 379; DB 5; Length 996;
 Best Local Similarity 31.8%; Pred. No. 3.9e-15;
 RESULT 790
 ID AAE18319 standard; protein; 1002 AA.
 DE Silk-like protein, SLP4.
 PN WO200200016-A1.
 PD 03-JAN-2002.
 PA (LUMI-) LUMINIS PTY LTD.
 PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.
 Query Match 16.0%; Score 379; DB 5; Length 1002;
 Best Local Similarity 31.8%; Pred. No. 3.9e-15;
 RESULT 791
 ID ABU36945 standard; protein; 588 AA.
 DE Protein encoded by Prokaryotic essential gene #22472.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 16.0%; Score 378; DB 6; Length 588;
 Best Local Similarity 30.1%; Pred. No. 2.7e-15;
 RESULT 792
 ID ADM40790 standard; protein; 588 AA.
 DE Mycobacterial disease detection method related RV3367 protein.

PN WO2003073101-A2.
 PD 04-SEP-2003.
 PA (UVNY) UNIV NEW YORK STATE.
 Query Match 16.0%; Score 378; DB 7; Length 588;
 Best Local Similarity 30.1%; Pred. No. 2.7e-15;
 RESULT 793
 ID AAW27178 standard; protein; 646 AA.
 DE Nephila clavipes spider silk protein.
 PN WO9708315-A1.
 PD 06-MAR-1997.
 PA (BASE/) BASEL R M.
 PA (ELIO/) ELION G R.
 Query Match 16.0%; Score 378; DB 2; Length 646;
 Best Local Similarity 29.0%; Pred. No. 3e-15;
 RESULT 794
 ID ADB61321 standard; protein; 646 AA.
 DE Spider silk related MasPi protein.
 PN WO2003060099-A2.
 PD 24-JUL-2003.
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
 PA (ALWA/) ALWATTARI A.
 Query Match 16.0%; Score 378; DB 7; Length 646;
 Best Local Similarity 31.5%; Pred. No. 3e-15;
 RESULT 795
 ID ADC35240 standard; protein; 646 AA.
 DE MasPi silk protein, SEQ ID 1.
 PN WO2003057727-A1.
 PD 17-JUL-2003.
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
 Query Match 16.0%; Score 378; DB 7; Length 646;
 Best Local Similarity 31.5%; Pred. No. 3e-15;
 RESULT 796
 ID ADM46149 standard; protein; 646 AA.
 DE Nephila clavipes spidroin 1 (MasPi) protein.
 PN WO2003057720-A2.
 PD 17-JUL-2003.
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
 Query Match 16.0%; Score 378; DB 7; Length 646;
 Best Local Similarity 31.5%; Pred. No. 3e-15;
 RESULT 797
 ID AAR95107 standard; protein; 1038 AA.
 DE Fibronectin cell binding seq. contg. silk like protein (SLP)III.
 PN US5514581-A.
 PD 07-MAY-1996.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.9%; Score 376.5; DB 2; Length 1038;
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;
 RESULT 798
 ID AAB63997 standard; protein; 1038 AA.
 DE FCB-SLP protein from pSY1521 SEQ ID 36.
 PN US6140072-A.
 PD 31-OCT-2000.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.9%; Score 376.5; DB 4; Length 1038;
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;
 RESULT 799
 ID AAB72727 standard; protein; 1038 AA.
 DE Repetitive protein polymer protein sequence #27.
 PN US6184348-B1.
 PD 06-FEB-2001.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.9%; Score 376.5; DB 4; Length 1038;
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;
 RESULT 800
 ID ADO08760 standard; protein; 452 AA.
 DE Novel surgical dressing-related protein SeqID47.
 PN JP2004049921-A.
 PD 19-FEB-2004.
 PA (SANN) SANYO CHEM IND LTD.
 PA (ALCA-) ALCARE KK.
 Query Match 15.9%; Score 375.5; DB 8; Length 452;
 Best Local Similarity 29.9%; Pred. No. 3e-15;
 RESULT 801

ID ABU36682 standard; protein; 914 AA.
DE Protein encoded by Prokaryotic essential gene #22209.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.9%; Score 375; DB 6; Length 914;
Best Local Similarity 33.0%; Pred. No. 6.3e-15;
RESULT 802
ID AAM50037 standard; protein; 1255 AA.
DE N. clavipes spidroin synthetic homologue SO1S01 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 15.8%; Score 374; DB 5; Length 1255;
Best Local Similarity 30.5%; Pred. No. 9.8e-15;
RESULT 803
ID AAM50039 standard; protein; 1880 AA.
DE N. clavipes spidroin synthetic homologue SO1S01S01 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 15.8%; Score 374; DB 5; Length 1880;
Best Local Similarity 30.5%; Pred. No. 1.4e-14;
RESULT 804
ID AAO16497 standard; protein; 520 AA.
DE Argiope trifasciata spider silk protein #1.
PN WO200299082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Query Match 15.8%; Score 373.5; DB 6; Length 520;
Best Local Similarity 30.0%; Pred. No. 4.5e-15;
RESULT 805
ID ABU36979 standard; protein; 584 AA.
DE Protein encoded by Prokaryotic essential gene #22506.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.8%; Score 373.5; DB 6; Length 584;
Best Local Similarity 32.3%; Pred. No. 5.1e-15;
RESULT 806
ID ABU36570 standard; protein; 667 AA.
DE Protein encoded by Prokaryotic essential gene #22097.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.8%; Score 373.5; DB 6; Length 667;
Best Local Similarity 28.5%; Pred. No. 5.7e-15;
RESULT 807
ID ADE28209 standard; protein; 203 AA.
DE Human MDT protein - SEQ ID 59.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.8%; Score 373; DB 7; Length 203;
Best Local Similarity 58.9%; Pred. No. 2e-15;
RESULT 808
ID ABU36802 standard; protein; 694 AA.
DE Protein encoded by Prokaryotic essential gene #22329.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.7%; Score 372; DB 6; Length 694;
Best Local Similarity 30.3%; Pred. No. 7.4e-15;
RESULT 809
ID ABU36862 standard; protein; 615 AA.
DE Protein encoded by Prokaryotic essential gene #22389.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.7%; Score 371; DB 6; Length 615;
Best Local Similarity 31.0%; Pred. No. 7.6e-15;
RESULT 810
ID AAY40097 standard; protein; 651 AA.
DE Spider silk protein spidroine major 1.
PN FR274588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 15.7%; Score 371; DB 2; Length 651;
Best Local Similarity 30.1%; Pred. No. 8e-15;
RESULT 811
ID AAU11781 standard; protein; 651 AA.
DE Spider natural silk protein Spidroin 1.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.7%; Score 371; DB 5; Length 651;
Best Local Similarity 30.1%; Pred. No. 8e-15;
RESULT 812
ID AAR14308 standard; protein; 718 AA.
DE N. clavipes dragline silk protein-1.
PN EP452925-A.
PD 23-OCT-1991.
PA (UYWY-) UNIV OF WYOMING.
Query Match 15.7%; Score 371; DB 2; Length 718;
Best Local Similarity 30.1%; Pred. No. 8.8e-15;
RESULT 813
ID AAW53346 standard; protein; 718 AA.
DE Nephila clavipes spider silk protein.
PN US5728810-A.
PD 17-MAR-1998.
PA (UYWY-) UNIV WYOMING.
Query Match 15.7%; Score 371; DB 2; Length 718;
Best Local Similarity 30.1%; Pred. No. 8.8e-15;
RESULT 814
ID AAY59070 standard; protein; 718 AA.
DE N. clavipes spider silk protein 1.
PN US5989894-A.
PD 23-NOV-1999.
PA (UYWY-) UNIV WYOMING.
Query Match 15.7%; Score 371; DB 3; Length 718;
Best Local Similarity 30.1%; Pred. No. 8.8e-15;
RESULT 815
ID ABU36634 standard; protein; 491 AA.
DE Protein encoded by Prokaryotic essential gene #22161.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.7%; Score 370.5; DB 6; Length 491;
Best Local Similarity 28.3%; Pred. No. 6.6e-15;
RESULT 816
ID AAR81318 standard; protein; 980 AA.
DE Adhesion protein.
PN WO9519791-A1.
PD 27-JUL-1995.
PA (USNA) US SEC OF NAVY.
PA (CELL-) CELLCO INC.
Query Match 15.7%; Score 370.5; DB 2; Length 980;
Best Local Similarity 29.6%; Pred. No. 1.3e-14;
RESULT 817
ID AAR05312 standard; protein; 1066 AA.
DE Sequence encoding SLP-LI monomer (similar to silk fibroin).
PN WO9005177-A.
PD 17-MAY-1990.
PA (SYTR) SYNTRO CORP.
Query Match 15.7%; Score 370; DB 2; Length 1066;
Best Local Similarity 27.9%; Pred. No. 1.5e-14;
RESULT 818
ID AAM50038 standard; protein; 989 AA.
DE N. clavipes spidroin synthetic homologue SO1SM12 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 15.6%; Score 369.5; DB 5; Length 989;
Best Local Similarity 30.8%; Pred. No. 1.5e-14;
RESULT 819
ID AAR41010 standard; protein; 2025 AA.

DE SELP1 multimeric protein.
 PN US5243038-A.
 PD 07-SEP-1993.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.6%; Score 369; DB 2; Length 2025;
 Best Local Similarity 27.4%; Pred. No. 3.1e-14;
 RESULT 820
 ID AAF82959 standard; protein; 2107 AA.
 DE SELP1 protein comprising gagags of silk fibroin and gvgvp of elastin.
 PN WO803533-A.
 PD 19-MAY-1988.
 PA (SYTR) SYNTHRO CORP.
 Query Match 15.6%; Score 369; DB 1; Length 2107;
 Best Local Similarity 27.4%; Pred. No. 3.3e-14;
 RESULT 821
 ID AAV78287 standard; protein; 1011 AA.
 DE SELPF amino acid sequence SEQ ID NO:94.
 PN US6018030-A.
 PD 25-JAN-2000.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 367; DB 3; Length 1011;
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;
 RESULT 822
 ID AG69277 standard; protein; 1011 AA.
 DE Silk/Elastin-like protein SELPF.
 PN US6355776-B1.
 PD 12-MAR-2002.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 367; DB 5; Length 1011;
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;
 RESULT 823
 ID ADE44989 standard; protein; 1011 AA.
 DE Recombinant structural protein SELPF protein seq id 94.
 PN US2003083464-A1.
 PD 01-MAY-2003.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 367; DB 7; Length 1011;
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;
 RESULT 824
 ID AAW26351 standard; protein; 1170 AA.
 DE SELPF synthetic protein.
 PN US5641648-A.
 PD 24-JUN-1997.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 367; DB 2; Length 1170;
 Best Local Similarity 27.8%; Pred. No. 2.5e-14;
 RESULT 825
 ID ABB67896 standard; protein; 610 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 30480.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 15.5%; Score 366; DB 4; Length 610;
 Best Local Similarity 32.5%; Pred. No. 1.5e-14;
 RESULT 826
 ID AAE36887 standard; protein; 691 AA.
 DE Dolomedes tenebrosus fibroin 2 protein.
 PN WO2003020916-A2.
 PD 13-MAR-2003.
 PA (UYWY-) UNIV WYOMING.
 Query Match 15.5%; Score 366; DB 6; Length 691;
 Best Local Similarity 27.0%; Pred. No. 1.7e-14;
 RESULT 827
 ID AAW53526 standard; protein; 695 AA.
 DE Amino acid sequence of FCB-SLPPII protein.
 PN WO9810063-A1.
 PD 12-MAR-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 2; Length 695;
 Best Local Similarity 27.3%; Pred. No. 1.7e-14;
 RESULT 828
 ID AAW26349 standard; protein; 766 AA.
 DE FCB-SLPPII (57 kDa) synthetic protein.

PN US5641648-A.
 PD 24-JUN-1997.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 2; Length 766;
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;
 RESULT 829
 ID AAY78285 standard; peptide; 766 AA.
 DE FCB-SLPPII amino acid sequence SEQ ID NO:88.
 PN US6018030-A.
 PD 25-JAN-2000.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 3; Length 766;
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;
 RESULT 830
 ID ABG69275 standard; protein; 766 AA.
 DE Fibronectin FCB portion/silk-like protein, FCB-SLPPII #1.
 PN US6355776-B1.
 PD 12-MAR-2002.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 5; Length 766;
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;
 RESULT 831
 ID ADE44983 standard; protein; 766 AA.
 DE Recombinant structural protein FCB-SLPPII protein seq id 88.
 PN US2003083464-A1.
 PD 01-MAY-2003.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 7; Length 766;
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;
 RESULT 832
 ID AAY78286 standard; protein; 979 AA.
 DE FCB-SLPPII amino acid sequence SEQ ID NO:89.
 PN US6018030-A.
 PD 25-JAN-2000.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 3; Length 979;
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;
 RESULT 833
 ID ABG69276 standard; protein; 979 AA.
 DE Fibronectin FCB portion/silk-like protein, FCB-SLPPII #2.
 PN US6355776-B1.
 PD 12-MAR-2002.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 5; Length 979;
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;
 RESULT 834
 ID ADE44984 standard; protein; 979 AA.
 DE Recombinant structural protein FCB-SLPPII protein seq id 89.
 PN US2003083464-A1.
 PD 01-MAY-2003.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 7; Length 979;
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;
 RESULT 835
 ID AAW26350 standard; protein; 1050 AA.
 DE FCB-SLPPII (72 kDa) synthetic protein.
 PN US5641648-A.
 PD 24-JUN-1997.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 2; Length 1050;
 Best Local Similarity 27.3%; Pred. No. 2.6e-14;
 RESULT 836
 ID AAW53527 standard; protein; 1170 AA.
 DE Amino acid sequence of SELPF protein.
 PN WO9810063-A1.
 PD 12-MAR-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 15.5%; Score 366; DB 2; Length 1170;
 Best Local Similarity 27.8%; Pred. No. 2.8e-14;
 RESULT 837
 ID AAW50042 standard; protein; 630 AA.
 DE N. clavipes spidroin synthetic homologue SO1 protein.
 PN DE10113781-A1.

PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENTIK & KULTURPFLANZE.
Query Match 15.4%; Score 365.5; DB 5; Length 630;
Best Local Similarity 29.6%; Pred. No. 1.7e-14;
RESULT 838
ID AAM50047 standard; protein; 676 AA.
DE N. clavipes spidroin synthetic homologue SO1 protein #2.
PN D810113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENTIK & KULTURPFLANZE.
Query Match 15.5%; Score 365.5; DB 5; Length 676;
Best Local Similarity 29.6%; Pred. No. 1.8e-14;
RESULT 839
ID ABU36623 standard; protein; 576 AA.
DE Protein encoded by Prokaryotic essential gene #22150.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.4%; Score 365; DB 6; Length 576;
Best Local Similarity 30.2%; Pred. No. 1.7e-14;
RESULT 840
ID ABU36439 standard; protein; 591 AA.
DE Protein encoded by Prokaryotic essential gene #21966.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.4%; Score 365; DB 6; Length 591;
Best Local Similarity 29.4%; Pred. No. 1.7e-14;
RESULT 841
ID ABG69270 standard; protein; 2018 AA.
DE Silk/Elastin-like protein SELP1.
PN US6355776-B1.
PD 12-MAR-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364.5; DB 5; Length 2018;
Best Local Similarity 27.4%; Pred. No. 5.9e-14;
RESULT 842
ID ADE44975 standard; protein; 2018 AA.
DE Recombinant structural protein SELPI protein seq id 80.
PN US2003083464-A1.
PD 01-MAY-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364.5; DB 7; Length 2018;
Best Local Similarity 27.4%; Pred. No. 5.9e-14;
RESULT 843
ID AAY78280 standard; peptide; 2100 AA.
DE SELPI amino acid sequence SEQ ID NO:80.
PN US6018030-A.
PD 25-JAN-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364.5; DB 3; Length 2100;
Best Local Similarity 27.4%; Pred. No. 6.1e-14;
RESULT 844
ID ABU36540 standard; protein; 606 AA.
DE Protein encoded by Prokaryotic essential gene #22067.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.4%; Score 364; DB 6; Length 606;
Best Local Similarity 29.8%; Pred. No. 2e-14;
RESULT 845
ID AAR95112 standard; protein; 649 AA.
DE Silk like protein (SLP)-L2.
PN US5514581-A.
PD 07-MAY-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 649;
Best Local Similarity 27.7%; Pred. No. 2.1e-14;
RESULT 846
ID AAB64002 standard; protein; 649 AA.
DE SLP-L1 protein SEQ ID 49.
PN US6140072-A.
PD 31-OCT-2000.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 649;
Best Local Similarity 27.7%; Pred. No. 2.1e-14;
RESULT 847
ID AAB72732 standard; protein; 649 AA.
DE Repetitive protein polymer protein sequence #32.
PN US6184348-B1.
PD 06-FEB-2001.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 649;
Best Local Similarity 27.7%; Pred. No. 2.1e-14;
RESULT 848
ID AAR95111 standard; protein; 784 AA.
DE Silk like protein (SLP)-L1.
PN US5514581-A.
PD 07-MAY-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 784;
Best Local Similarity 31.3%; Pred. No. 2.6e-14;
RESULT 849
ID AAB64001 standard; protein; 784 AA.
DE SLP-L1 protein SEQ ID 48.
PN US6140072-A.
PD 31-OCT-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 784;
Best Local Similarity 31.3%; Pred. No. 2.6e-14;
RESULT 850
ID AAB72731 standard; protein; 784 AA.
DE Repetitive protein polymer protein sequence #31.
PN US6184348-B1.
PD 06-FEB-2001.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 4; Length 784;
Best Local Similarity 31.3%; Pred. No. 2.6e-14;
RESULT 851
ID AAR05309 standard; protein; 946 AA.
DE SLP-L2 polymer (similar to silk fibroin).
PN WO9005177-A.
PD 17-MAY-1990.
PA (SYTR) SYNTRO CORP.
Query Match 15.4%; Score 364; DB 2; Length 946;
Best Local Similarity 27.7%; Pred. No. 3.1e-14;
RESULT 852
ID AAW01496 standard; protein; 1018 AA.
DE Silk-like protein SLP-L3.0 polymer.
PN WO9501998-A2.
PD 19-JAN-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 1018;
Best Local Similarity 30.5%; Pred. No. 3.3e-14;
RESULT 853
ID AAW26345 standard; protein; 2107 AA.
DE SELPI synthetic elastomeric protein.
PN US5641648-A.
PD 24-JUN-1997.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 2107;
Best Local Similarity 27.4%; Pred. No. 6.6e-14;
RESULT 854
ID AAW53521 standard; protein; 2107 AA.
DE Amino acid sequence of the SELPI protein.
PN WO9810063-A1.
PD 12-MAR-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.4%; Score 364; DB 2; Length 2107;
Best Local Similarity 27.4%; Pred. No. 6.6e-14;
RESULT 855
ID ABU36685 standard; protein; 639 AA.
DE Protein encoded by Prokaryotic essential gene #22212.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 15.4%; Score 363; DB 6; Length 639;
Best Local Similarity 30.5%; Pred. No. 2.4e-14;
RESULT 856
ID AAR99057 standard; protein; 604 AA.
DE Spider dragline variant, DP-1B.16 polymer.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.3%; Score 362; DB 2; Length 604;
Best Local Similarity 29.7%; Pred. No. 2.7e-14;
RESULT 857
ID AAR95109 standard; protein; 1332 AA.
DE Silk like protein (SLP)-C.
PN US5514581-A.
PD 07-MAY-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.3%; Score 362; DB 2; Length 1332;
Best Local Similarity 28.3%; Pred. No. 5.7e-14;
RESULT 858
ID AAB63999 standard; protein; 1332 AA.
DE SLP-C protein sequence SEQ ID 41.
PN US6140072-A.
PD 31-OCT-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.3%; Score 362; DB 4; Length 1332;
Best Local Similarity 28.3%; Pred. No. 5.7e-14;
RESULT 859
ID AAB72729 standard; protein; 1332 AA.
DE Repetitive protein polymer protein sequence #29.
PN US6184348-B1.
PD 06-FEB-2001.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.3%; Score 362; DB 4; Length 1332;
Best Local Similarity 28.3%; Pred. No. 5.7e-14;
RESULT 860
ID AAR92960 standard; protein; 2055 AA.
DE SELP2 protein comprising gagags of silk fibroin and gvgvp of elastin.
PN WO8803533-A.
PD 19-MAY-1988.
PA (SVTR) SYNTRO CORP.
Query Match 15.3%; Score 360.5; DB 1; Length 2055;
Best Local Similarity 25.6%; Pred. No. 1.1e-13;
RESULT 861
ID ABU36590 standard; protein; 562 AA.
DE Protein encoded by Prokaryotic essential gene #23117.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.2%; Score 360; DB 6; Length 562;
Best Local Similarity 28.9%; Pred. No. 3.3e-14;
RESULT 862
ID ABB76672 standard; protein; 655 AA.
DE Protein related to Bombyx mori silk fibroin.
PN WO200240528-A1.
PD 23-MAY-2002.
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Query Match 15.2%; Score 360; DB 5; Length 655;
Best Local Similarity 28.7%; Pred. No. 3.8e-14;
RESULT 863
ID ABU36665 standard; protein; 1011 AA.
DE Protein encoded by Prokaryotic essential gene #22192.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 15.2%; Score 359.5; DB 6; Length 1011;
Best Local Similarity 31.2%; Pred. No. 6.2e-14;
RESULT 864
ID AAE36926 standard; protein; 490 AA.
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #1.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 15.2%; Score 359; DB 6; Length 490;

Best Local Similarity 27.9%; Pred. No. 3.3e-14;
RESULT 865
ID AAQ16492 standard; protein; 525 AA.
DE Phidippus audax fibronin 1 protein.
PN WO200299082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Query Match 15.2%; Score 359; DB 6; Length 525;
Best Local Similarity 28.9%; Pred. No. 3.6e-14;
RESULT 866
ID AAE36893 standard; protein; 525 AA.
DE Phidippus audax fibronin 1 protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 15.2%; Score 359; DB 6; Length 525;
Best Local Similarity 28.9%; Pred. No. 3.6e-14;
RESULT 867
ID AAE36886 standard; protein; 854 AA.
DE Delomedes tenebrosus fibroin 1 protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 15.2%; Score 359; DB 6; Length 854;
Best Local Similarity 26.2%; Pred. No. 5.7e-14;
RESULT 868
ID AAY40099 standard; protein; 615 AA.
DE Spider silk protein spidroin minor 1.
PN FR2774588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 15.2%; Score 358.5; DB 2; Length 615;
Best Local Similarity 28.7%; Pred. No. 4.4e-14;
RESULT 869
ID AAR41011 standard; protein; 2055 AA.
DE SELP2 multimeric protein.
PN US5243038-A.
PD 07-SEP-1993.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.2%; Score 358.5; DB 2; Length 2055;
Best Local Similarity 25.6%; Pred. No. 1.4e-13;
RESULT 870
ID AAW26346 standard; protein; 2055 AA.
DE SELP2 synthetic elastomeric protein.
PN US5641648-A.
PD 24-JUN-1997.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.2%; Score 358.5; DB 2; Length 2055;
Best Local Similarity 25.6%; Pred. No. 1.4e-13;
RESULT 871
ID AAW53522 standard; protein; 2055 AA.
DE Amino acid sequence of the SELP2 protein.
PN WO9810083-A1.
PD 12-MAR-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.2%; Score 358.5; DB 2; Length 2055;
Best Local Similarity 25.6%; Pred. No. 1.4e-13;
RESULT 872
ID AAY78281 standard; peptide; 2055 AA.
DE SELP2 amino acid sequence SEQ ID NO:81.
PN US6018030-A.
PD 25-JAN-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.2%; Score 358.5; DB 3; Length 2055;
Best Local Similarity 25.6%; Pred. No. 1.4e-13;
RESULT 873
ID ADE44976 standard; protein; 2055 AA.
DE Recombinant structural protein SELP2 protein seq id 81.
PN US2003083464-A1.
PD 01-MAY-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.2%; Score 358.5; DB 7; Length 2055;
Best Local Similarity 25.6%; Pred. No. 1.4e-13;

RESULT 874
ID AAR99053 standard; protein; 606 AA.
DE Spider dragline variant, DP-1A.9 polymer.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.2%; Score 358; DB 2; Length 606;
Best Local Similarity 29.2%; Pred. No. 4.7e-14;
RESULT 875
ID AAR99055 standard; protein; 606 AA.
DE Spider dragline variant, DP-1B.9 polymer.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.2%; Score 358; DB 2; Length 606;
Best Local Similarity 30.3%; Pred. No. 4.7e-14;
RESULT 876
ID AAY40101 standard; protein; 606 AA.
DE Polymer of an analogue of spider silk protein spidroine major 1.
PN FR2774588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 15.2%; Score 358; DB 2; Length 606;
Best Local Similarity 30.3%; Pred. No. 4.7e-14;
RESULT 877
ID AAY40102 standard; protein; 606 AA.
DE Polymer of an analogue of spider silk protein spidroine major 1.
PN FR2774588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 15.2%; Score 358; DB 2; Length 606;
Best Local Similarity 30.3%; Pred. No. 4.7e-14;
RESULT 878
ID AAY40100 standard; protein; 606 AA.
DE Polymer of an analogue of spider silk protein spidroine major 1.
PN FR2774588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 15.2%; Score 358; DB 2; Length 606;
Best Local Similarity 29.2%; Pred. No. 4.7e-14;
RESULT 879
ID AAU11793 standard; protein; 809 AA.
DE Dragline protein 1 analogue DP-1B 8mer.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.2%; Score 358; DB 5; Length 809;
Best Local Similarity 30.3%; Pred. No. 6.2e-14;
RESULT 880
ID AAU11797 standard; protein; 818 AA.
DE Dragline protein 1 analogue DP-1B/his tag 8mer.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.2%; Score 358; DB 5; Length 818;
Best Local Similarity 30.3%; Pred. No. 6.3e-14;
RESULT 881
ID AAU11794 standard; protein; 1617 AA.
DE Dragline protein 1 analogue DP-1B 16mer.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.2%; Score 358; DB 5; Length 1617;
Best Local Similarity 30.3%; Pred. No. 1.2e-13;
RESULT 882
ID AAU11798 standard; protein; 1626 AA.
DE Dragline protein 1 analogue DP-1B/his tag 16mer.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.2%; Score 358; DB 5; Length 1626;
Best Local Similarity 30.3%; Pred. No. 1.2e-13;
RESULT 883

ID AAO16494 standard; protein; 761 AA.
DE Kukulcania hibernalis spider silk protein #1.
PN WO20029082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Query Match 15.1%; Score 357; DB 6; Length 761;
Best Local Similarity 28.1%; Pred. No. 6.7e-14;
RESULT 884
ID ABG69271 standard; protein; 2055 AA.
DE Silk/Elastin-like protein SELP2.
PN US6355776-B1.
PD 12-MAR-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 15.0%; Score 354.5; DB 5; Length 2055;
Best Local Similarity 25.6%; Pred. No. 2.5e-13;
RESULT 885
ID AAW01494 standard; protein; 945 AA.
DE Silk-like protein SLP-F9 polymer.
PN WO9501998-A2.
PD 19-JAN-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES.
Query Match 15.0%; Score 354; DB 2; Length 945;
Best Local Similarity 25.6%; Pred. No. 1.3e-13;
RESULT 886
ID ABU34417 standard; protein; 505 AA.
DE Protein encoded by Prokaryotic essential gene #19944.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.9%; Score 353; DB 6; Length 505;
Best Local Similarity 32.4%; Pred. No. 8e-14;
RESULT 887
ID AAP82961 standard; protein; 2257 AA.
DE SEPL3 protein comprising gagage of silk fibroin and gvgvp of elastin.
PN WO8803533-A.
PD 19-MAY-1988.
PA (SYTR) SYNTRO CORP.
Query Match 14.9%; Score 352.5; DB 1; Length 2257;
Best Local Similarity 29.6%; Pred. No. 3.6e-13;
RESULT 888
ID ABU36613 standard; protein; 603 AA.
DE Protein encoded by Prokaryotic essential gene #22140.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.9%; Score 352; DB 6; Length 603;
Best Local Similarity 30.0%; Pred. No. 1.1e-13;
RESULT 889
ID AAR80254 standard; peptide; 1056 AA.
DE Polymer SELP3.
PN WO9524478-A1.
PD 14-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 14.9%; Score 351.5; DB 2; Length 1056;
Best Local Similarity 26.5%; Pred. No. 2e-13;
RESULT 890
ID ABP53475 standard; protein; 1056 AA.
DE Protein polymer SELP3 polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPF/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match 14.9%; Score 351.5; DB 5; Length 1056;
Best Local Similarity 26.5%; Pred. No. 2e-13;
RESULT 891
ID ABU36437 standard; protein; 957 AA.
DE Protein encoded by Prokaryotic essential gene #21964.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.9%; Score 351; DB 6; Length 957;
Best Local Similarity 28.0%; Pred. No. 2e-13;
RESULT 892

ID ABU36826 standard; protein; 461 AA.
 DE Protein encoded by Prokaryotic essential gene #22353.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 14.8%; Score 350.5; DB 6; Length 461;
 Best Local Similarity 31.3%; Pred. No. 1e-13;
 RESULT 893
 ID AAR41012 standard; protein; 2257 AA.
 DE SLP3 multimeric protein.
 PN US5243038-A.
 PD 07-SEP-1993.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;
 RESULT 894
 ID AAW26347 standard; protein; 2257 AA.
 DE SLP3 synthetic elastomeric protein.
 PN US5641648-A.
 PD 24-JUN-1997.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;
 RESULT 895
 ID AAW53523 standard; protein; 2257 AA.
 DE Amino acid sequence of the SLP3 protein.
 PN WO9810063-A1.
 PD 12-MAR-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;
 RESULT 896
 ID AAY78282 standard; peptide; 2257 AA.
 DE SLP3 amino acid sequence SEQ ID NO:82.
 PN US6018030-A.
 PD 25-JAN-2000.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 14.8%; Score 350.5; DB 3; Length 2257;
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;
 RESULT 897
 ID AAG69272 standard; protein; 2257 AA.
 DE Silk/Elastin-like protein SLP3.
 PN US6355776-B1.
 PD 12-MAR-2002.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 14.8%; Score 350.5; DB 5; Length 2257;
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;
 RESULT 898
 ID ADE44977 standard; protein; 2257 AA.
 DE Recombinant structural protein SLP3 protein seq id 82.
 PN US2003083464-A1.
 PD 01-MAY-2003.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 14.8%; Score 350.5; DB 7; Length 2257;
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;
 RESULT 899
 ID ADQ19957 standard; protein; 316 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2777.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 14.8%; Score 350; DB 8; Length 316;
 Best Local Similarity 35.3%; Pred. No. 7.8e-14;
 RESULT 900
 ID ABU36684 standard; protein; 618 AA.
 DE Protein encoded by Prokaryotic essential gene #22211.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 14.8%; Score 349; DB 6; Length 618;
 Best Local Similarity 29.9%; Pred. No. 1.7e-13;
 RESULT 901
 ID AAB82611 standard; protein; 528 AA.

DE Spider recombinant silk protein pETNCD5.
 PN WO200153333-A1.
 PD 26-JUL-2001.
 PA (MELL/) MELLO C M.
 PA (ARCI/) ARCIDIACONO S.
 PA (BUTL/) BUTLER M M.
 PA (USSA) US SEC OF ARMY.
 Query Match 14.7%; Score 348.5; DB 4; Length 528;
 Best Local Similarity 29.0%; Pred. No. 1.6e-13;
 RESULT 902
 ID AAR80168 standard; protein; 831 AA.
 DE PMISSI MISP spider silk protein insert product.
 PN WO9525165-A1.
 PD 21-SEP-1995.
 PA (UWVY-) UNIV WYOMING.
 Query Match 14.7%; Score 348.5; DB 2; Length 831;
 Best Local Similarity 28.1%; Pred. No. 2.4e-13;
 RESULT 903
 ID AAE36869 standard; protein; 648 AA.
 DE Argiope trifasciata major ampullate spidroin 1 (MasPl) protein.
 PN WO2003020916-A2.
 PD 13-MAR-2003.
 PA (UWVY-) UNIV WYOMING.
 Query Match 14.6%; Score 346; DB 6; Length 648;
 Best Local Similarity 27.3%; Pred. No. 2.7e-13;
 RESULT 904
 ID ADO08772 standard; protein; 441 AA.
 DE Novel surgical dressing-related protein SeqID59.
 PN JP2004049921-A.
 PD 19-FEB-2004.
 PA (SANN) SANYO CHEM IND LTD.
 PA (ALCA-) ALCARE KK.
 Query Match 14.6%; Score 345.5; DB 8; Length 441;
 Best Local Similarity 27.2%; Pred. No. 2e-13;
 RESULT 905
 ID AAW31853 standard; protein; 898 AA.
 DE Mycobacterium tuberculosis 77 kDa protein.
 PN WO9741252-A2.
 PD 06-NOV-1997.
 PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.
 Query Match 14.6%; Score 344.5; DB 2; Length 898;
 Best Local Similarity 26.8%; Pred. No. 4.6e-13;
 RESULT 906
 ID AAM17023 standard; protein; 283 AA.
 DE Peptide #3457 encoded by probe for measuring cervical gene expression.
 PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 14.6%; Score 344; DB 4; Length 283;
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;
 RESULT 907
 ID ABB36017 standard; peptide; 283 AA.
 DE Peptide #3523 encoded by human foetal liver single exon probe.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 14.6%; Score 344; DB 4; Length 283;
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;
 RESULT 908
 ID AAW29514 standard; protein; 283 AA.
 DE Peptide #3551 encoded by probe for measuring placental gene expression.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 14.6%; Score 344; DB 4; Length 283;
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;
 RESULT 909
 ID ABB30839 standard; peptide; 283 AA.
 DE Peptide #3490 encoded by breast cell single exon nucleic acid probe.
 PN WO200157271-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 14.6%; Score 344; DB 4; Length 283;

Best Local Similarity 34.4%; Pred. No. 1.6e-13;
RESULT 910
ID ABB21422 standard; protein; 283 AA.
DE Protein #3421 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.6%; Score 344; DB 4; Length 283;
Best Local Similarity 34.4%; Pred. No. 1.6e-13;
RESULT 911
ID AAM69190 standard; protein; 283 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29456.
PN WO200157276-A2.
PD 03-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.6%; Score 344; DB 4; Length 283;
Best Local Similarity 34.4%; Pred. No. 1.6e-13;
RESULT 912
ID AAM56810 standard; protein; 283 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28915.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.6%; Score 344; DB 4; Length 283;
Best Local Similarity 34.4%; Pred. No. 1.6e-13;
RESULT 913
ID AAG50867 standard; peptide; 283 AA.
DE Human liver peptide, SEQ ID No 29515.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.6%; Score 344; DB 4; Length 283;
Best Local Similarity 34.4%; Pred. No. 1.6e-13;
RESULT 914
ID AAM04731 standard; protein; 283 AA.
DE Peptide #3413 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.6%; Score 344; DB 4; Length 283;
Best Local Similarity 34.4%; Pred. No. 1.6e-13;
RESULT 915
ID ABG38794 standard; peptide; 283 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28459.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.6%; Score 344; DB 5; Length 283;
Best Local Similarity 34.4%; Pred. No. 1.6e-13;
RESULT 916
ID AAE36839 standard; protein; 525 AA.
DE Protein encoded by Prokaryotic essential gene #22366.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.6%; Score 344; DB 6; Length 525;
Best Local Similarity 30.4%; Pred. No. 3e-13;
RESULT 917
ID AAE36884 standard; protein; 651 AA.
DE Argiope trifasciata flagelliform silk protein (Flag).
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 14.6%; Score 344; DB 6; Length 651;
Best Local Similarity 28.4%; Pred. No. 3.6e-13;
RESULT 918
ID AAB83609 standard; protein; 681 AA.
DE Spider recombinant silk protein PQE((SP1)4/(SP2)1)4.
PN WO200153333-A1.
PD 26-JUL-2001.
PA (MELL/) MELLO C M.
PA (ARCI/) ARCIDIACONO S.
PA (BUTL/) BUTLER M M.

PA (USSA) US SEC OF ARMY.
Query Match 14.5%; Score 343; DB 4; Length 681;
Best Local Similarity 28.3%; Pred. No. 4.4e-13;
RESULT 919
ID AAB82610 standard; protein; 691 AA.
DE Spider recombinant silk protein pET((SP1)4/(SP2)1)4.
PN WO200153333-A1.
PD 26-JUL-2001.
PA (MELL/) MELLO C M.
PA (ARCI/) ARCIDIACONO S.
PA (BUTL/) BUTLER M M.
PA (USSA) US SEC OF ARMY.
Query Match 14.5%; Score 343; DB 4; Length 691;
Best Local Similarity 28.3%; Pred. No. 4.4e-13;
RESULT 920
ID ADB61323 standard; protein; 629 AA.
DE Spider silk related ADP-3 protein.
PN WO2003060099-A2.
PD 24-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
PA (ALWA/) ALWATTARI A.
Query Match 14.5%; Score 342.5; DB 7; Length 629;
Best Local Similarity 29.5%; Pred. No. 4.4e-13;
RESULT 921
ID ADC35242 standard; protein; 629 AA.
DE ADP-3 silk protein, SEQ ID 3.
PN WO2003057727-A1.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 14.5%; Score 342.5; DB 7; Length 629;
Best Local Similarity 29.5%; Pred. No. 4.4e-13;
RESULT 922
ID ADM46151 standard; protein; 629 AA.
DE Nephila clavipes ADP-3 protein.
PN WO2003057720-A2.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 14.5%; Score 342.5; DB 7; Length 629;
Best Local Similarity 29.5%; Pred. No. 4.4e-13;
RESULT 923
ID AAM50045 standard; protein; 773 AA.
DE N. clavipes spidroin homologue SMI2-70xELP for plant expression.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPRP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 14.5%; Score 342.5; DB 5; Length 773;
Best Local Similarity 29.4%; Pred. No. 5.3e-13;
RESULT 924
ID AAM50046 standard; protein; 777 AA.
DE N. clavipes spidroin homologue SMI2-70xELP for E. coli expression.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPRP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 14.5%; Score 342.5; DB 5; Length 777;
Best Local Similarity 29.4%; Pred. No. 5.3e-13;
RESULT 925
ID ADO08787 standard; protein; 482 AA.
DE Novel surgical dressing-related protein SeqID74.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANVO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 14.5%; Score 342; DB 8; Length 482;
Best Local Similarity 27.1%; Pred. No. 3.6e-13;
RESULT 926
ID ABU36689 standard; protein; 515 AA.
DE Protein encoded by Prokaryotic essential gene #22216.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.5%; Score 342; DB 6; Length 515;
Best Local Similarity 29.3%; Pred. No. 3.9e-13;
RESULT 927

ID ABU36423 standard; protein; 487 AA.
DE Protein encoded by Prokaryotic essential gene #21950.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.4%; Score 339.5; DB 6; Length 487;
Best Local Similarity 29.9%; Pred. No. 5.2e-13;
RESULT 928
ID AAE36885 standard; protein; 1002 AA.
DE Argiope trifasciata flag protein fragment.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 14.3%; Score 337; DB 6; Length 1002;
Best Local Similarity 29.9%; Pred. No. 1.5e-12;
RESULT 929
ID AAE18320 standard; protein; 968 AA.
DE Silk elastin combination protein, SELP3.
PN WO200200016-A1.
PD 03-JAN-2002.
PA (LUMI-) LUMINIS PTY LTD.
PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.
Query Match 14.2%; Score 336.5; DB 5; Length 968;
Best Local Similarity 29.6%; Pred. No. 1.5e-12;
RESULT 930
ID ABP53479 standard; protein; 1169 AA.
DE Protein polymer SELPPF polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKI E R.
Query Match 14.2%; Score 336; DB 5; Length 1169;
Best Local Similarity 30.5%; Pred. No. 2e-12;
RESULT 931
ID ADO08775 standard; protein; 482 AA.
DE Novel surgical dressing-related protein SeqID62.
PN JF2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 14.2%; Score 335; DB 8; Length 482;
Best Local Similarity 30.6%; Pred. No. 9.8e-13;
RESULT 932
ID ADP31119 standard; protein; 8973 AA.
DE Human secreted protein SEQ ID #1886.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 14.2%; Score 335; DB 8; Length 8973;
Best Local Similarity 29.9%; Pred. No. 1.6e-11;
RESULT 933
ID AAW79137 standard; protein; 261 AA.
DE FLGA Gly-ala insert present in chimeric IkappaB construct.
PN WO9822577-A1.
PD 28-MAY-1998.
PA (MASU/) MASUCCI M G.
Query Match 14.2%; Score 334.5; DB 2; Length 261;
Best Local Similarity 29.1%; Pred. No. 5.8e-13;
RESULT 934
ID AAE36927 standard; protein; 440 AA.
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #2.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 14.1%; Score 334; DB 6; Length 440;
Best Local Similarity 27.9%; Pred. No. 1e-12;
RESULT 935
ID ABP72662 standard; protein; 498 AA.
DE Rv181c gene product of Mycobacterium tuberculosis.
PN WO2003018754-A2.
PD 06-MAR-2003.
PA (NEUR-) NEURONZ LTD.
PA (NEUR-) NEURONZ BIOSCIENCES INC.

Query Match 14.1%; Score 334; DB 6; Length 498;
Best Local Similarity 29.3%; Pred. No. 1.2e-12;
RESULT 936
ID ABU36686 standard; protein; 498 AA.
DE Protein encoded by Prokaryotic essential gene #22213.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 14.1%; Score 334; DB 6; Length 498;
Best Local Similarity 29.3%; Pred. No. 1.2e-12;
RESULT 937
ID ABB68951 standard; protein; 342 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33645.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.1%; Score 332.5; DB 4; Length 342;
Best Local Similarity 29.5%; Pred. No. 1e-12;
RESULT 938
ID AAM50043 standard; protein; 364 AA.
DE N. clavipes spidroin synthetic homologue SM12 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 14.0%; Score 331.5; DB 5; Length 364;
Best Local Similarity 29.3%; Pred. No. 1.2e-12;
RESULT 939
ID AAE36868 standard; protein; 447 AA.
DE Argiope aurantia major ampullate spidroin 1 (Maspl) protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 14.0%; Score 330; DB 6; Length 447;
Best Local Similarity 29.5%; Pred. No. 1.8e-12;
RESULT 940
ID ADK51951 standard; protein; 780 AA.
DE Repeat protein polymer repeat sequence, SEQ ID 19.
PN WO2003099465-A1.
PD 04-DEC-2003.
PA (DOWO) DOW CORNING CORP.
PA (GEMV) GENECOR INT INC.
Query Match 13.9%; Score 329; DB 8; Length 780;
Best Local Similarity 26.9%; Pred. No. 3.6e-12;
RESULT 941
ID ADR70468 standard; protein; 780 AA.
DE Silk-elastin polymer SELP47K.
PN US2004180027-A1.
PD 16-SEP-2004.
PA (KUMA/) KUMAR M.
PA (CUEV/) CUEVAS W A.
Query Match 13.9%; Score 329; DB 8; Length 780;
Best Local Similarity 26.9%; Pred. No. 3.6e-12;
RESULT 942
ID ADO08759 standard; protein; 302 AA.
DE Novel surgical dressing-related protein SeqID46.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 13.8%; Score 326.5; DB 8; Length 302;
Best Local Similarity 29.6%; Pred. No. 2.1e-12;
RESULT 943
ID ABB81230 standard; protein; 334 AA.
DE Mycobacterium bovis BCG strain Pasteur PE-PCRS protein sequence.
PN WO954487-A2.
PD 28-OCT-1999.
PA (INSP) INST PASTEUR.
Query Match 13.8%; Score 326.5; DB 3; Length 334;
Best Local Similarity 30.0%; Pred. No. 2.3e-12;
RESULT 944
ID ABU36981 standard; protein; 439 AA.
DE Protein encoded by Prokaryotic essential gene #22508.
PN WO200277183-A2.

PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.8%; Score 325.5; DB 6; Length 439;
Best Local Similarity 29.0%; Pred. No. 3.4e-12;
RESULT 945
ID ADO08784 standard; protein; 471 AA.
DE Novel surgical dressing-related protein SeqID171.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 13.7%; Score 324.5; DB 8; Length 471;
Best Local Similarity 28.1%; Pred. No. 4.2e-12;
RESULT 946
ID ADO08764 standard; protein; 482 AA.
DE Novel surgical dressing-related protein SeqID51.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 13.7%; Score 324; DB 8; Length 482;
Best Local Similarity 29.3%; Pred. No. 4.6e-12;
RESULT 947
ID ADR70478 standard; protein; 1038 AA.
DE Silk-elastin polymer SEMP 67K.
PN US2004180027-A1.
PD 16-SEP-2004.
PA (KUMA/) KUMAR M.
PA (CUEV/) CUEVAS W A.
Query Match 13.7%; Score 324; DB 8; Length 1038;
Best Local Similarity 25.0%; Pred. No. 9.6e-12;
RESULT 948
ID AAR80255 standard; peptide; 972 AA.
DE Polymer SEMP4.
PN WO9524478-A1.
PD 14-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 13.6%; Score 322.5; DB 2; Length 972;
Best Local Similarity 24.8%; Pred. No. 1.1e-11;
RESULT 949
ID ABP53476 standard; protein; 972 AA.
DE Protein polymer SEMP4 polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match 13.6%; Score 322.5; DB 5; Length 972;
Best Local Similarity 24.8%; Pred. No. 1.1e-11;
RESULT 950
ID AAB70185 standard; peptide; 504 AA.
DE Peptide dendrimer carrier #10.
PN WO200107469-A2.
PD 01-FEB-2001.
PA (VERD/) VERDINI A.
Query Match 13.6%; Score 321.5; DB 4; Length 504;
Best Local Similarity 29.1%; Pred. No. 6.9e-12;
RESULT 951
ID AAB70186 standard; peptide; 1016 AA.
DE Peptide dendrimer carrier #11.
PN WO200107469-A2.
PD 01-FEB-2001.
PA (VERD/) VERDINI A.
Query Match 13.6%; Score 321.5; DB 4; Length 1016;
Best Local Similarity 29.1%; Pred. No. 1.3e-11;
RESULT 952
ID AAB70187 standard; peptide; 2040 AA.
DE Peptide dendrimer carrier #12.
PN WO200107469-A2.
PD 01-FEB-2001.
PA (VERD/) VERDINI A.
Query Match 13.6%; Score 321.5; DB 4; Length 2040;
Best Local Similarity 29.1%; Pred. No. 2.6e-11;
RESULT 953

ID ABU36473 standard; protein; 594 AA.
DE Protein encoded by Prokaryotic essential gene #22000.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.5%; Score 320; DB 6; Length 594;
Best Local Similarity 31.4%; Pred. No. 1e-11;
RESULT 954
ID ABB70834 standard; protein; 620 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39294.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.5%; Score 320; DB 4; Length 620;
Best Local Similarity 26.7%; Pred. No. 1e-11;
RESULT 955
ID AAE36881 standard; protein; 1953 AA.
DE Nephila madagascariensis major ampullate spidroin 2 (Masps2)-like protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 13.5%; Score 320; DB 6; Length 1953;
Best Local Similarity 26.9%; Pred. No. 3.1e-11;
RESULT 956
ID ADP31118 standard; protein; 5820 AA.
DE Human secreted protein SEQ ID #1885.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 13.5%; Score 318.5; DB 8; Length 5820;
Best Local Similarity 29.2%; Pred. No. 1.1e-10;
RESULT 957
ID ABB81229 standard; protein; 318 AA.
DE Mycobacterium tuberculosis strain H37Rv PE-PGRS protein sequence.
PN WO9554487-A2.
PD 28-OCT-1999.
PA (INSP) INST PASTEUR.
Query Match 13.5%; Score 318; DB 3; Length 318;
Best Local Similarity 32.2%; Pred. No. 7.3e-12;
RESULT 958
ID ADR70473 standard; protein; 884 AA.
DE Silk-elastin polymer SEMP 47-E13.
PN US2004180027-A1.
PD 16-SEP-2004.
PA (KUMA/) KUMAR M.
PA (CUEV/) CUEVAS W A.
Query Match 13.5%; Score 318; DB 8; Length 884;
Best Local Similarity 26.6%; Pred. No. 1.9e-11;
RESULT 959
ID AAR80253 standard; peptide; 988 AA.
DE Polymer SEMP7.
PN WO9524478-A1.
PD 14-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 13.4%; Score 317.5; DB 2; Length 988;
Best Local Similarity 28.6%; Pred. No. 2.3e-11;
RESULT 960
ID ABP53474 standard; protein; 988 AA.
DE Protein polymer SEMP7 polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match 13.4%; Score 317.5; DB 5; Length 988;
Best Local Similarity 28.6%; Pred. No. 2.3e-11;
RESULT 961
ID ADO59401 standard; protein; 2655 AA.
DE Antheraea yamamai fibroin.
PN KR2002094304-A.
PD 18-DEC-2002.
PA (RURA-) RURAL DEV ADMINISTRATION.
Query Match 13.4%; Score 317; DB 7; Length 2655;
Best Local Similarity 25.6%; Pred. No. 6.4e-11;

RESULT 962
 ID ADO08778 standard; protein; 506 AA.
 DE Novel surgical dressing-related protein SeqID65.
 PN JP2004049921-A.
 PD 19-FEB-2004.
 PA (SANN) SANYO CHEM IND LTD.
 PA (ALCA-) ALCARE KK.
 Query Match 13.4%; Score 316; DB 8; Length 506;
 Best Local Similarity 28.3%; Pred. No. 1.5e-11;
 RESULT 963
 ID ADR70479 standard; protein; 965 AA.
 DE Silk-elastin polymer SELLP 58.
 PN US2004180027-A1.
 PD 16-SEP-2004.
 PA (KUMA/) KUMAR M.
 PA (CUEV/) CUEVAS W A.
 Query Match 13.4%; Score 315.5; DB 8; Length 965;
 Best Local Similarity 26.4%; Pred. No. 3e-11;
 RESULT 964
 ID AAM94219 standard; protein; 116 AA.
 DE Human reproductive system related antigen SEQ ID NO: 2877.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.3%; Score 314; DB 4; Length 116;
 Best Local Similarity 98.2%; Pred. No. 4.9e-12;
 RESULT 965
 ID AAB70180 standard; peptide; 1488 AA.
 DE Peptide dendrimer carrier #5.
 PN WO200107469-A2.
 PD 01-FEB-2001.
 PA (VERD/) VERDINI A.
 Query Match 13.2%; Score 312; DB 4; Length 1488;
 Best Local Similarity 28.9%; Pred. No. 7.4e-11;
 RESULT 966
 ID ADG98556 standard; protein; 200 AA.
 DE Poly Gly flexible linker.
 PN US2003176333-A1.
 PD 18-SEP-2003.
 PA (RIGE-) RIGEL PHARM INC.
 Query Match 13.1%; Score 309.5; DB 7; Length 200;
 Best Local Similarity 32.3%; Pred. No. 1.6e-11;
 RESULT 967
 ID ADJ84541 standard; protein; 200 AA.
 DE T2R G-protein coupled receptor related linker seq id 94.
 PN US2004038312-A1.
 PD 26-FEB-2004.
 PA (ZUKE/) ZUKER C S.
 PA (ADLE/) ADLER J E.
 PA (HOON/) HOON M.
 PA (RYBA/) RYBA N.
 PA (MUEL/) MUELLER K.
 Query Match 13.1%; Score 309.5; DB 8; Length 200;
 Best Local Similarity 32.3%; Pred. No. 1.6e-11;
 RESULT 968
 ID ADM96215 standard; protein; 200 AA.
 DE Poly Gly flexible linker.
 PN US2004071708-A1.
 PD 15-APR-2004.
 PA (IMMU-) IMMUSOL INC.
 Query Match 13.1%; Score 309.5; DB 8; Length 200;
 Best Local Similarity 32.3%; Pred. No. 1.6e-11;
 RESULT 969
 ID ADO08771 standard; protein; 296 AA.
 DE Novel surgical dressing-related protein SeqID58.
 PN JP2004049921-A.
 PD 19-FEB-2004.
 PA (SANN) SANYO CHEM IND LTD.
 PA (ALCA-) ALCARE KK.
 Query Match 13.1%; Score 309.5; DB 8; Length 296;
 Best Local Similarity 27.5%; Pred. No. 2.3e-11;
 RESULT 970
 ID ABG71303 standard; protein; 201 AA.
 DE PINPOINT poly-Gly linker protein.
 PN US6444421-B1.
 PD 03-SEP-2002.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 13.1%; Score 309; DB 5; Length 201;
 Best Local Similarity 31.9%; Pred. No. 1.7e-11;
 RESULT 971
 ID AAW05704 standard; peptide; 235 AA.
 DE Glycine-rich repeat sequence of EBV nuclear antigen.
 PN WO9632483-A1.
 PD 17-OCT-1996.
 PA (MASU/) MASUCCI M.
 Query Match 13.0%; Score 308; DB 2; Length 235;
 Best Local Similarity 29.6%; Pred. No. 2.2e-11;
 RESULT 972
 ID AAW79126 standard; protein; 235 AA.
 DE Epstein Barr Virus EBNA1 protein gly-ala repeat region.
 PN WO9822577-A1.
 PD 28-MAY-1998.
 PA (MASU/) MASUCCI M G.
 Query Match 13.0%; Score 308; DB 2; Length 235;
 Best Local Similarity 29.6%; Pred. No. 2.2e-11;
 RESULT 973
 ID AAB70188 standard; peptide; 465 AA.
 DE Peptide dendrimer carrier #13.
 PN WO200107469-A2.
 PD 01-FEB-2001.
 PA (VERD/) VERDINI A.
 Query Match 12.9%; Score 305.5; DB 4; Length 465;
 Best Local Similarity 27.9%; Pred. No. 6.1e-11;
 RESULT 974
 ID ABB61734 standard; protein; 1039 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 11994.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 12.9%; Score 305.5; DB 4; Length 1039;
 Best Local Similarity 27.5%; Pred. No. 1.3e-10;
 RESULT 975
 ID ADP31138 standard; protein; 1350 AA.
 DE Human secreted protein SEQ ID #1905.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 12.9%; Score 304.5; DB 8; Length 1350;
 Best Local Similarity 26.0%; Pred. No. 2e-10;
 RESULT 976
 ID ADP31137 standard; protein; 1719 AA.
 DE Human secreted protein SEQ ID #1904.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 12.9%; Score 304.5; DB 8; Length 1719;
 Best Local Similarity 26.0%; Pred. No. 2.5e-10;
 RESULT 977
 ID ADO08774 standard; protein; 322 AA.
 DE Novel surgical dressing-related protein SeqID61.
 PN JP2004049921-A.
 PD 19-FEB-2004.
 PA (SANN) SANYO CHEM IND LTD.
 PA (ALCA-) ALCARE KK.
 Query Match 12.8%; Score 303.5; DB 8; Length 322;
 Best Local Similarity 31.6%; Pred. No. 5.7e-11;
 RESULT 978
 ID ADS28501 standard; protein; 592 AA.
 DE Bacterial polypeptide #17534.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.

Query Match 12.8%; Score 302; DB 8; Length 592;
Best Local Similarity 27.7%; Pred. No. 1.3e-10;
RESULT 979
ID AAR99059 standard; protein; 714 AA.
DE Spider dragline variant, DP-2A polymer.
PN WO9429450-A2.
PD 22-DEC-1994.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 12.8%; Score 302; DB 2; Length 714;
Best Local Similarity 28.4%; Pred. No. 1.5e-10;
RESULT 980
ID RAY40103 standard; protein; 714 AA.
DE Polymer of an analogue of spider silk protein spidroine major 2.
PN FR2774588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 12.8%; Score 302; DB 2; Length 714;
Best Local Similarity 28.4%; Pred. No. 1.5e-10;
RESULT 981
ID ADO08790 standard; protein; 506 AA.
DE Novel surgical dressing-related protein SeqID77.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
Query Match 12.7%; Score 301; DB 8; Length 506;
Best Local Similarity 26.6%; Pred. No. 1.3e-10;
RESULT 982
ID ADS88365 standard; protein; 622 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 220.
PN WO2004035783-A2.
PD 23-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 12.7%; Score 300.5; DB 8; Length 622;
Best Local Similarity 26.2%; Pred. No. 1.6e-10;
RESULT 983
ID ABP53481 standard; protein; 768 AA.
DE Protein polymer SELP8K polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPPE/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match 12.7%; Score 300.5; DB 5; Length 768;
Best Local Similarity 26.8%; Pred. No. 2e-10;
RESULT 984
ID AAR80341 standard; protein; 884 AA.
DE Protein polymer adhesive substrate SELP8K.
PN WO9523611-A1.
PD 08-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.7%; Score 300.5; DB 2; Length 884;
Best Local Similarity 26.8%; Pred. No. 2.3e-10;
RESULT 985
ID AAW09213 standard; protein; 884 AA.
DE SELP8K polymer.
PN WO9634618-A1.
PD 07-NOV-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.7%; Score 300.5; DB 2; Length 884;
Best Local Similarity 26.8%; Pred. No. 2.3e-10;
RESULT 986
ID AAW53541 standard; protein; 884 AA.
DE Expected amino acid sequence of pPT0345 encoding SELP8K polymer.
PN WO9810063-A1.
PD 12-MAR-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.7%; Score 300.5; DB 2; Length 884;
Best Local Similarity 26.8%; Pred. No. 2.3e-10;
RESULT 987
ID AAW49728 standard; protein; 884 AA.
DE SELP8K polymer.
PN US5773577-A.
PD 30-JUN-1998.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.7%; Score 300.5; DB 2; Length 884;
Best Local Similarity 26.8%; Pred. No. 2.3e-10;
RESULT 988
ID AAY51882 standard; protein; 884 AA.
DE Plasmid pPT0345 protein fragment containing SELP8K polymer units.
PN US6033654-A.
PD 07-MAR-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.7%; Score 300.5; DB 3; Length 884;
Best Local Similarity 26.8%; Pred. No. 2.3e-10;
RESULT 989
ID ABG31412 standard; protein; 884 AA.
DE SELP8K polymer encoded by plasmid pPT0345.
PN US6423333-B1.
PD 23-JUL-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.7%; Score 300.5; DB 5; Length 884;
Best Local Similarity 26.8%; Pred. No. 2.3e-10;
RESULT 990
ID ABW01628 standard; protein; 884 AA.
DE Plasmid pPT0345 SELP8K polymer protein.
PN US2003104589-A1.
PD 05-JUN-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.7%; Score 300.5; DB 7; Length 884;
Best Local Similarity 26.8%; Pred. No. 2.3e-10;
RESULT 991
ID AAW56163 standard; protein; 738 AA.
DE New DNA sequence isolated from Pinctada fucata.
PN JP10080285-A.
PD 31-MAR-1998.
PA (MIKI-) MIKIMOTO SEIYAKU KK.
Query Match 12.7%; Score 300; DB 2; Length 738;
Best Local Similarity 24.4%; Pred. No. 2.1e-10;
RESULT 992
ID AAE36879 standard; protein; 373 AA.
DE Latrodectus geometricus major ampullate spidroin 2 (MaSp2) protein #1.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 12.7%; Score 299; DB 6; Length 373;
Best Local Similarity 28.0%; Pred. No. 1.2e-10;
RESULT 993
ID AAR80256 standard; peptide; 1024 AA.
DE Polymer SELP5.
PN WO9524478-A1.
PD 14-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.5%; Score 296.5; DB 2; Length 1024;
Best Local Similarity 21.8%; Pred. No. 4.7e-10;
RESULT 994
ID ABP53477 standard; protein; 1024 AA.
DE Protein polymer SELP5 polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPPE/) CAPPELLO J. E R.
PA (STED/) STEDRONSKY E R.
Query Match 12.5%; Score 296.5; DB 5; Length 1024;
Best Local Similarity 21.8%; Pred. No. 4.7e-10;
RESULT 995
ID RAY40098 standard; protein; 531 AA.
DE Spider silk protein spidroine major 2.
PN FR2774588-A1.
PD 13-AUG-1999.
PA (OREA) L'OREAL SA.
Query Match 12.5%; Score 296; DB 2; Length 531;
Best Local Similarity 27.7%; Pred. No. 2.7e-10;
RESULT 996
ID AAR14309 standard; protein; 595 AA.
DE N.clavipes dragline silk protein-2.
PN EP452925-A.
PD 23-OCT-1991.

PA (UYWY-) UNIV OF WYOMING.
 Query Match 12.5%; Score 296; DB 2; Length 595;
 Best Local Similarity 27.7%; Pred. No. 3e-10;
 RESULT 997
 ID AAW53347 standard; protein; 595 AA.
 DE Nephila clavipes spider silk protein.
 PN US728810-A.
 PD 17-MAR-1998.
 PA (UYWY-) UNIV WYOMING.
 Query Match 12.5%; Score 296; DB 2; Length 595;
 Best Local Similarity 27.7%; Pred. No. 3e-10;
 RESULT 998
 ID AAY9071 standard; protein; 595 AA.
 DE N. clavipes spider silk protein 2.
 PN US989894-A.
 PD 23-NOV-1999.
 PA (UYWY-) UNIV WYOMING.
 Query Match 12.5%; Score 296; DB 3; Length 595;
 Best Local Similarity 27.7%; Pred. No. 3e-10;
 RESULT 999
 ID AAO16488 standard; protein; 624 AA.
 DE Nephila clavipes dragline silk fibronin protein.
 PN WO20029082-A2.
 PD 12-DEC-2002.
 PA (UYWY-) UNIV WYOMING.
 Query Match 12.5%; Score 296; DB 6; Length 624;
 Best Local Similarity 27.7%; Pred. No. 3.1e-10;
 RESULT 1000
 ID AOC35241 standard; protein; 627 AA.
 DE Maspi silk protein, SEQ ID 2.
 PN WO2003057727-A1.
 PD 17-JUL-2003.
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
 Query Match 12.5%; Score 296; DB 7; Length 627;
 Best Local Similarity 27.7%; Pred. No. 3.1e-10;
 RESULT 1001
 ID AAR80252 standard; peptide; 832 AA.
 DE Polymer SELP8.
 PN WO9524478-A1.
 PD 14-SEP-1995.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 12.5%; Score 294.5; DB 2; Length 832;
 Best Local Similarity 27.1%; Pred. No. 5.1e-10;
 RESULT 1002
 ID ABP53473 standard; protein; 832 AA.
 DE Protein polymer SELP8 polymer block amino acid sequence.
 PN US2002045567-A1.
 PD 18-APR-2002.
 PA (CAPP/) CAPPELLO J.
 PA (STED/) STEDRONSKY E R.
 Query Match 12.5%; Score 294.5; DB 5; Length 832;
 Best Local Similarity 27.1%; Pred. No. 5.1e-10;
 RESULT 1003
 ID AAB23358 standard; protein; 674 AA.
 DE Human trophinin protein from residue 69 to 749.
 PN US6111089-A.
 PD 29-AUG-2000.
 PA (BURN-) BURNHAM INST.
 Query Match 12.4%; Score 294; DB 3; Length 674;
 Best Local Similarity 28.7%; Pred. No. 4.4e-10;
 RESULT 1004
 ID ADC86917 standard; protein; 821 AA.
 DE Human GPCR protein SEQ ID NO:1370.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 12.4%; Score 294; DB 7; Length 821;
 Best Local Similarity 31.1%; Pred. No. 5.4e-10;
 RESULT 1005
 ID ABB67074 standard; protein; 586 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 28014.
 PN WO200171042-A2.

PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 12.4%; Score 293.5; DB 4; Length 586;
 Best Local Similarity 26.6%; Pred. No. 4.2e-10;
 RESULT 1006
 ID ABB62822 standard; protein; 586 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15258.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 12.4%; Score 293.5; DB 4; Length 586;
 Best Local Similarity 26.6%; Pred. No. 4.2e-10;
 RESULT 1007
 ID ADS96696 standard; protein; 586 AA.
 DE Drosophila melanogaster protein, SEQ ID 317.
 PN WO2004039999-A2.
 PD 13-MAY-2004.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 12.4%; Score 293.5; DB 8; Length 586;
 Best Local Similarity 26.6%; Pred. No. 4.2e-10;
 RESULT 1008
 ID ADA07852 standard; protein; 611 AA.
 DE Pinctada margaritifera nacrein.
 PN US2003027258-A1.
 PD 06-FEB-2003.
 PA (CHAN/) CHANG F F.
 PA (LIHH/) LI H.
 PA (HSIE/) HSIEH-LI H M.
 Query Match 12.4%; Score 293.5; DB 6; Length 611;
 Best Local Similarity 26.5%; Pred. No. 4.3e-10;
 RESULT 1009
 ID ABO23517 standard; protein; 256 AA.
 DE Mycobacterium tuberculosis outlier protein #1.
 PN US2003039963-A1.
 PD 27-FEB-2003.
 PA (BRAH/) BRAHMACHARI S K.
 PA (RAMA/) RAMACHANDRAN S.
 PA (NAND/) NANDI T.
 PA (BHIM/) BHIMARAO C.
 Query Match 12.4%; Score 293; DB 7; Length 256;
 Best Local Similarity 31.1%; Pred. No. 2e-10;
 RESULT 1010
 ID ADO08786 standard; protein; 322 AA.
 DE Novel surgical dressing-related protein SeqID73.
 PN JP2004049921-A.
 PD 19-FEB-2004.
 PA (SANN) SANYO CHEM IND LTD.
 PA (ALCA-) ALCARE KK.
 Query Match 12.4%; Score 292.5; DB 8; Length 322;
 Best Local Similarity 28.8%; Pred. No. 2.7e-10;
 RESULT 1011
 ID AAE36889 standard; protein; 912 AA.
 DE Plectreureys tristic fibroin 1 protein.
 PN WO2003020916-A2.
 PD 13-MAR-2003.
 PA (UYWY-) UNIV WYOMING.
 Query Match 12.4%; Score 292; DB 6; Length 912;
 Best Local Similarity 23.4%; Pred. No. 7.9e-10;
 RESULT 1012
 ID AAR94895 standard; protein; 749 AA.
 DE Human trophinin.
 PN WO9610414-A1.
 PD 11-APR-1996.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 Query Match 12.3%; Score 290.5; DB 2; Length 749;
 Best Local Similarity 27.8%; Pred. No. 8.1e-10;
 RESULT 1013
 ID AAB23357 standard; protein; 749 AA.
 DE Human trophinin protein.
 PN US6111089-A.
 PD 23-AUG-2000.
 PA (BURN-) BURNHAM INST.
 Query Match 12.3%; Score 290.5; DB 3; Length 749;

Best Local Similarity 27.6%; Pred. No. 8.1e-10;
RESULT 1014
ID ABO60408 standard; protein; 805 AA.
DE Human genome derived single exon protein #6642.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 12.3%; Score 290.5; DB 8; Length 805;
Best Local Similarity 27.6%; Pred. No. 8.6e-10;
RESULT 1015
ID AAB94744 standard; protein; 814 AA.
DE Human protein sequence SEQ ID NO:15790.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.3%; Score 290.5; DB 4; Length 814;
Best Local Similarity 27.6%; Pred. No. 8.7e-10;
RESULT 1016
ID AAM94034 standard; protein; 814 AA.
DE Human stomach cancer expressed polypeptide SEQ ID NO 139.
PN WO200109317-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 12.3%; Score 290.5; DB 4; Length 814;
Best Local Similarity 27.6%; Pred. No. 8.7e-10;
RESULT 1017
ID AAU32728 standard; protein; 1406 AA.
DE Novel human secreted protein #3219.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.3%; Score 290.5; DB 4; Length 1406;
Best Local Similarity 27.6%; Pred. No. 1.5e-09;
RESULT 1018
ID AAY04999 standard; protein; 388 AA.
DE Mycobacterium species protein sequence 50C.
PN WO9909186-A2.
PD 25-FEB-1999.
PA (INSP) INST PASTEUR.
Query Match 12.2%; Score 289; DB 2; Length 388;
Best Local Similarity 30.4%; Pred. No. 5.3e-10;
RESULT 1019
ID ADB61322 standard; protein; 627 AA.
DE Spider silk related MaspII protein.
PN WO2003060099-A2.
PD 24-JUL-2003.
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.
PA (ALMA/) ALMATTARI A.
Query Match 12.2%; Score 289; DB 7; Length 627;
Best Local Similarity 28.2%; Pred. No. 8.4e-10;
RESULT 1020
ID ADM46150 standard; protein; 627 AA.
DE Nephila clavipes spidroin 2 (MasPII) protein.
PN WO2003057720-A2.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 12.2%; Score 289; DB 7; Length 627;
Best Local Similarity 28.2%; Pred. No. 8.4e-10;
RESULT 1021
ID AAF53466 standard; protein; 768 AA.
DE SELP8 related amino acid sequence #2.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match 12.2%; Score 288.5; DB 5; Length 768;
Best Local Similarity 26.6%; Pred. No. 1.1e-09;
RESULT 1022
ID AAR80335 standard; protein; 877 AA.
DE Protein polymeric adhesion substrate 1-G.
PN WO9523611-A1.

PD 08-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.2%; Score 288.5; DB 2; Length 877;
Best Local Similarity 26.6%; Pred. No. 1.2e-09;
RESULT 1023
ID AAM49724 standard; protein; 877 AA.
DE Protein polymer adhesive substrate PPAS1-G.
PN US5773577-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 12.2%; Score 288.5; DB 2; Length 877;
Best Local Similarity 26.6%; Pred. No. 1.2e-09;
RESULT 1024
ID ADO8763 standard; protein; 322 AA.
DE Novel surgical dressing-related protein SeqID50.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 12.1%; Score 286; DB 8; Length 322;
Best Local Similarity 29.8%; Pred. No. 6.8e-10;
RESULT 1025
ID AAE36882 standard; protein; 563 AA.
DE Nephila madagascariensis major ampullate spidroin 2 (MasP2) protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 12.1%; Score 286; DB 6; Length 563;
Best Local Similarity 26.3%; Pred. No. 1.2e-09;
RESULT 1026
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.1%; Score 286; DB 4; Length 2112;
Best Local Similarity 24.3%; Pred. No. 4.1e-09;
RESULT 1027
ID AAM78356 standard; protein; 536 AA.
DE Human protein SEQ ID NO 1018.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 285; DB 4; Length 536;
Best Local Similarity 29.6%; Pred. No. 1.3e-09;
RESULT 1028
ID AAM50044 standard; protein; 271 AA.
DE N. clavipes spidroin synthetic homologue SF1 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 12.0%; Score 283.5; DB 5; Length 271;
Best Local Similarity 29.7%; Pred. No. 8.2e-10;
RESULT 1029
ID AAB06023 standard; protein; 401 AA.
DE Polar gelatin P tetramer, P4.
PN EP1014176-A2.
PD 28-JUN-2000.
PA (FUJF) FUJI PHOTO FILM BV.
Query Match 12.0%; Score 283.5; DB 3; Length 401;
Best Local Similarity 33.9%; Pred. No. 1.2e-09;
RESULT 1030
ID AAY72375 standard; protein; 599 AA.
DE Amphiphilic recombinant collagen-like polymer, NIN2P4.
PN EP1063565-A1.
PD 27-DEC-2000.
PA (FUJF) FUJI PHOTO FILM BV.
Query Match 12.0%; Score 283.5; DB 4; Length 599;
Best Local Similarity 33.9%; Pred. No. 1.8e-09;
RESULT 1031
ID AAY72374 standard; protein; 599 AA.
DE Amphiphilic recombinant collagen-like polymer, NIN1P4.
PN EP1063565-A1.

PD 27-DEC-2000.
PA (FOUJF) FUJII PHOTO FILM BV.
Query Match 12.0%; Score 283.5; DB 4; Length 599;
Best Local Similarity 33.9%; Pred. No. 1.8e-09;
RESULT 1032
ID AAB23367 standard; protein; 1160 AA.
DE Mouse troponin protein.
PN US6111089-A.
PD 29-AUG-2000.
PA (BURN-) BURNHAM INST.
Query Match 12.0%; Score 283; DB 3; Length 1160;
Best Local Similarity 29.6%; Pred. No. 3.5e-09;
RESULT 1033
ID ADO08783 standard; protein; 316 AA.
DE Novel surgical dressing-related protein SeqID70.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 12.0%; Score 282.5; DB 8; Length 316;
Best Local Similarity 27.6%; Pred. No. 1.1e-09;
RESULT 1034
ID ADH58964 standard; protein; 258 AA.
DE Silk protein related protein #SEQ ID 33.
PN WO2003100065-A1.
PD 04-DEC-2003.
PA (UYNI-) UNIV JAPAN TOKYO AGR.
Query Match 11.9%; Score 280.5; DB 8; Length 258;
Best Local Similarity 29.4%; Pred. No. 1.2e-09;
RESULT 1035
ID AAB36876 standard; protein; 444 AA.
DE Argiophe trifasciata major ampullate spidroin 2 (MasP2) protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 11.8%; Score 280; DB 6; Length 444;
Best Local Similarity 27.1%; Pred. No. 2.2e-09;
RESULT 1036
ID AON35278 standard; protein; 1028 AA.
DE Helical domain of type III collagen #2.
PN WO2004028404-A2.
PD 08-APR-2004.
PA (FIBR-) FIBROGEN INC.
Query Match 11.8%; Score 280; DB 8; Length 1028;
Best Local Similarity 27.4%; Pred. No. 4.8e-09;
RESULT 1037
ID AON35277 standard; protein; 1313 AA.
DE Helical domain of type III collagen.
PN WO2004028404-A2.
PD 08-APR-2004.
PA (FIBR-) FIBROGEN INC.
Query Match 11.8%; Score 280; DB 8; Length 1313;
Best Local Similarity 27.4%; Pred. No. 6.1e-09;
RESULT 1038
ID ADE61480 standard; protein; 1380 AA.
DE Rat Protein AAC05725, SEQ ID NO 7400.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.8%; Score 280; DB 7; Length 1380;
Best Local Similarity 31.7%; Pred. No. 6.4e-09;
RESULT 1039
ID ABB50291 standard; protein; 1466 AA.
DE Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 11.8%; Score 280; DB 4; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1040
ID ABB90747 standard; protein; 1466 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 226.

PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 11.8%; Score 280; DB 5; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1041
ID ABUS4454 standard; protein; 1466 AA.
DE Human tumour endothelial marker TEM 15.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 11.8%; Score 280; DB 6; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1042
ID ABR47418 standard; protein; 1466 AA.
DE Breast cancer associated protein sequence SEQ ID NO:68.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 11.8%; Score 280; DB 6; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1043
ID ADP65248 standard; protein; 1466 AA.
DE Human alpha 1 type III collagen preproprotein.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 11.8%; Score 280; DB 7; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1044
ID ADP65210 standard; protein; 1466 AA.
DE Human alpha 1 type III collagen preproprotein.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 11.8%; Score 280; DB 7; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1045
ID ADQ26091 standard; protein; 1466 AA.
DE Type III, alpha 1 collagen.
PN WO2004056386-A2.
PD 08-JUL-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 11.8%; Score 280; DB 8; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1046
ID ADQ29677 standard; protein; 1466 AA.
DE Human colorectal cancer-associated protein #32.
PN EPI439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 11.8%; Score 280; DB 8; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1047
ID ADR16802 standard; protein; 1466 AA.
DE Human collagen III alpha2 (III) fragment protein.
PN US2004151731-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
Query Match 11.8%; Score 280; DB 8; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1048
ID ADR16427 standard; protein; 1466 AA.
DE Human collagen I alpha2 (III) fragment protein.
PN US2004151732-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
PA (PELU/) PELUSE S.
Query Match 11.8%; Score 280; DB 8; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1049
ID ABM80366 standard; protein; 1466 AA.

DE Tumour-associated antigenic target (TAT) polypeptide PRO2665, SEQ:922.
PN W0204030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 11.8%; Score 280; DB 8; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1050
ID ADR67267 standard; protein; 1466 AA.
DE Human bladder cancer associated amino acid sequence.
PN W02004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 11.8%; Score 280; DB 8; Length 1466;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1051
ID ABG15191 standard; protein; 1469 AA.
DE Novel human diagnostic protein #15182.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 280; DB 4; Length 1469;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1052
ID ADE03939 standard; protein; 1470 AA.
DE Novel protein-related contig polypeptide sequence #465.
PN W02003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 280; DB 7; Length 1470;
Best Local Similarity 27.4%; Pred. No. 6.8e-09;
RESULT 1053
ID ABR42661 standard; protein; 1726 AA.
DE Decorin-modified pro-alpha chain.
PN W02003035692-A2.
PD 01-MAY-2003.
PA (UYMA-) UNIV VICTORIA MANCHESTER.
Query Match 11.8%; Score 280; DB 6; Length 1726;
Best Local Similarity 27.4%; Pred. No. 7.9e-09;
RESULT 1054
ID ADO08777 standard; protein; 338 AA.
DE Novel surgical dressing-related protein SeqID64.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 11.8%; Score 279; DB 8; Length 338;
Best Local Similarity 29.2%; Pred. No. 1.9e-09;
RESULT 1055
ID ADP99004 standard; protein; 1096 AA.
DE C. albicans specific gene, CAYMR047C, protein sequence.
PN W02004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 11.8%; Score 279; DB 8; Length 1096;
Best Local Similarity 27.4%; Pred. No. 5.9e-09;
RESULT 1056
ID AAW78355 standard; protein; 526 AA.
DE Human protein SEQ ID NO 1017.
PN W0200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 278.5; DB 4; Length 526;
Best Local Similarity 27.7%; Pred. No. 3.1e-09;
RESULT 1057
ID ABG95081 standard; protein; 526 AA.
DE Human translocation (12; 16)(q13; p11) protein #2.
PN W0200269900-A2.

PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 11.8%; Score 278.5; DB 5; Length 526;
Best Local Similarity 27.7%; Pred. No. 3.1e-09;
RESULT 1058
ID ADI26117 standard; protein; 526 AA.
DE Human protein that promotes STAT6 activation #41.
PN W02003104277-A2.
PD 18-DEC-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 11.8%; Score 278.5; DB 8; Length 526;
Best Local Similarity 27.7%; Pred. No. 3.1e-09;
RESULT 1059
ID ABM81732 standard; protein; 526 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82568, SEQ:4466.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 11.8%; Score 278.5; DB 8; Length 526;
Best Local Similarity 27.7%; Pred. No. 3.1e-09;
RESULT 1060
ID ADS88302 standard; protein; 526 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 157.
PN W02004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 11.8%; Score 278.5; DB 8; Length 526;
Best Local Similarity 27.7%; Pred. No. 3.1e-09;
RESULT 1061
ID ABB61650 standard; protein; 2280 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11742.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.8%; Score 278.5; DB 4; Length 2280;
Best Local Similarity 26.3%; Pred. No. 1.3e-08;
RESULT 1062
ID AAR71704 standard; protein; 1078 AA.
DE Collagen alpha 1 (III) chain precursor.
PN W09508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 11.8%; Score 278; DB 2; Length 1078;
Best Local Similarity 27.4%; Pred. No. 6.7e-09;
RESULT 1063
ID ABU40120 standard; protein; 237 AA.
DE Protein encoded by Prokaryotic essential gene #25647.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.7%; Score 277; DB 6; Length 237;
Best Local Similarity 30.7%; Pred. No. 1.8e-09;
RESULT 1064
ID ABP53461 standard; protein; 768 AA.
DE SELP5 related amino acid sequence #3.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match 11.7%; Score 276.5; DB 5; Length 768;
Best Local Similarity 23.1%; Pred. No. 6e-09;
RESULT 1065
ID ADE59683 standard; protein; 1372 AA.
DE Rat Protein P02466, SEQ ID NO 5579.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.7%; Score 276.5; DB 7; Length 1372;
Best Local Similarity 30.4%; Pred. No. 1e-08;
RESULT 1066
ID ADD45148 standard; protein; 1372 AA.
DE Rat Protein P02466, SEQ ID NO 10581.

PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 11.7%; Score 276.5; DB 7; Length 1372;
 Best Local Similarity 30.4%; Pred. No. 1e-08;
 RESULT 1067
 ID ADD45604 standard; protein; 1372 AA.
 DE Rat Protein P02466, SEQ ID NO 11270.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 11.7%; Score 276.5; DB 7; Length 1372;
 Best Local Similarity 30.4%; Pred. No. 1e-08;
 RESULT 1068
 ID ADE59687 standard; protein; 1372 AA.
 DE Rat Protein P02466, SEQ ID NO 5593.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 11.7%; Score 276.5; DB 7; Length 1372;
 Best Local Similarity 30.4%; Pred. No. 1e-08;
 RESULT 1069
 ID ADD47529 standard; protein; 1372 AA.
 DE Rat Protein AAD41775, SEQ ID NO 13225.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 11.7%; Score 276.5; DB 7; Length 1372;
 Best Local Similarity 30.4%; Pred. No. 1e-08;
 RESULT 1070
 ID AAY84548 standard; protein; 1040 AA.
 DE A human collagen 1 (alpha2) protein helical region.
 PN EP92586-A2.
 PD 12-APR-2000.
 PA (USSU) US SURGICAL CORP.
 Query Match 11.7%; Score 276; DB 3; Length 1040;
 Best Local Similarity 29.8%; Pred. No. 8.6e-09;
 RESULT 1071
 ID AAY84547 standard; protein; 1040 AA.
 DE A human collagen 1 (alpha2) protein helical region.
 PN EP92586-A2.
 PD 12-APR-2000.
 PA (USSU) US SURGICAL CORP.
 Query Match 11.7%; Score 276; DB 3; Length 1040;
 Best Local Similarity 29.8%; Pred. No. 8.6e-09;
 RESULT 1072
 ID AAY96125 standard; peptide; 1078 AA.
 DE Collagen type III alpha-1.
 PN US6110689-A.
 PD 29-AUG-2000.
 PA (OSTE-) OSTROMETER AS.
 Query Match 11.7%; Score 276; DB 3; Length 1078;
 Best Local Similarity 27.4%; Pred. No. 8.9e-09;
 RESULT 1073
 ID AAE16478 standard; protein; 1078 AA.
 DE Human collagen alpha1 (III) protein.
 PN US6323314-B1.
 PD 27-NOV-2001.
 PA (OSTE-) OSTROMETER AS.
 Query Match 11.7%; Score 276; DB 5; Length 1078;
 Best Local Similarity 27.4%; Pred. No. 8.9e-09;
 RESULT 1074
 ID ABB80736 standard; protein; 1078 AA.
 DE Collagen type III-alpha1 protein.
 PN US6355442-B1.
 PD 12-MAR-2002.
 PA (OSTE-) OSTROMETER BIOTECH AS.
 Query Match 11.7%; Score 276; DB 5; Length 1078;
 Best Local Similarity 27.4%; Pred. No. 8.9e-09;

RESULT 1075
 ID ABB09628 standard; peptide; 1078 AA.
 DE Amino acid sequence of human collagen type III alpha1.
 PN US6342361-B1.
 PD 29-JAN-2002.
 PA (OSTE-) OSTROMETER BIOTECH AS.
 Query Match 11.7%; Score 276; DB 5; Length 1078;
 Best Local Similarity 27.4%; Pred. No. 8.9e-09;
 RESULT 1076
 ID ADP13078 standard; protein; 1078 AA.
 DE Human collagen alpha1(III) chain precursor.
 PN US2003119058-A1.
 PD 26-JUN-2003.
 PA (OSTE-) OSTROMETER AS.
 Query Match 11.7%; Score 276; DB 7; Length 1078;
 Best Local Similarity 27.4%; Pred. No. 8.9e-09;
 RESULT 1077
 ID AAY56801 standard; protein; 1366 AA.
 DE Human preproalpha 2 (I) collagen.
 PN EP967226-A2.
 PD 29-DEC-1999.
 PA (COHE-) COHESION TECHNOLOGIES INC.
 Query Match 11.7%; Score 276; DB 3; Length 1366;
 Best Local Similarity 29.8%; Pred. No. 1.1e-08;
 RESULT 1078
 ID ABB90751 standard; protein; 1366 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 234.
 PN W0200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 11.7%; Score 276; DB 5; Length 1366;
 Best Local Similarity 29.8%; Pred. No. 1.1e-08;
 RESULT 1079
 ID ABB90766 standard; protein; 1366 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 265.
 PN W0200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 11.7%; Score 276; DB 5; Length 1366;
 Best Local Similarity 29.8%; Pred. No. 1.1e-08;
 RESULT 1080
 ID ABB90741 standard; protein; 1366 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 214.
 PN W0200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 11.7%; Score 276; DB 5; Length 1366;
 Best Local Similarity 29.8%; Pred. No. 1.1e-08;
 RESULT 1081
 ID ABU54448 standard; protein; 1366 AA.
 DE Human tumour endothelial marker TEM 10.
 PN W0200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 11.7%; Score 276; DB 6; Length 1366;
 Best Local Similarity 29.8%; Pred. No. 1.1e-08;
 RESULT 1082
 ID ABU54473 standard; protein; 1366 AA.
 DE Human tumour endothelial marker TEM 40.
 PN W0200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 11.7%; Score 276; DB 6; Length 1366;
 Best Local Similarity 29.8%; Pred. No. 1.1e-08;
 RESULT 1083
 ID ABU54458 standard; protein; 1366 AA.
 DE Human tumour endothelial marker TEM 20.
 PN W0200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 11.7%; Score 276; DB 6; Length 1366;
 Best Local Similarity 29.8%; Pred. No. 1.1e-08;
 RESULT 1084
 ID ABB0736 standard; protein; 1078 AA.
 DE Collagen type III-alpha1 protein.

ID ABR92065 standard; protein; 1366 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:38.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.7%; Score 276; DB 6; Length 1366;
Best Local Similarity 29.8%; Pred. No. 1.1e-08;
RESULT 1085
ID ADK70437 standard; protein; 1366 AA.
DE Respiratory disease differentially expressed protein #3.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 11.7%; Score 276; DB 8; Length 1366;
Best Local Similarity 29.8%; Pred. No. 1.1e-08;
RESULT 1086
ID ADQ29669 standard; protein; 1366 AA.
DE Human colorectal cancer-associated protein #24.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 11.7%; Score 276; DB 8; Length 1366;
Best Local Similarity 29.8%; Pred. No. 1.1e-08;
RESULT 1087
ID ABO59421 standard; protein; 208 AA.
DE Human genome derived single exon protein #5655.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 11.6%; Score 275; DB 8; Length 208;
Best Local Similarity 32.1%; Pred. No. 2.1e-09;
RESULT 1088
ID ABG95084 standard; protein; 525 AA.
DE Human translocation (12; 16)(q13; p11) protein #5.
PN WO200269900-A2.
PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 11.6%; Score 275; DB 5; Length 525;
Best Local Similarity 27.5%; Pred. No. 5.1e-09;
RESULT 1089
ID ADR14649 standard; protein; 525 AA.
DE Human NP-kappaB pathway-associated protein SeqID650.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 11.6%; Score 275; DB 8; Length 525;
Best Local Similarity 27.5%; Pred. No. 5.1e-09;
RESULT 1090
ID ABB61800 standard; protein; 944 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12192.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 11.6%; Score 275; DB 4; Length 944;
Best Local Similarity 24.4%; Pred. No. 9e-09;
RESULT 1091
ID ADH13201 standard; protein; 593 AA.
DE Human malignant neoplasia-related protein SeqID50.
PN EP1355034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
Query Match 11.6%; Score 274; DB 8; Length 593;
Best Local Similarity 36.9%; Pred. No. 6.7e-09;
RESULT 1092
ID ADF5631 standard; protein; 600 AA.
DE Protein (SEQ ID 1) related to oyster pearl keratin protein.
PN JP2003012696-A.
PD 15-JAN-2003.
PA (MATS/) MATSUSHIRO A.
Query Match 11.6%; Score 274; DB 7; Length 600;
Best Local Similarity 30.3%; Pred. No. 1.8e-08;
RESULT 1102

Best Local Similarity 24.5%; Pred. No. 6.7e-09;
RESULT 1093
ID AAG23582 standard; protein; 730 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35222.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.6%; Score 274; DB 3; Length 730;
Best Local Similarity 28.9%; Pred. No. 8.1e-09;
RESULT 1094
ID AAG29581 standard; protein; 752 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35221.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 11.6%; Score 274; DB 3; Length 752;
Best Local Similarity 28.9%; Pred. No. 8.3e-09;
RESULT 1095
ID ADN35279 standard; protein; 1313 AA.
DE Synthetic collagen used as sealant tissue protein.
PN WO2004028404-A2.
PD 08-APR-2004.
PA (FIER-) FIBROGEN INC.
Query Match 11.6%; Score 274; DB 8; Length 1313;
Best Local Similarity 27.2%; Pred. No. 1.4e-08;
RESULT 1096
ID AAU31850 standard; protein; 2367 AA.
DE Novel human secreted protein #2341.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.6%; Score 273; DB 4; Length 2367;
Best Local Similarity 27.0%; Pred. No. 2.9e-08;
RESULT 1097
ID AAW49739 standard; protein; 479 AA.
DE Protein polymer adhesive substrate PPAS2-F.
PN US5773577-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 11.5%; Score 272.5; DB 2; Length 479;
Best Local Similarity 26.2%; Pred. No. 6.7e-09;
RESULT 1098
ID ABO77606 standard; protein; 619 AA.
DE Pseudomonas aeruginosa polypeptide #9781.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 11.5%; Score 272.5; DB 7; Length 619;
Best Local Similarity 25.2%; Pred. No. 8.6e-09;
RESULT 1099
ID ADK51953 standard; protein; 696 AA.
DE Repeat protein polymer repeat sequence, SEQ ID 21.
PN WO2003099465-A1.
PD 04-DEC-2003.
PA (DOWO) DOW CORNING CORP.
PA (GEMV) GENECOR INT INC.
Query Match 11.5%; Score 272.5; DB 8; Length 696;
Best Local Similarity 28.6%; Pred. No. 9.6e-09;
RESULT 1100
ID AAW09214 standard; protein; 1065 AA.
DE CLP6 polymer.
PN WO9634618-A1.
PD 07-NOV-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 11.5%; Score 272.5; DB 2; Length 1065;
Best Local Similarity 27.7%; Pred. No. 1.4e-08;
RESULT 1101
ID ABB57364 standard; protein; 1373 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1029.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UTNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 11.5%; Score 272.5; DB 5; Length 1373;
Best Local Similarity 30.3%; Pred. No. 1.8e-08;
RESULT 1102

ID AAB82608 standard; protein; 291 AA.
 DE Spider recombinant silk protein pOE(spl)7.
 PD WO200153333-A1.
 PA (MELL/) MELLO C M.
 PA (ARCI/) ARCIACONO S.
 PA (BUTL/) BUTLER M M.
 PA (USSA) US SEC OF ARMY.
 Query Match
 Best Local Similarity 11.5%; Score 272; DB 4; Length 291;
 RESULT 1103
 ID AAB20586 standard; protein; 671 AA.
 DE Novel human diagnostic protein #20577.
 PD WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 11.5%; Score 272; DB 4; Length 671;
 RESULT 1104
 ID AAF3470 standard; peptide; 696 AA.
 DE SELP9K related amino acid sequence #1.
 PD US2002045567-A1.
 PD 18-APR-2002.
 PA (CAPP/) CAPPELLO J.
 PA (STED/) STEDRONSKY E R.
 Query Match
 Best Local Similarity 11.5%; Score 272; DB 5; Length 696;
 RESULT 1105
 ID AAF3482 standard; protein; 696 AA.
 DE Protein polymer SELP9K polymer block amino acid sequence.
 PD US2002045567-A1.
 PD 18-APR-2002.
 PA (CAPP/) CAPPELLO J.
 PA (STED/) STEDRONSKY E R.
 Query Match
 Best Local Similarity 11.5%; Score 272; DB 5; Length 696;
 RESULT 1106
 ID ADK51955 standard; protein; 696 AA.
 DE Repeat protein polymer repeat sequence, SEQ ID 23.
 PD WO2003099465-A1.
 PD 04-DEC-2003.
 PA (DOMO) DOW CORNING CORP.
 PA (GEMV) GENENCOR INT INC.
 Query Match
 Best Local Similarity 11.5%; Score 272; DB 8; Length 696;
 RESULT 1107
 ID ABU36642 standard; protein; 370 AA.
 DE Protein encoded by Prokaryotic essential gene #22169.
 PD WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 11.5%; Score 271.5; DB 6; Length 370;
 RESULT 1108
 ID AAM79339 standard; protein; 569 AA.
 DE Human protein SEQ ID NO 2985.
 PD WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 11.5%; Score 271.5; DB 4; Length 569;
 RESULT 1109
 ID AAM79340 standard; protein; 569 AA.
 DE Human protein SEQ ID NO 2986.
 PD WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 11.5%; Score 271.5; DB 4; Length 569;
 RESULT 1110
 ID AAR80324 standard; protein; 762 AA.
 DE Protein polymeric adhesion substrate 1-A.
 PD WO9523611-A1.

PD 08-SEP-1995.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;
 RESULT 1111
 ID AAW57666 standard; peptide; 762 AA.
 DE Collagen-like polymer.
 PD US5773249-A.
 PD 30-JUN-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;
 RESULT 1112
 ID AAW53535 standard; protein; 762 AA.
 DE Amino acid sequence of the plasmid encoding fibrin gamma PPAS1-A.
 PD WO9810063-A1.
 PD 12-MAR-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;
 RESULT 1113
 ID AAW49713 standard; protein; 762 AA.
 DE Protein polymer adhesive substrate PPAS1-A.
 PD US5773577-A.
 PD 30-JUN-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match
 Best Local Similarity 11.5%; Score 271; DB 2; Length 762;
 RESULT 1114
 ID ABO58348 standard; protein; 2338 AA.
 DE Human genome derived single exon protein #4582.
 PD US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match
 Best Local Similarity 11.5%; Score 271; DB 8; Length 2338;
 RESULT 1115
 ID ADR16801 standard; protein; 1366 AA.
 DE Human collagen I alpha2 (I) chain protein.
 PD US2004151731-A1.
 PD 05-AUG-2004.
 PA (JICH/) JICHA D L.
 Query Match
 Best Local Similarity 11.4%; Score 270.5; DB 8; Length 1366;
 RESULT 1116
 ID ADR16426 standard; protein; 1366 AA.
 DE Human collagen I alpha2 (I) chain protein.
 PD US2004151732-A1.
 PD 05-AUG-2004.
 PA (JICH/) JICHA D L.
 PA (PELU/) PELUSE S.
 Query Match
 Best Local Similarity 11.4%; Score 270.5; DB 8; Length 1366;
 RESULT 1117
 ID ADR99147 standard; protein; 1366 AA.
 DE Collagen, type 1, alpha 2, COL1A2, SEQ ID 153.
 PD WO2004078035-A2.
 PD 16-SEP-2004.
 PA (FARB) BAYER PHARM CORP.
 Query Match
 Best Local Similarity 11.4%; Score 270.5; DB 8; Length 1366;
 RESULT 1118
 ID ADC87061 standard; protein; 920 AA.
 DE Human GPCR protein SEQ ID NO:1514.
 PD EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match
 Best Local Similarity 11.4%; Score 270; DB 7; Length 920;
 RESULT 1119

ID AAR28916 standard; protein; 1196 AA.
DE Type III procollagen (prior art).
PN WO9219754-A1.
PD 12-NOV-1992.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 11.4%; Score 270; DB 2; Length 1196;
Best Local Similarity 29.0%; Pred. No. 2.3e-08;
RESULT 1120
ID AAE02537 standard; protein; 1466 AA.
DE Porcine alaphal(III) collagen.
PN WO200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 11.4%; Score 270; DB 4; Length 1466;
Best Local Similarity 29.0%; Pred. No. 2.8e-08;
RESULT 1121
ID AAE36870 standard; protein; 360 AA.
DE Latrodectus geometricus major ampullate spideroin 1 (MaSp1) protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 11.4%; Score 269.5; DB 6; Length 360;
Best Local Similarity 25.1%; Pred. No. 7.8e-09;
RESULT 1122
ID ADP31413 standard; protein; 951 AA.
DE Human secreted protein SEQ ID #2180.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 11.4%; Score 269.5; DB 8; Length 951;
Best Local Similarity 25.8%; Pred. No. 2e-08;
RESULT 1123
ID AEG31413 standard; protein; 1065 AA.
DE CLP6 polymer encoded by plasmid pPT0246.
PN US6423333-B1.
PD 23-JUL-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 11.4%; Score 269.5; DB 5; Length 1065;
Best Local Similarity 26.7%; Pred. No. 2.2e-08;
RESULT 1124
ID ABB70198 standard; protein; 272 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37386.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE-) PE CORP NY.
Query Match 11.4%; Score 269; DB 4; Length 272;
Best Local Similarity 29.9%; Pred. No. 6.4e-09;
RESULT 1125
ID ADC3284 standard; protein; 410 AA.
DE ADF-4 silk protein.
PN WO2003057727-A1.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 11.4%; Score 269; DB 7; Length 410;
Best Local Similarity 27.1%; Pred. No. 9.5e-09;
RESULT 1126
ID ADP31157 standard; protein; 474 AA.
DE Human secreted protein SEQ ID #1924.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 11.4%; Score 269; DB 8; Length 474;
Best Local Similarity 28.9%; Pred. No. 1.1e-08;
RESULT 1127
ID AAB70184 standard; peptide; 248 AA.
DE Peptide dendrimer carrier #9.
PN WO200107469-A2.
PD 01-FEB-2001.
PA (VERD/) VERDINI A.
Query Match 11.4%; Score 268.5; DB 4; Length 248;
Best Local Similarity 31.2%; Pred. No. 6.3e-09;
RESULT 1128
ID ADL92144 standard; protein; 1027 AA.
DE Amino acid sequence of human collagen type I alpha2.

DE Collagen protein sequence.
PN WO200309862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Query Match 11.4%; Score 268.5; DB 8; Length 1027;
Best Local Similarity 27.7%; Pred. No. 2.4e-08;
RESULT 1129
ID AAR80327 standard; protein; 762 AA.
DE Protein polymeric adhesion substrate 1-B.
PN WO9523611-A1.
PD 08-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 11.3%; Score 268; DB 2; Length 762;
Best Local Similarity 27.9%; Pred. No. 2e-08;
RESULT 1130
ID AAW57668 standard; peptide; 762 AA.
DE Collagen-like polymer.
PN US773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 11.3%; Score 268; DB 2; Length 762;
Best Local Similarity 27.9%; Pred. No. 2e-08;
RESULT 1131
ID AAW49715 standard; protein; 762 AA.
DE Protein polymer adhesive substrate PPAS1-B.
PN US773257-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 11.3%; Score 268; DB 2; Length 762;
Best Local Similarity 27.9%; Pred. No. 2e-08;
RESULT 1132
ID AAR71702 standard; protein; 1366 AA.
DE Collagen alpha 2 (I) chain precursor.
PN WO9508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 11.3%; Score 267.5; DB 2; Length 1366;
Best Local Similarity 30.3%; Pred. No. 3.7e-08;
RESULT 1133
ID AAY96123 standard; peptide; 1366 AA.
DE Collagen type I alpha-2.
PN US6110689-A.
PD 29-AUG-2000.
PA (OSTE-) OSTEOMETER AS.
Query Match 11.3%; Score 267.5; DB 3; Length 1366;
Best Local Similarity 30.3%; Pred. No. 3.7e-08;
RESULT 1134
ID ABB50293 standard; protein; 1366 AA.
DE Collagen type I alpha-2 ovarian tumour marker protein, SEQ ID NO:76.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 11.3%; Score 267.5; DB 4; Length 1366;
Best Local Similarity 30.3%; Pred. No. 3.7e-08;
RESULT 1135
ID AAE16476 standard; protein; 1366 AA.
DE Human collagen alpha 2-type I protein.
PN US6323314-B1.
PD 27-NOV-2001.
PA (OSTE-) OSTEOMETER AS.
Query Match 11.3%; Score 267.5; DB 5; Length 1366;
Best Local Similarity 30.3%; Pred. No. 3.7e-08;
RESULT 1136
ID ABB80734 standard; protein; 1366 AA.
DE Protein sequence related to human collagen.
PN US6355442-B1.
PD 12-MAR-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 11.3%; Score 267.5; DB 5; Length 1366;
Best Local Similarity 30.3%; Pred. No. 3.7e-08;
RESULT 1137
ID ABB09626 standard; peptide; 1366 AA.
DE Amino acid sequence of human collagen type I alpha2.

PN US6342361-B1.
FD 29-JAN-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match
Best Local Similarity 11.3%; Score 267.5; DB 5; Length 1366;
RESULT 1138
ID ADF13076 standard; protein; 1366 AA.
DE Human procollagen alpha2(I) chain precursor.
PN US2003119058-A1.
PD 26-JUN-2003.
PA (OSTE-) OSTEOMETER AS.
Query Match
Best Local Similarity 11.3%; Score 267.5; DB 7; Length 1366;
RESULT 1139
ID ADF1438 standard; protein; 675 AA.
DE Human secreted protein SEQ ID #2205.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 11.3%; Score 266.5; DB 8; Length 675;
RESULT 1140
ID ABB64222 standard; protein; 317 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19458.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 11.3%; Score 266; DB 4; Length 317;
RESULT 1141
ID ADA07853 standard; protein; 568 AA.
DE Pinctada maxima naearein.
PN US2003027258-A1.
PD 06-FEB-2003.
PA (CHAN/) CHANG F F.
PA (LIHH/) LI H.
PA (HSIE/) HSIEH-LI H M.
Query Match
Best Local Similarity 11.2%; Score 265.5; DB 6; Length 568;
RESULT 1142
ID AAE02536 standard; protein; 1366 AA.
DE Porcine alpha2(I) collagen.
PN W0200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 11.2%; Score 265.5; DB 4; Length 1366;
RESULT 1143
ID AAU79907 standard; protein; 343 AA.
DE Fragment for resistance against dehydration stress, protein #5.
PN W0200226800-A1.
PD 04-APR-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match
Best Local Similarity 11.2%; Score 265; DB 5; Length 343;
RESULT 1144
ID ABG28641 standard; protein; 399 AA.
DE Novel human diagnostic protein #28632.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 4; Length 399;
RESULT 1145
ID AAU79272 standard; protein; 536 AA.
DE Phenolic acid esterase amino acid sequence.
PN GB2324302-A.
PD 21-OCT-1998.
PA (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.
PA (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 2; Length 536;
RESULT 1146
ID AAK51954 standard; protein; 1008 AA.
DE Repeat protein polymer repeat sequence, SEQ ID 22.
PN W0200309465-A1.
PD 04-DEC-2003.
PA (DOMO) DOM CORNING CORP.
PA (GEMV) GENENCOR INT INC.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 8; Length 1008;
RESULT 1147
ID ADR70477 standard; protein; 1063 AA.
DE Collagen-like protein.
PN US2004180027-A1.
PD 16-SEP-2004.
PA (KUMA/) KUMAR M.
PA (CUEV/) CUEVAS W A.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 8; Length 1063;
RESULT 1148
ID AAR37748 standard; protein; 1065 AA.
DE Collagen-like polymer DCP6 encoded by clone pPT 0246.
PN W09310154-A1.
PD 27-MAY-1993.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 2; Length 1065;
RESULT 1149
ID AAR93259 standard; protein; 1065 AA.
DE Collagen-like polymer sequence D gene 6 polymer protein (pPT0246).
PN US5496712-A.
PD 05-MAR-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 2; Length 1065;
RESULT 1150
ID AAW57656 standard; peptide; 1065 AA.
DE Collagen-like polymer.
PN US5773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 2; Length 1065;
RESULT 1151
ID AAY51883 standard; protein; 1065 AA.
DE Plasmid pPT0246 protein fragment containing CLP6 polymer units.
PN US6033654-A.
PD 07-MAR-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 3; Length 1065;
RESULT 1152
ID ABW01629 standard; protein; 1065 AA.
DE Plasmid pPT0246 CLP6 polymer protein.
PN US2003104589-A1.
PD 05-JUN-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match
Best Local Similarity 11.2%; Score 264.5; DB 7; Length 1065;
RESULT 1153
ID AAE02534 standard; protein; 1466 AA.
DE Bovine alpha1(III) collagen #2.
PN W0200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 11.1%; Score 262.5; DB 4; Length 1466;
RESULT 1154
ID AAE02533 standard; protein; 1466 AA.
DE Bovine alpha1(III) collagen #1.
PN W0200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match
Best Local Similarity 11.1%; Score 262.5; DB 4; Length 1466;
RESULT 1155

RESULT 1155
ID ADF63307 standard; protein; 553 AA.
DE Human lung specific protein sequence SEQ ID NO:64.
PN WO2003102137-A2.
PD 11-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 11.1%; Score 262; DB 8; Length 553;
Best Local Similarity 26.1%; Pred. No. 3.4e-08;
RESULT 1156
ID ABB58985 standard; protein; 1937 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3747.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 11.1%; Score 261.5; DB 4; Length 1937;
Best Local Similarity 24.9%; Pred. No. 1.2e-07;
RESULT 1157
ID ADR86371 standard; protein; 1049 AA.
DE Aspergillus fumigatus essential gene protein #421.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA PHARM INC.
Query Match 11.0%; Score 261; DB 8; Length 1049;
Best Local Similarity 23.7%; Pred. No. 7.2e-08;
RESULT 1158
ID ABB63141 standard; protein; 828 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16215.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 11.0%; Score 260.5; DB 4; Length 828;
Best Local Similarity 26.5%; Pred. No. 6.2e-08;
RESULT 1159
ID ADQ08606 standard; protein; 1104 AA.
DE Ciona intestinalis nervous system associated protein SeqID8.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JTGYODAN.
Query Match 11.0%; Score 260.5; DB 8; Length 1104;
Best Local Similarity 28.6%; Pred. No. 8.1e-08;
RESULT 1160
ID AAE36880 standard; protein; 399 AA.
DE Latrodectus geometricus major ampullate spideroin 2 (MasP2) protein #2.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 11.0%; Score 259.5; DB 6; Length 399;
Best Local Similarity 27.3%; Pred. No. 3.5e-08;
RESULT 1161
ID ADP31162 standard; protein; 537 AA.
DE Human secreted protein SEQ ID #1929.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 11.0%; Score 259; DB 8; Length 537;
Best Local Similarity 25.9%; Pred. No. 5e-08;
RESULT 1162
ID ABG95083 standard; protein; 462 AA.
DE Human translocation (12; 16)(q13; p11) protein #4.
PN WO200269900-A2.
PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 10.9%; Score 258.5; DB 5; Length 462;
Best Local Similarity 32.7%; Pred. No. 4.7e-08;
RESULT 1163
ID ADP31163 standard; protein; 594 AA.
DE Human secreted protein SEQ ID #1930.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.9%; Score 258; DB 8; Length 594;
Best Local Similarity 26.2%; Pred. No. 6.4e-08;
RESULT 1164
ID AAR37751 standard; protein; 1077 AA.
DE CLIP 3.1 monomer containing peptide.
PN WO9310154-A1.
PD 27-MAY-1993.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.9%; Score 258; DB 2; Length 1077;
Best Local Similarity 28.7%; Pred. No. 1.1e-07;
RESULT 1165
ID ADI26113 standard; protein; 518 AA.
DE Human protein that promotes STAT6 activation #39.
PN WO2003104277-A2.
PD 18-DEC-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 10.9%; Score 257.5; DB 8; Length 518;
Best Local Similarity 26.2%; Pred. No. 6e-08;
RESULT 1166
ID ABB71788 standard; protein; 385 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42156.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.9%; Score 257; DB 4; Length 385;
Best Local Similarity 35.4%; Pred. No. 4.9e-08;
RESULT 1167
ID ADP31164 standard; protein; 534 AA.
DE Human secreted protein SEQ ID #1931.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.9%; Score 257; DB 8; Length 534;
Best Local Similarity 26.0%; Pred. No. 6.7e-08;
RESULT 1168
ID AAR37746 standard; protein; 633 AA.
DE Collagen-like polymer DCP5 encoded by clone pPT 0232.
PN WO9310154-A1.
PD 27-MAY-1993.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.9%; Score 257; DB 2; Length 633;
Best Local Similarity 30.4%; Pred. No. 7.8e-08;
RESULT 1169
ID AAR93257 standard; protein; 633 AA.
DE Collagen-like polymer sequence D gene 5 polymer protein (pPT0232).
PN US5496712-A.
PD 05-MAR-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.9%; Score 257; DB 2; Length 633;
Best Local Similarity 30.4%; Pred. No. 7.8e-08;
RESULT 1170
ID AAW57655 standard; peptide; 633 AA.
DE Collagen-like polymer.
PN US5773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.9%; Score 257; DB 2; Length 633;
Best Local Similarity 30.4%; Pred. No. 7.8e-08;
RESULT 1171
ID ABU17075 standard; protein; 974 AA.
DE Protein encoded by Prokaryotic essential gene #2602.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.9%; Score 257; DB 6; Length 974;
Best Local Similarity 24.1%; Pred. No. 1.2e-07;
RESULT 1172
ID AAR37745 standard; protein; 1065 AA.
DE Collagen-like polymer DCP4 encoded by clone pPT 0249.
PN WO9310154-A1.
PD 27-MAY-1993.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.9%; Score 257; DB 2; Length 1065;
Best Local Similarity 28.0%; Pred. No. 1.3e-07;
RESULT 1173

ID AAR93256 standard; protein; 1065 AA.
DE Collagen-like polymer sequence D gene 4 polymer protein (pPT0249).
PN US5496712-A.
PD 05-MAR-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.9%; Score 257; DB 2; Length 1065;
Best Local Similarity 28.0%; Pred. No. 1.3e-07;
RESULT 1174
ID AAW57654 standard; peptide; 1065 AA.
DE Collagen-like polymer.
PN US5773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.9%; Score 257; DB 2; Length 1065;
Best Local Similarity 28.0%; Pred. No. 1.3e-07;
RESULT 1175
ID AAM50035 standard; protein; 230 AA.
DE N. clavipes spidroin synthetic homologue SE1 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 10.8%; Score 255.5; DB 5; Length 230;
Best Local Similarity 30.0%; Pred. No. 3.7e-08;
RESULT 1176
ID ADI26207 standard; protein; 589 AA.
DE Human protein that promotes STAT6 activation #86.
PN WO2003104277-A2.
PD 18-DEC-2003.
PA (ASAH) ASAHI KASEI KK.
Query Match 10.8%; Score 255.5; DB 8; Length 589;
Best Local Similarity 26.0%; Pred. No. 9e-08;
RESULT 1177
ID ABO53050 standard; protein; 592 AA.
DE Human putative spliceosome associated protein (SAP) #26.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 10.8%; Score 255.5; DB 6; Length 592;
Best Local Similarity 26.0%; Pred. No. 9.1e-08;
RESULT 1178
ID ADI26209 standard; protein; 592 AA.
DE Human protein that promotes STAT6 activation #87.
PN WO2003104277-A2.
PD 18-DEC-2003.
PA (ASAH) ASAHI KASEI KK.
Query Match 10.8%; Score 255.5; DB 8; Length 592;
Best Local Similarity 26.0%; Pred. No. 9.1e-08;
RESULT 1179
ID ABB66654 standard; protein; 499 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26754.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.8%; Score 254.5; DB 4; Length 499;
Best Local Similarity 26.3%; Pred. No. 8.9e-08;
RESULT 1180
ID ADN99871 standard; protein; 632 AA.
DE Novel human protein sequence #687.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.7%; Score 254; DB 8; Length 632;
Best Local Similarity 34.2%; Pred. No. 1.2e-07;
RESULT 1181
ID ABP53478 standard; protein; 1040 AA.
DE Protein polymer SELP6 polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match 10.7%; Score 254; DB 5; Length 1040;
Best Local Similarity 22.9%; Pred. No. 1.9e-07;

RESULT 1182
ID ABM83560 standard; protein; 1417 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3809.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.7%; Score 254; DB 8; Length 1417;
Best Local Similarity 27.4%; Pred. No. 2.6e-07;
RESULT 1183
ID ADE55694 standard; protein; 1419 AA.
DE Rat Protein AAR79780, SEQ ID NO 1513.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.7%; Score 254; DB 7; Length 1419;
Best Local Similarity 26.4%; Pred. No. 2.6e-07;
RESULT 1184
ID ABG61861 standard; protein; 1487 AA.
DE Prostate cancer-associated protein #62.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.7%; Score 254; DB 5; Length 1487;
Best Local Similarity 27.4%; Pred. No. 2.7e-07;
RESULT 1185
ID ABP56769 standard; protein; 1487 AA.
DE Collagen IIA protein.
PN WO2002100426-A1.
PD 19-DEC-2002.
PA (SMIN) SMITH & NEPHEW PLC.
Query Match 10.7%; Score 254; DB 6; Length 1487;
Best Local Similarity 27.4%; Pred. No. 2.7e-07;
RESULT 1186
ID AAG77793 standard; protein; 1745 AA.
DE Human pro-alpha-3(V) fibrillar procollagen polypeptide.
PN WO200164871-A2.
PD 07-SEP-2001.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 10.7%; Score 254; DB 4; Length 1745;
Best Local Similarity 27.6%; Pred. No. 3.2e-07;
RESULT 1187
ID ABB97234 standard; protein; 1745 AA.
DE Novel human protein SEQ ID NO: 502.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 254; DB 5; Length 1745;
Best Local Similarity 27.6%; Pred. No. 3.2e-07;
RESULT 1188
ID ADQ19841 standard; protein; 1745 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2660.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.7%; Score 254; DB 8; Length 1745;
Best Local Similarity 27.6%; Pred. No. 3.2e-07;
RESULT 1189
ID AAM50048 standard; protein; 264 AA.
DE N. clavipes spidroin synthetic homologue FA2 protein #2.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 10.7%; Score 253; DB 5; Length 264;
Best Local Similarity 30.7%; Pred. No. 6e-08;
RESULT 1190
ID ADK51957 standard; protein; 780 AA.
DE Repeat protein polymer repeat sequence, SEQ ID 25.
PN WO2003099465-A1.
PD 04-DEC-2003.
PA (DOWO) DOW CORNING CORP.
PA (GEMV) GENENCOR INT INC.
Query Match 10.7%; Score 253; DB 8; Length 780;
Best Local Similarity 10.7%;

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Best Local Similarity 29.2%; Pred. No. 1.7e-07;
RESULT 1191
ID ADC21544 standard; protein; 1014 AA.
DE Human type II collagen protein sequence.
PN WO2003006603-A2.
PD 23-JAN-2003.
PA (AREX-) AREXIS AB.
Query Match 10.7%; Score 253; DB 7; Length 1014;
Best Local Similarity 27.4%; Pred. No. 2.2e-07;
RESULT 1192
ID AAE16477 standard; protein; 1020 AA.
DE Collagen like protein, CLP3.1.
PN WO200200016-A1.
PD 03-JAN-2002.
PA (LUMI-) LUMINIS PTY LTD.
PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.
Query Match 10.7%; Score 253; DB 5; Length 1020;
Best Local Similarity 29.2%; Pred. No. 2.2e-07;
RESULT 1193
ID AAR93261 standard; protein; 1077 AA.
DE CLP 3.1 polymer sequence (pPT0297).
PN US5496712-A.
PD 05-MAR-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.7%; Score 253; DB 2; Length 1077;
Best Local Similarity 29.2%; Pred. No. 2.3e-07;
RESULT 1194
ID AAW57657 standard; peptide; 1077 AA.
DE Collagen-like polymer.
PN US5773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.7%; Score 253; DB 2; Length 1077;
Best Local Similarity 29.2%; Pred. No. 2.3e-07;
RESULT 1195
ID ABP60377 standard; peptide; 1217 AA.
DE Bombyx mori sericin SEQ ID NO 2.
PN WO200286133-A1.
PD 31-OCT-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match 10.7%; Score 253; DB 6; Length 1217;
Best Local Similarity 27.0%; Pred. No. 2.6e-07;
RESULT 1196
ID AAR59751 standard; protein; 1418 AA.
DE Type II collagen.
PN WO9414070-A1.
PD 23-JUN-1994.
PA (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.
Query Match 10.7%; Score 253; DB 2; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1197
ID AAR71703 standard; protein; 1418 AA.
DE Collagen alpha 1 (II) chain precursor.
PN WO9508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 2; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1198
ID RAY96124 standard; peptide; 1418 AA.
DE Collagen type II alpha-1.
PN US6110689-A.
PD 29-AUG-2000.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 3; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1199
ID AAB35624 standard; protein; 1418 AA.
DE Human type II collagen.
PN US6132976-A.
PD 17-OCT-2000.
PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
Query Match 10.7%; Score 253; DB 4; Length 1418;

Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1200
ID AAE16477 standard; protein; 1418 AA.
DE Human collagen alpha (II) protein.
PN US6323314-B1.
PD 27-NOV-2001.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1201
ID ABB80735 standard; protein; 1418 AA.
DE Collagen type II-alpha protein.
PN US6355442-B1.
PD 12-MAR-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1202
ID ABG93927 standard; protein; 1418 AA.
DE Human polypeptide orthologous to DACC-2.
PN WO200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1203
ID ABB09627 standard; peptide; 1418 AA.
DE Amino acid sequence of human collagen type II alpha1.
PN US6342361-B1.
PD 29-JAN-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 10.7%; Score 253; DB 5; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1204
ID ADF13077 standard; protein; 1418 AA.
DE Human collagen alpha(II) chain precursor.
PN US2003119058-A1.
PD 26-JUN-2003.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.7%; Score 253; DB 7; Length 1418;
Best Local Similarity 27.1%; Pred. No. 3e-07;
RESULT 1205
ID ADP31446 standard; protein; 1755 AA.
DE Human secreted protein SEQ ID #2213.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.7%; Score 252.5; DB 8; Length 1755;
Best Local Similarity 24.2%; Pred. No. 3.9e-07;
RESULT 1206
ID AAO16498 standard; protein; 227 AA.
DE Argiope trifasciata spider silk protein #2.
PN WO200299082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Query Match 10.7%; Score 252; DB 6; Length 227;
Best Local Similarity 29.2%; Pred. No. 6e-08;
RESULT 1207
ID AAP90064 standard; protein; 429 AA.
DE Antigenic protein for malaria vaccination.
PN USN7238746-N.
PD 21-MAR-1989.
PA (USSH-) NAT INST OF HEALTH.
Query Match 10.7%; Score 252; DB 1; Length 429;
Best Local Similarity 19.9%; Pred. No. 1.1e-07;
RESULT 1208
ID RAA61562 standard; protein; 1487 AA.
DE Human type II collagen alpha-chain protein.
PN WO9835235-A1.
PD 13-AUG-1998.
PA (UYSH-) UNIV SHEFFIELD.
Query Match 10.7%; Score 252; DB 2; Length 1487;
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Best Local Similarity 27.1%; Pred. No. 3.6e-07;
RESULT 1209
ID AEG3945 standard; protein; 1497 AA.
DE Mouse polypeptide orthologous to DACC-10.
PN W0200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 10.7%; Score 252; DB 5; Length 1497;
Best Local Similarity 26.0%; Pred. No. 3.6e-07;
RESULT 1210
ID ADE77159 standard; protein; 462 AA.
DE Human protein expressed in a liver disorder #83.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 10.6%; Score 251.5; DB 8; Length 462;
Best Local Similarity 29.9%; Pred. No. 1.3e-07;
RESULT 1211
ID ADF31648 standard; protein; 889 AA.
DE Human secreted protein SEQ ID #2415.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.6%; Score 251.5; DB 8; Length 889;
Best Local Similarity 26.6%; Pred. No. 2.4e-07;
RESULT 1212
ID AAP70709 standard; protein; 402 AA.
DE Plasmodium cynomolgi sporozoite circumsporozoite protein.
PN W08700533-A.
PD 29-JAN-1987.
PA (UYNY) UNIV NEW YORK STATE.
PA (ARNO/) ARNOT D E.
Query Match 10.6%; Score 251; DB 1; Length 402;
Best Local Similarity 25.5%; Pred. No. 1.2e-07;
RESULT 1213
ID ADD45053 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 10485.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.6%; Score 251; DB 7; Length 1453;
Best Local Similarity 27.7%; Pred. No. 4.1e-07;
RESULT 1214
ID ADD45057 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 10489.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.6%; Score 251; DB 7; Length 1453;
Best Local Similarity 27.7%; Pred. No. 4.1e-07;
RESULT 1215
ID ADD48341 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 14041.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.6%; Score 251; DB 7; Length 1453;
Best Local Similarity 27.7%; Pred. No. 4.1e-07;
RESULT 1216
ID ADD45049 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 10481.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.6%; Score 251; DB 7; Length 1453;
Best Local Similarity 27.7%; Pred. No. 4.1e-07;
RESULT 1217
ID ADD48337 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 14037.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.6%; Score 251; DB 7; Length 1453;
Best Local Similarity 27.7%; Pred. No. 4.1e-07;
RESULT 1218
ID ADD48345 standard; protein; 1453 AA.
DE Rat Protein CAB01633, SEQ ID NO 14045.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.6%; Score 251; DB 7; Length 1453;
Best Local Similarity 27.7%; Pred. No. 4.1e-07;
RESULT 1219
ID AAM50040 standard; protein; 219 AA.
DE N. clavipes spidroin synthetic homologue FA2 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match 10.6%; Score 250.5; DB 5; Length 219;
Best Local Similarity 32.8%; Pred. No. 7.1e-08;
RESULT 1220
ID ADC35282 standard; protein; 360 AA.
DE ADF-1 silk protein.
PN W02003057727-A1.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 10.6%; Score 250.5; DB 7; Length 360;
Best Local Similarity 25.7%; Pred. No. 1.1e-07;
RESULT 1221
ID AAG92278 standard; protein; 585 AA.
DE C glutamicum protein fragment SEQ ID NO: 6032.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 10.6%; Score 250.5; DB 4; Length 585;
Best Local Similarity 24.9%; Pred. No. 1.8e-07;
RESULT 1222
ID AAG28100 standard; protein; 274 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33192.
PN EPI33405-A2.
PD 06-SEP-2000.
Query Match 10.6%; Score 250; DB 3; Length 274;
Best Local Similarity 30.2%; Pred. No. 9.5e-08;
RESULT 1223
ID AAU08231 standard; protein; 597 AA.
DE Polypeptide encoded by Mycobacterium tuberculosis clone mTCC#3.
PN W0200162893-A2.
PD 30-AUG-2001.
PA (CORI-) CORIXA CORP.
Query Match 10.6%; Score 250; DB 4; Length 597;
Best Local Similarity 26.7%; Pred. No. 2e-07;
RESULT 1224
ID ABU25538 standard; protein; 669 AA.
DE Protein encoded by Prokaryotic essential gene #11065.
PN W020027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.6%; Score 249.5; DB 6; Length 669;
Best Local Similarity 43.6%; Pred. No. 2.4e-07;
RESULT 1225
ID ADJ67574 standard; protein; 702 AA.
DE Human ovarian specific polypeptide SEQ ID NO:288.
PN W02004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 10.6%; Score 249.5; DB 8; Length 702;
Best Local Similarity 27.8%; Pred. No. 2.5e-07;
RESULT 1226
ID ABB60516 standard; protein; 1190 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 8340.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.5%; Score 249; DB 4; Length 1190;
Best Local Similarity 29.1%; Pred. No. 4.4e-07;
RESULT 1227
ID AAR79480 standard; protein; 1442 AA.
DE Rat type II collagen.
PN W09522611-A2.
PD 24-AUG-1995.
PA (UNMI) UNIV MICHIGAN.
Query Match 10.5%; Score 248.5; DB 2; Length 1442;
Best Local Similarity 24.3%; Pred. No. 5.7e-07;
RESULT 1228
ID AAU79906 standard; protein; 267 AA.
DE Fragment for resistance against dehydration stress, protein #4.
PN W0200226800-A1.
PD 04-APR-2002.
PA (SEIR-) SEIREN CO LTD.
Query Match 10.5%; Score 247.5; DB 5; Length 267;
Best Local Similarity 33.6%; Pred. No. 1.3e-07;
RESULT 1229
ID ABB60010 standard; protein; 399 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6822.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.5%; Score 247.5; DB 4; Length 399;
Best Local Similarity 25.0%; Pred. No. 1.9e-07;
RESULT 1230
ID AAY50936 standard; protein; 590 AA.
DE Human adult skin cDNA clone vdl_1 derived protein #1.
PN W0955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 10.5%; Score 247.5; DB 3; Length 590;
Best Local Similarity 24.3%; Pred. No. 2.8e-07;
RESULT 1231
ID ABP75534 standard; protein; 601 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 718.
PN W0200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.5%; Score 247.5; DB 6; Length 601;
Best Local Similarity 24.3%; Pred. No. 2.9e-07;
RESULT 1232
ID AAG77792 standard; protein; 1739 AA.
DE Murine pro-alpha-3(V) fibrillar procollagen polypeptide.
PN W0200164871-A2.
PD 07-SEP-2001.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 10.5%; Score 247.5; DB 4; Length 1739;
Best Local Similarity 26.6%; Pred. No. 7.9e-07;
RESULT 1233
ID ABU36445 standard; protein; 3300 AA.
DE Protein encoded by Prokaryotic essential gene #21972.
PN W020027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.5%; Score 247.5; DB 6; Length 3300;
Best Local Similarity 24.0%; Pred. No. 1.5e-06;
RESULT 1234
ID ADA33477 standard; protein; 975 AA.
DE Acinetobacter baumannii protein #638.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.5%; Score 247; DB 6; Length 975;
Best Local Similarity 24.3%; Pred. No. 4.9e-07;
RESULT 1235
ID ADO08789 standard; protein; 338 AA.
DE Novel surgical dressing-related protein SeqID76.
PN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 10.4%; Score 246.5; DB 8; Length 338;
Best Local Similarity 28.5%; Pred. No. 1.9e-07;
RESULT 1236
ID AAY06239 standard; protein; 595 AA.
DE Mouse recombinant type I collagen COL1A1-2.
PN EP926543-A1.
PD 30-JUN-1999.
PA (FUJF) FUJII PHOTO FILM BV.
Query Match 10.4%; Score 246.5; DB 2; Length 595;
Best Local Similarity 28.6%; Pred. No. 3.3e-07;
RESULT 1237
ID AAY06240 standard; protein; 822 AA.
DE Mouse recombinant type I collagen COL1A1-3.
PN EP926543-A1.
PD 30-JUN-1999.
PA (FUJF) FUJII PHOTO FILM BV.
Query Match 10.4%; Score 246.5; DB 2; Length 822;
Best Local Similarity 28.6%; Pred. No. 4.4e-07;
RESULT 1238
ID AAR71701 standard; protein; 1341 AA.
DE Collagen alpha 1 (I) chain precursor.
PN W09508115-A1.
PD 23-MAR-1995.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.4%; Score 246.5; DB 2; Length 1341;
Best Local Similarity 27.8%; Pred. No. 7.1e-07;
RESULT 1239
ID AAY96122 standard; peptide; 1341 AA.
DE Collagen type I alpha-1.
PN US6110689-A.
PD 29-AUG-2000.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.4%; Score 246.5; DB 3; Length 1341;
Best Local Similarity 27.8%; Pred. No. 7.1e-07;
RESULT 1240
ID AAE16475 standard; protein; 1341 AA.
DE Human collagen alphas (I) protein.
PN US6323314-B1.
PD 27-NOV-2001.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.4%; Score 246.5; DB 5; Length 1341;
Best Local Similarity 27.8%; Pred. No. 7.1e-07;
RESULT 1241
ID ABB80733 standard; protein; 1341 AA.
DE Collagen type I-alpha protein.
PN US6355442-B1.
PD 12-MAR-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 10.4%; Score 246.5; DB 5; Length 1341;
Best Local Similarity 27.8%; Pred. No. 7.1e-07;
RESULT 1242
ID ABB09625 standard; peptide; 1341 AA.
DE Amino acid sequence of human collagen type I alpha1.
PN US6342361-B1.
PD 29-JAN-2002.
PA (OSTE-) OSTEOMETER BIOTECH AS.
Query Match 10.4%; Score 246.5; DB 5; Length 1341;
Best Local Similarity 27.8%; Pred. No. 7.1e-07;
RESULT 1243
ID ADF13075 standard; protein; 1341 AA.
DE Human collagen alphas (I) chain precursor.
PN US2003119058-A1.
PD 26-JUN-2003.
PA (OSTE-) OSTEOMETER AS.
Query Match 10.4%; Score 246.5; DB 7; Length 1341;
Best Local Similarity 27.8%; Pred. No. 7.1e-07;
RESULT 1244
ID ABG93948 standard; protein; 1453 AA.
DE Mouse polypeptide orthologous to DACC-11.

PN WO200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 10.4%; Score 246.5; DB 5; Length 1453;
Best Local Similarity 28.6%; Pred. No. 7.7e-07;
RESULT 1245
ID AAR60620 standard; protein; 1958 AA.
DE Protein from ORF2 of Pseudorabies virus large latency transcript.
PN US5352596-A.
PD 04-OCT-1994.
PA (USDA) US SEC OF AGRIC.
Query Match 10.4%; Score 246.5; DB 2; Length 1958;
Best Local Similarity 23.7%; Pred. No. 1e-06;
RESULT 1246
ID ABO23520 standard; protein; 354 AA.
DE Mycobacterium tuberculosis outlier protein #4.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match 10.4%; Score 245.5; DB 7; Length 354;
Best Local Similarity 26.0%; Pred. No. 2.3e-07;
RESULT 1247
ID ADC21591 standard; protein; 1014 AA.
DE Mouse type II collagen protein sequence.
PN WO2003006603-A2.
PD 23-JAN-2003.
PA (AREX-) AREXIS AB.
Query Match 10.4%; Score 245.5; DB 7; Length 1014;
Best Local Similarity 24.9%; Pred. No. 6.3e-07;
RESULT 1248
ID AAE02535 standard; protein; 1449 AA.
DE Porcine alpha1(I) collagen.
PN WO200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 10.4%; Score 245.5; DB 4; Length 1449;
Best Local Similarity 28.9%; Pred. No. 8.8e-07;
RESULT 1249
ID ABG93928 standard; protein; 1487 AA.
DE Mouse polypeptide orthologous to DACC-2.
PN WO200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 10.4%; Score 245.5; DB 5; Length 1487;
Best Local Similarity 24.9%; Pred. No. 9e-07;
RESULT 1250
ID AAG28101 standard; protein; 267 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33193.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.4%; Score 245; DB 3; Length 267;
Best Local Similarity 30.2%; Pred. No. 1.9e-07;
RESULT 1251
ID AAB35148 standard; protein; 894 AA.
DE Human NFAR-2 SEQ ID NO: 4.
PN WO200077205-A1.
PD 21-DEC-2000.
PA (BARB/) BARBER G N.
PA (SAUN/) SAUNDERS L.
PA (PERK/) PERKINS D J.
Query Match 10.4%; Score 245; DB 4; Length 894;
Best Local Similarity 28.3%; Pred. No. 6e-07;
RESULT 1252
ID ADA03105 standard; protein; 894 AA.
DE Nucleotide therapy testing protein #11.
PN WO2003023031-A1.
PD 20-MAR-2003.
PA (NNSH) NIPPON SHINYAKU CO LTD.

Query Match 10.4%; Score 245; DB 6; Length 894;
Best Local Similarity 28.3%; Pred. No. 6e-07;
RESULT 1253
ID ADJ66639 standard; protein; 894 AA.
DE Interleukin enhancer binding factor 3 for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
Query Match 10.4%; Score 245; DB 8; Length 894;
Best Local Similarity 28.3%; Pred. No. 6e-07;
RESULT 1254
ID ADL56761 standard; protein; 894 AA.
DE Human cell derived viral RNA binding protein 110.
PN WO2004029199-A2.
PD 08-APR-2004.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 10.4%; Score 245; DB 8; Length 894;
Best Local Similarity 28.3%; Pred. No. 6e-07;
RESULT 1255
ID ADQ20794 standard; protein; 894 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3614.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.4%; Score 245; DB 8; Length 894;
Best Local Similarity 28.3%; Pred. No. 6e-07;
RESULT 1256
ID ADE31110 standard; protein; 906 AA.
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 242.
PN WO2003062376-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.4%; Score 245; DB 7; Length 906;
Best Local Similarity 28.3%; Pred. No. 6e-07;
RESULT 1257
ID AAG41604 standard; protein; 1424 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51784.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.4%; Score 245; DB 3; Length 1424;
Best Local Similarity 32.9%; Pred. No. 9.3e-07;
RESULT 1258
ID AAG41603 standard; protein; 1457 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51783.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.4%; Score 245; DB 3; Length 1457;
Best Local Similarity 32.9%; Pred. No. 9.5e-07;
RESULT 1259
ID AAG30466 standard; protein; 1598 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36428.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.4%; Score 245; DB 3; Length 1598;
Best Local Similarity 32.9%; Pred. No. 1e-06;
RESULT 1260
ID AAG30465 standard; protein; 1599 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36427.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.4%; Score 245; DB 3; Length 1599;
Best Local Similarity 32.9%; Pred. No. 1e-06;
RESULT 1261
ID AAG41602 standard; protein; 1637 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51782.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 10.4%; Score 245; DB 3; Length 1637;
Best Local Similarity 32.9%; Pred. No. 1.1e-06;
RESULT 1262
ID AAG30464 standard; protein; 1684 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36426.
PN EP1033405-A2.

PD 06-SEP-2000.
Query Match 10.4%; Score 245; DB 3; Length 1684;
Best Local Similarity 32.9%; Pred. No. 1.1e-06;
RESULT 1263
ID ADJ69005 standard; protein; 1684 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID811.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 10.4%; Score 245; DB 7; Length 1684;
Best Local Similarity 32.9%; Pred. No. 1.1e-06;
RESULT 1264
ID ADE87052 standard; protein; 886 AA.
DE Human pancreatic cell protein sequence SeqID512.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 10.3%; Score 244.5; DB 7; Length 886;
Best Local Similarity 27.8%; Pred. No. 6.3e-07;
RESULT 1265
ID AAW09218 standard; protein; 1002 AA.
DE SELPOK polymer.
PN WO9634618-A1.
PD 07-NOV-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.3%; Score 244.5; DB 2; Length 1002;
Best Local Similarity 29.2%; Pred. No. 7.1e-07;
RESULT 1266
ID AAW53544 standard; protein; 1002 AA.
DE Amino acid sequence of SELPOK peptide 2.
PN WO9810063-A1.
PD 12-MAR-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.3%; Score 244.5; DB 2; Length 1002;
Best Local Similarity 29.2%; Pred. No. 7.1e-07;
RESULT 1267
ID AAY51888 standard; protein; 1002 AA.
DE Plasmid pPT0364 protein fragment containing SELPOK polymer units.
PN US6033654-A.
PD 07-MAR-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.3%; Score 244.5; DB 3; Length 1002;
Best Local Similarity 29.2%; Pred. No. 7.1e-07;
RESULT 1268
ID ABG31418 standard; protein; 1002 AA.
DE SELPOK protein encoded by plasmid pPT0364.
PN US6423333-B1.
PD 23-JUL-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.3%; Score 244.5; DB 5; Length 1002;
Best Local Similarity 29.2%; Pred. No. 7.1e-07;
RESULT 1269
ID ASW01634 standard; protein; 1002 AA.
DE Plasmid pPT0364 SELPOK polymer protein.
PN US2003104589-A1.
PD 05-JUN-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.3%; Score 244.5; DB 7; Length 1002;
Best Local Similarity 29.2%; Pred. No. 7.1e-07;
RESULT 1270
ID AAY84544 standard; protein; 1057 AA.
DE A human collagen 1 (alpha) protein helical region.
PN EP992586-A2.
PD 12-APR-2000.
PA (USSU) US SURGICAL CORP.
Query Match 10.3%; Score 244.5; DB 3; Length 1057;
Best Local Similarity 27.8%; Pred. No. 7.5e-07;
RESULT 1271
ID AAY84403 standard; protein; 1058 AA.
DE Amino acid sequence of human type 1 (alpha) collagen polypeptide.
PN WO200014201-A1.
PD 16-MAR-2000.

PA (USSU) US SURGICAL CORP.
PA (PAOL/) PAOLELLA D N.
PA (GRUS/) GRUSKIN E A.
PA (BUEC/) BUECHTER D D.
Query Match 10.3%; Score 244.5; DB 3; Length 1058;
Best Local Similarity 27.8%; Pred. No. 7.5e-07;
RESULT 1272
ID RAY84540 standard; protein; 1107 AA.
DE Amino acid sequence of a chimeric collagen 1 (alpha)/decorin protein.
PN EP992586-A2.
PD 12-APR-2000.
PA (USSU) US SURGICAL CORP.
Query Match 10.3%; Score 244.5; DB 3; Length 1107;
Best Local Similarity 27.8%; Pred. No. 7.8e-07;
RESULT 1273
ID ADE87050 standard; protein; 1161 AA.
DE Human pancreatic cell protein sequence SeqID510.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 10.3%; Score 244.5; DB 7; Length 1161;
Best Local Similarity 27.8%; Pred. No. 8.2e-07;
RESULT 1274
ID AAY84538 standard; protein; 1171 AA.
DE A chimeric collagen 1 (alpha)/TGF-beta1 protein.
PN EP992586-A2.
PD 12-APR-2000.
PA (USSU) US SURGICAL CORP.
Query Match 10.3%; Score 244.5; DB 3; Length 1171;
Best Local Similarity 27.8%; Pred. No. 8.3e-07;
RESULT 1275
ID ADE87057 standard; protein; 1211 AA.
DE Human pancreatic cell protein sequence SeqID517.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 10.3%; Score 244.5; DB 7; Length 1211;
Best Local Similarity 27.8%; Pred. No. 8.5e-07;
RESULT 1276
ID ADE87062 standard; protein; 1226 AA.
DE Human pancreatic cell protein sequence SeqID522.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 10.3%; Score 244.5; DB 7; Length 1226;
Best Local Similarity 27.8%; Pred. No. 8.6e-07;
RESULT 1277
ID RAY84539 standard; protein; 1388 AA.
DE Amino acid sequence of a chimeric collagen 1 (alpha)/decorin protein.
PN EP992586-A2.
PD 12-APR-2000.
PA (USSU) US SURGICAL CORP.
Query Match 10.3%; Score 244.5; DB 3; Length 1388;
Best Local Similarity 27.8%; Pred. No. 9.7e-07;
RESULT 1278
ID REG93947 standard; protein; 1461 AA.
DE Human polypeptide orthologous to DACC-11.
PN WO200264625-A1.
PD 22-AUG-2002.
PA (ADPP-) ADP PHARM PTY LTD.
PA (UNSY) UNIV SYDNEY.
Query Match 10.3%; Score 244.5; DB 5; Length 1461;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1279
ID AAW68485 standard; protein; 1464 AA.
DE Human recombinant collagen protein.
PN WO9827202-A1.
PD 25-JUN-1998.
PA (BIOC-) BIOCEM SA.
Query Match 10.3%; Score 244.5; DB 2; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1280
ID AAU14136 standard; protein; 1464 AA.

DE Human novel protein #7.
FN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 244.5; DB 4; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1281
ID ADD45059 standard; protein; 1464 AA.
DE Human Protein P02452, SEQ ID NO 10491.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.3%; Score 244.5; DB 7; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1282
ID ADD45055 standard; protein; 1464 AA.
DE Human Protein P02452, SEQ ID NO 10487.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.3%; Score 244.5; DB 7; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1283
ID ADD45051 standard; protein; 1464 AA.
DE Human Protein P02452, SEQ ID NO 10483.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.3%; Score 244.5; DB 7; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1284
ID ADE87048 standard; protein; 1464 AA.
DE Human pancreatic cell protein sequence SeqID508.
FN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 10.3%; Score 244.5; DB 7; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1285
ID ADR16800 standard; protein; 1464 AA.
DE Human collagen I alpha1 (I) chain protein.
FN US2004151731-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
Query Match 10.3%; Score 244.5; DB 8; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1286
ID ADR16425 standard; protein; 1464 AA.
DE Human collagen I alpha1 (I) chain protein.
FN US2004151732-A1.
PD 05-AUG-2004.
PA (JICH/) JICHA D L.
PA (PELU/) PELUSE S.
Query Match 10.3%; Score 244.5; DB 8; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1287
ID ADR99144 standard; protein; 1464 AA.
DE Collagen, type I, alpha 1, COL1A1, SEQ ID 150.
FN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 10.3%; Score 244.5; DB 8; Length 1464;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1288
ID ABG22679 standard; protein; 1518 AA.
DE Novel human diagnostic protein #22670.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.3%; Score 244.5; DB 4; Length 1518;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1289
ID ADE87051 standard; protein; 1536 AA.
DE Human pancreatic cell protein sequence SeqID511.
FN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 10.3%; Score 244.5; DB 7; Length 1536;
Best Local Similarity 27.8%; Pred. No. 1e-06;
RESULT 1290
ID ABG53065 standard; protein; 441 AA.
DE Human putative spliceosome associated protein (SAP) #42.
FN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 10.3%; Score 244; DB 6; Length 441;
Best Local Similarity 28.3%; Pred. No. 3.5e-07;
RESULT 1291
ID ADA03117 standard; protein; 591 AA.
DE Nucleotide therapy testing protein #23.
FN WO2003023031-A1.
PD 20-MAR-2003.
PA (NNNSH) NIPPON SHINYAKU CO LTD.
Query Match 10.3%; Score 244; DB 6; Length 591;
Best Local Similarity 29.0%; Pred. No. 4.6e-07;
RESULT 1292
ID ADO08795 standard; protein; 316 AA.
DE Novel surgical dressing-related protein SeqID82.
FN JP2004049921-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match 10.3%; Score 243.5; DB 8; Length 316;
Best Local Similarity 25.3%; Pred. No. 2.7e-07;
RESULT 1293
ID AAE36862 standard; protein; 714 AA.
DE Human collagen type II protein.
FN WO2003021226-A2.
PD 13-MAR-2003.
PA (PHAA) PHARMACIA CORP.
Query Match 10.3%; Score 243; DB 6; Length 714;
Best Local Similarity 27.1%; Pred. No. 6.4e-07;
RESULT 1294
ID ADI3185 standard; protein; 714 AA.
DE Human collagen type II-related protein.
FN US2003219843-A1.
PD 27-NOV-2003.
PA (WELS/) WELSCH D J.
PA (DUFF/) DUFFIN K L.
PA (NEMI/) NEMIROVSKIY O V.
PA (DUFF/) DUFFIELD D R.
PA (SUNY/) SUNYER T.
PA (HOWA/) HOWARD C P.
PA (ABRA/) ABRAMS M.
Query Match 10.3%; Score 243; DB 8; Length 714;
Best Local Similarity 27.1%; Pred. No. 6.4e-07;
RESULT 1295
ID ADF31573 standard; protein; 906 AA.
DE Human secreted protein SEQ ID #2340.
FN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.3%; Score 243; DB 8; Length 906;
Best Local Similarity 25.8%; Pred. No. 8e-07;
RESULT 1296
ID ABB70775 standard; protein; 1357 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39117.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.3%; Score 243; DB 4; Length 1357;
Best Local Similarity 22.9%; Pred. No. 1.2e-06;

PD 26-AUG-1999.
 PA (CORI-) CORIXA CORP.
 Query Match 10.2%; Score 240.5; DB 2; Length 943;
 Best Local Similarity 24.5%; Pred. No. 1.2e-06;
 RESULT 1315
 ID AAR89472 standard; protein; 1107 AA.
 DE Collagen/decorsin(aa46-93) fusion protein.
 PN CA2151547-A.
 PD 11-DEC-1995.
 PA (USSU) US SURGICAL CORP.
 Query Match 10.2%; Score 240.5; DB 2; Length 1107;
 Best Local Similarity 27.6%; Pred. No. 1.4e-06;
 RESULT 1316
 ID AAR89469 standard; protein; 1169 AA.
 DE Collagen/BMP-2B fusion protein.
 PN CA2151547-A.
 PD 11-DEC-1995.
 PA (USSU) US SURGICAL CORP.
 Query Match 10.2%; Score 240.5; DB 2; Length 1169;
 Best Local Similarity 27.6%; Pred. No. 1.5e-06;
 RESULT 1317
 ID AAY84537 standard; protein; 1169 AA.
 DE Amino acid sequence of a chimeric collagen 1 (alpha1)/BMP-2B protein.
 PN EF992586-A2.
 PD 12-APR-2000.
 PA (USSU) US SURGICAL CORP.
 Query Match 10.2%; Score 240.5; DB 3; Length 1169;
 Best Local Similarity 27.6%; Pred. No. 1.5e-06;
 RESULT 1318
 ID AAR89470 standard; protein; 1171 AA.
 DE Collagen/TGF-beta-1 fusion protein.
 PN CA2151547-A.
 PD 11-DEC-1995.
 PA (USSU) US SURGICAL CORP.
 Query Match 10.2%; Score 240.5; DB 2; Length 1171;
 Best Local Similarity 27.6%; Pred. No. 1.5e-06;
 RESULT 1319
 ID AAR89471 standard; protein; 1388 AA.
 DE Collagen/decorsin fusion protein.
 PN CA2151547-A.
 PD 11-DEC-1995.
 PA (USSU) US SURGICAL CORP.
 Query Match 10.2%; Score 240.5; DB 2; Length 1388;
 Best Local Similarity 27.6%; Pred. No. 1.7e-06;
 RESULT 1320
 ID AAO16358 standard; protein; 7339 AA.
 DE Human translocated promoter region (TPR) protein, SEQ ID NO 6.
 PN WO200299050-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 10.2%; Score 240.5; DB 6; Length 7339;
 Best Local Similarity 24.3%; Pred. No. 8.4e-06;
 RESULT 1321
 ID AAR80350 standard; protein; 338 AA.
 DE Protein polymeric adhesion substrate 2-F.
 PN WO9523611-A1.
 PD 08-SEP-1995.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 10.2%; Score 240; DB 2; Length 338;
 Best Local Similarity 29.6%; Pred. No. 4.8e-07;
 RESULT 1322
 ID ABU36649 standard; protein; 678 AA.
 DE Protein encoded by Prokaryotic essential gene #22176.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 10.2%; Score 240; DB 6; Length 678;
 Best Local Similarity 27.5%; Pred. No. 9.3e-07;
 RESULT 1323
 ID ADD89022 standard; protein; 1212 AA.
 DE TAT262.
 PN WO2003057160-A2.
 PD 17-JUL-2003.

PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 240; DB 7; Length 1212;
 Best Local Similarity 26.2%; Pred. No. 1.6e-06;
 RESULT 1324
 ID AAM40863 standard; protein; 1669 AA.
 DE Human polypeptide SEQ ID NO 5794.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 10.2%; Score 240; DB 4; Length 1669;
 Best Local Similarity 26.2%; Pred. No. 2.2e-06;
 RESULT 1325
 ID AAB70178 standard; peptide; 183 AA.
 DE Peptide dendrimer carrier #3.
 PN WO200107469-A2.
 PD 01-FEB-2001.
 PA (VERD/) VERDINI A.
 Query Match 10.1%; Score 239.5; DB 4; Length 183;
 Best Local Similarity 29.7%; Pred. No. 2.8e-07;
 RESULT 1326
 ID ADP31574 standard; protein; 366 AA.
 DE Human secreted protein SEQ ID #2341.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 10.1%; Score 239.5; DB 8; Length 366;
 Best Local Similarity 26.3%; Pred. No. 5.5e-07;
 RESULT 1327
 ID ADP31575 standard; protein; 384 AA.
 DE Human secreted protein SEQ ID #2342.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 10.1%; Score 239.5; DB 8; Length 384;
 Best Local Similarity 26.3%; Pred. No. 5.8e-07;
 RESULT 1328
 ID ABU17351 standard; protein; 469 AA.
 DE Protein encoded by Prokaryotic essential gene #2878.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 10.1%; Score 239.5; DB 6; Length 469;
 Best Local Similarity 28.2%; Pred. No. 7e-07;
 RESULT 1329
 ID AAY84541 standard; protein; 1057 AA.
 DE Amino acid sequence of a human collagen 1 (alpha1) protein.
 PN EF992586-A2.
 PD 12-APR-2000.
 PA (USSU) US SURGICAL CORP.
 Query Match 10.1%; Score 239.5; DB 3; Length 1057;
 Best Local Similarity 26.7%; Pred. No. 1.5e-06;
 RESULT 1330
 ID AAB82454 standard; protein; 1464 AA.
 DE Human pro-alpha-1 chain of type I procollagen.
 PN WO200144455-A2.
 PD 21-JUN-2001.
 PA (ASTR) ASTRAZENECA AB.
 Query Match 10.1%; Score 239.5; DB 4; Length 1464;
 Best Local Similarity 26.7%; Pred. No. 2.1e-06;
 RESULT 1331
 ID ABB90764 standard; protein; 1464 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 261.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UIJO) UNIV JOHNS HOPKINS.
 Query Match 10.1%; Score 239.5; DB 5; Length 1464;
 Best Local Similarity 26.7%; Pred. No. 2.1e-06;
 RESULT 1332
 ID ABP68610 standard; protein; 1464 AA.
 DE Human pancreatic cancer expressed protein SEQ ID NO 159.
 PN WO200260317-A2.
 PD 08-AUG-2002.

PA (CORI-) CORIXA CORP.
Query Match 10.1%; Score 239.5; DB 5; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1333
ID ABUS4471 standard; protein; 1464 AA.
DE Human tumour endothelial marker TEM 38.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 10.1%; Score 239.5; DB 6; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1334
ID ABR47417 standard; protein; 1464 AA.
DE Breast cancer associated protein sequence SEQ ID NO:65.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.1%; Score 239.5; DB 6; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1335
ID ABR92064 standard; protein; 1464 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:36.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.1%; Score 239.5; DB 6; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1336
ID ADD14142 standard; protein; 1464 AA.
DE Human src biomarker polypeptide SEQ ID NO:331.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.1%; Score 239.5; DB 7; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1337
ID ADP65246 standard; protein; 1464 AA.
DE Human alpha 1 type I collagen preproprotein, Collagen I, alpha-1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.1%; Score 239.5; DB 7; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1338
ID ADQ19470 standard; protein; 1464 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2289.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.1%; Score 239.5; DB 8; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1339
ID ADQ29653 standard; protein; 1464 AA.
DE Human colorectal cancer-associated protein #8.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 10.1%; Score 239.5; DB 8; Length 1464;
Best Local Similarity 26.7%; Pred. No. 2.1e-06;
RESULT 1340
ID ADP65203 standard; protein; 1629 AA.
DE Human alpha 2 type XI collagen, isoform 3 preproprotein.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 10.1%; Score 239.5; DB 7; Length 1629;
Best Local Similarity 25.7%; Pred. No. 2.3e-06;
RESULT 1341
ID ABB57334 standard; protein; 1669 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:933.
PN WO200188188-A2.
PD 22-NOV-2001.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 10.1%; Score 239.5; DB 5; Length 1669;
Best Local Similarity 27.7%; Pred. No. 2.4e-06;
RESULT 1342
ID ABU22680 standard; protein; 584 AA.
DE Protein encoded by Prokaryotic essential gene #8207.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.1%; Score 239; DB 6; Length 584;
Best Local Similarity 26.2%; Pred. No. 9.3e-07;
RESULT 1343
ID AAB68072 standard; protein; 662 AA.
DE Amino acid sequence of a recombinant human gelatin.
PN WO200134801-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 10.1%; Score 239; DB 4; Length 662;
Best Local Similarity 27.6%; Pred. No. 1e-06;
RESULT 1344
ID AAE02718 standard; protein; 662 AA.
DE Human alpha (I) type I collagen helical domain (residues 531-1192).
PN WO200134646-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 10.1%; Score 239; DB 4; Length 662;
Best Local Similarity 27.6%; Pred. No. 1e-06;
RESULT 1345
ID ADB84306 standard; protein; 662 AA.
DE Recombinant gelatin #18.
PN US2003064074-A1.
PD 03-APR-2003.
PA (CHAN/) CHANG R C.
PA (KIVI/) KIVIRIKKO K I.
PA (NEFF/) NEFF T B.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
Query Match 10.1%; Score 239; DB 7; Length 662;
Best Local Similarity 27.6%; Pred. No. 1e-06;
RESULT 1346
ID AAE02532 standard; protein; 1463 AA.
DE Bovine alpha (I) collagen.
PN WO200134647-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 10.1%; Score 239; DB 4; Length 1463;
Best Local Similarity 27.7%; Pred. No. 2.2e-06;
RESULT 1347
ID AAU84266 standard; protein; 1806 AA.
DE Human endometrial cancer related protein, COL1A1.
PN WO200209573-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 10.1%; Score 239; DB 5; Length 1806;
Best Local Similarity 24.7%; Pred. No. 2.7e-06;
RESULT 1348
ID ABJ05596 standard; protein; 1806 AA.
DE Breast cancer-associated protein 61.
PN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.1%; Score 239; DB 5; Length 1806;
Best Local Similarity 24.7%; Pred. No. 2.7e-06;
RESULT 1349
ID ABR58545 standard; protein; 1806 AA.
DE Human cancer related protein SEQ ID NO:202.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.1%; Score 239; DB 6; Length 1806;
Best Local Similarity 24.7%; Pred. No. 2.7e-06;
RESULT 1350
ID ABU56581 standard; protein; 1806 AA.

DE Lung cancer-associated polypeptide #174.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 10.1%; Score 239; DB 6; Length 1806;
 Best Local Similarity 24.7%; Pred. No. 2.7e-06;
 RESULT 1351
 ID ADP31114 standard; protein; 1288 AA.
 DE Human secreted protein SEQ ID #1881.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 10.1%; Score 238.5; DB 8; Length 1288;
 Best Local Similarity 24.5%; Pred. No. 2.1e-06;
 RESULT 1352
 ID ADP48530 standard; protein; 1420 AA.
 DE Full-length chicken type II collagen.
 PN WO2004052910-A1.
 PD 24-JUN-2004.
 PA (AFFI-) AFFILIATED HOSPITAL ACAD MILITARY SCI PL.
 Query Match 10.1%; Score 238.5; DB 8; Length 1420;
 Best Local Similarity 26.2%; Pred. No. 2.3e-06;
 RESULT 1353
 ID AAB68062 standard; protein; 500 AA.
 DE Amino acid sequence of a recombinant human gelatin.
 PN WO200134801-A2.
 PD 17-MAY-2001.
 PA (FIBR-) FIBROGEN INC.
 Query Match 10.1%; Score 238; DB 4; Length 500;
 Best Local Similarity 25.6%; Pred. No. 9.2e-07;
 RESULT 1354
 ID AAE02708 standard; protein; 500 AA.
 DE Human alpha (I) type I collagen helical domain (residues 531-1030).
 PN WO200134646-A2.
 PD 17-MAY-2001.
 PA (FIBR-) FIBROGEN INC.
 Query Match 10.1%; Score 238; DB 4; Length 500;
 Best Local Similarity 25.6%; Pred. No. 9.2e-07;
 RESULT 1355
 ID ADB84295 standard; protein; 500 AA.
 DE Recombinant gelatin #8.
 PN US2003064074-A1.
 PD 03-APR-2003.
 PA (CHAN/) CHANG R C.
 PA (KIVI/) KIVIRIKKO K I.
 PA (NEFF/) NEFF T B.
 PA (OLSE/) OLSEN D R.
 PA (POLA/) POLAREK J W.
 Query Match 10.1%; Score 238; DB 7; Length 500;
 Best Local Similarity 25.6%; Pred. No. 9.2e-07;
 RESULT 1356
 ID ADE87059 standard; protein; 614 AA.
 DE Human pancreatic cell protein sequence SeqID519.
 PN WO2003060145-A2.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 10.1%; Score 238; DB 7; Length 614;
 Best Local Similarity 27.5%; Pred. No. 1.1e-06;
 RESULT 1357
 ID ADE87063 standard; protein; 615 AA.
 DE Human pancreatic cell protein sequence SeqID523.
 PN WO2003060145-A2.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 10.1%; Score 238; DB 7; Length 615;
 Best Local Similarity 27.5%; Pred. No. 1.1e-06;
 RESULT 1358
 ID ADE87058 standard; protein; 691 AA.
 DE Human pancreatic cell protein sequence SeqID518.
 PN WO2003060145-A2.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 10.1%; Score 238; DB 7; Length 691;
 Best Local Similarity 27.5%; Pred. No. 1.1e-06;
 RESULT 1359
 ID AAE36875 standard; protein; 349 AA.
 DE Argiopo aurantia major ampullate spidroin 2 (MaSp2) protein.
 PN WO2003020916-A2.
 PD 13-MAR-2003.
 PA (UYWY-) UNIV WYOMING.
 Query Match 10.1%; Score 237.5; DB 6; Length 349;
 Best Local Similarity 23.5%; Pred. No. 7e-07;
 RESULT 1360
 ID AAR80330 standard; protein; 682 AA.
 DE Protein polymeric adhesion substrate 1-C.
 PN WO9523611-A1.
 PD 08-SEP-1995.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 10.1%; Score 237.5; DB 2; Length 682;
 Best Local Similarity 28.1%; Pred. No. 1.3e-06;
 RESULT 1361
 ID AAW57670 standard; peptide; 682 AA.
 DE Collagen-like polymer.
 PN US5773249-A.
 PD 30-JUN-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 10.1%; Score 237.5; DB 2; Length 682;
 Best Local Similarity 28.1%; Pred. No. 1.3e-06;
 RESULT 1362
 ID AAW49717 standard; protein; 682 AA.
 DE Protein polymer adhesive substrate PPAS1-C.
 PN US5773577-A.
 PD 30-JUN-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 10.1%; Score 237.5; DB 2; Length 682;
 Best Local Similarity 28.1%; Pred. No. 1.3e-06;
 RESULT 1363
 ID AAG36619 standard; protein; 273 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 44903.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 10.0%; Score 237; DB 3; Length 273;
 Best Local Similarity 32.9%; Pred. No. 5.9e-07;
 RESULT 1364
 ID AAG36618 standard; protein; 309 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 44902.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 10.0%; Score 237; DB 3; Length 309;
 Best Local Similarity 32.9%; Pred. No. 6.7e-07;
 RESULT 1365
 ID ABR40002 standard; protein; 1606 AA.
 DE Human collagen XXII alternatively spliced variant protein.
 PN WO2003012121-A2.
 PD 13-FEB-2003.
 PA (GENO) GEN HOSPITAL CORP.
 Query Match 10.0%; Score 237; DB 6; Length 1606;
 Best Local Similarity 22.3%; Pred. No. 3.2e-06;
 RESULT 1366
 ID AAW53519 standard; protein; 1412 AA.
 DE Amino acid sequence of the EBSI protein.
 PN WO9810063-A1.
 PD 12-MAR-1998.
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 Query Match 10.0%; Score 236.5; DB 2; Length 1412;
 Best Local Similarity 28.0%; Pred. No. 3.1e-06;
 RESULT 1367
 ID AAP82957 standard; protein; 1413 AA.
 DE EBSI protein comprising gagags of silk fibroin and gvgvp of elastin.
 PN WO803533-A.
 PD 19-MAY-1988.
 PA (SYTR) SYNTRO CORP.
 Query Match 10.0%; Score 236.5; DB 1; Length 1413;
 Best Local Similarity 28.0%; Pred. No. 3.1e-06;
 RESULT 1368
 ID AAR41008 standard; protein; 1413 AA.

DE EBSI multimeric protein.
PN US5243038-A.
PD 07-SEP-1993.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.0%; Score 236.5; DB 2; Length 1413;
Best Local Similarity 28.0%; Pred. No. 3.1e-06;
RESULT 1369
ID AAW26343 standard; protein; 1413 AA.
DE EBSI synthetic elastomeric protein.
PN US5641648-A.
PD 24-JUN-1997.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.0%; Score 236.5; DB 2; Length 1413;
Best Local Similarity 28.0%; Pred. No. 3.1e-06;
RESULT 1370
ID AAY78278 standard; protein; 1464 AA.
DE EBSI protein sequence SEQ ID NO:74.
PN US6018030-A.
PD 25-JAN-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.0%; Score 236.5; DB 3; Length 1464;
Best Local Similarity 28.0%; Pred. No. 3.2e-06;
RESULT 1371
ID ABG69268 standard; protein; 1465 AA.
DE Elastin-like protein EBSI (not defined).
PN US6355776-B1.
PD 12-MAR-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.0%; Score 236.5; DB 5; Length 1465;
Best Local Similarity 28.0%; Pred. No. 3.2e-06;
RESULT 1372
ID ABE44969 standard; protein; 1465 AA.
DE Recombinant structural protein EBSI protein seq id 74.
PN US2003083464-A1.
PD 01-MAY-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 10.0%; Score 236.5; DB 7; Length 1465;
Best Local Similarity 28.0%; Pred. No. 3.2e-06;
RESULT 1373
ID ABG74869 standard; protein; 643 AA.
DE Human cytokeraatin-1 protein.
PN WO2003002600-A1.
PD 09-JAN-2003.
PA (BRAH-) BRAHMS AG.
Query Match 10.0%; Score 235.5; DB 6; Length 643;
Best Local Similarity 39.8%; Pred. No. 1.7e-06;
RESULT 1374
ID ADQ17549 standard; protein; 644 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 366.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.0%; Score 235.5; DB 8; Length 644;
Best Local Similarity 39.8%; Pred. No. 1.7e-06;
RESULT 1375
ID ABB65175 standard; protein; 1180 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22317.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 10.0%; Score 235.5; DB 4; Length 1180;
Best Local Similarity 26.1%; Pred. No. 3e-06;
RESULT 1376
ID AAM39077 standard; protein; 1672 AA.
DE Human polypeptide SEQ ID NO 2222.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 235.5; DB 4; Length 1672;
Best Local Similarity 26.0%; Pred. No. 4.2e-06;
RESULT 1377
ID AAB70107 standard; protein; 936 AA.
DE Gelatin protein.
PN WO2004048938-A2.
PN JP2000325095-A.
PD 28-NOV-2000.
PA (MIYA-) MIYAGI KAGAKU KOSYO KK.
PA (DAII-) DAIICHI KAKAGU YAKUHIN KK.
Query Match 9.9%; Score 235; DB 4; Length 936;
Best Local Similarity 23.9%; Pred. No. 2.6e-06;
RESULT 1378
ID ABP56960 standard; protein; 2189 AA.
DE E. maxima 250 kDa antigen homologous protein sequence SEQ ID NO:7.
PN WO2003004684-A2.
PD 16-JAN-2003.
PA (WITC/) WITCOMBE D.
PA (SMIT/) SMITH N C.
PA (WALL/) WALLACH M.
Query Match 9.9%; Score 235; DB 6; Length 2189;
Best Local Similarity 27.6%; Pred. No. 5.8e-06;
RESULT 1379
ID AAB68066 standard; protein; 510 AA.
DE Amino acid sequence of a recombinant human gelatin.
PN WO200134801-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 9.9%; Score 234.5; DB 4; Length 510;
Best Local Similarity 26.9%; Pred. No. 1.5e-06;
RESULT 1380
ID AAE02712 standard; protein; 510 AA.
DE Recombinant human gelatin #1.
PN WO200134646-A2.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 9.9%; Score 234.5; DB 4; Length 510;
Best Local Similarity 26.9%; Pred. No. 1.5e-06;
RESULT 1381
ID ADB84299 standard; protein; 510 AA.
DE Recombinant gelatin #12.
PN US2003064074-A1.
PD 03-APR-2003.
PA (CHAN/) CHANG R C.
PA (KIVI/) KIVIRIKKO K I.
PA (NEFF/) NEFF T B.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
Query Match 9.9%; Score 234.5; DB 7; Length 510;
Best Local Similarity 26.9%; Pred. No. 1.5e-06;
RESULT 1382
ID AAR80251 standard; peptide; 936 AA.
DE Polymer SELP0.
PN WO9524478-A1.
PD 14-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.9%; Score 234.5; DB 2; Length 936;
Best Local Similarity 28.5%; Pred. No. 2.7e-06;
RESULT 1383
ID ABP53472 standard; protein; 936 AA.
DE Protein polymer SELP0 polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKY B R.
Query Match 9.9%; Score 234.5; DB 5; Length 936;
Best Local Similarity 28.5%; Pred. No. 2.7e-06;
RESULT 1384
ID ABU56436 standard; protein; 2944 AA.
DE Lung cancer-associated polypeptide #29.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 9.9%; Score 234.5; DB 6; Length 2944;
Best Local Similarity 26.2%; Pred. No. 8.2e-06;
RESULT 1385
ID ADQ18966 standard; protein; 2944 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1785.
PN WO2004048938-A2.

PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.9%; Score 234.5; DB 8; Length 2944;
Best Local Similarity 26.2%; Pred. No. 8.2e-06;
RESULT 1386
ID AQQ39966 standard; protein; 2944 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1629.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.9%; Score 234.5; DB 8; Length 2944;
Best Local Similarity 26.2%; Pred. No. 8.2e-06;
RESULT 1387
ID ADN23131 standard; protein; 3507 AA.
DE Bacterial polypeptide #5784.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.9%; Score 234.5; DB 8; Length 3507;
Best Local Similarity 22.6%; Pred. No. 9.7e-06;
RESULT 1388
ID ABR40001 standard; protein; 1626 AA.
DE Human collagen XXII.
PD 13-FEB-2003.
PA (GEOH) GEN HOSPITAL CORP.
Query Match 9.9%; Score 234; DB 6; Length 1626;
Best Local Similarity 26.1%; Pred. No. 5e-06;
RESULT 1389
ID AAG36620 standard; protein; 263 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44904.
PD EPI033405-A2.
Query Match 9.9%; Score 233.5; DB 3; Length 263;
Best Local Similarity 34.9%; Pred. No. 9.4e-07;
RESULT 1390
ID AGS51723 standard; protein; 258 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65674.
PD EPI033405-A2.
Query Match 9.9%; Score 233; DB 3; Length 258;
Best Local Similarity 30.0%; Pred. No. 9.9e-07;
RESULT 1391
ID AAE36929 standard; protein; 387 AA.
DE Nephila clavipes flagelliform (flag) consensus protein.
PD 13-MAR-2003.
PA (UYWV-) UNIV WYOMING.
Query Match 9.9%; Score 233; DB 6; Length 387;
Best Local Similarity 27.1%; Pred. No. 1.5e-06;
RESULT 1392
ID AAB70182 standard; peptide; 564 AA.
DE Peptide dendrimer carrier #7.
PD 01-FEB-2001.
PA (VERD/) VERDINI A.
Query Match 9.9%; Score 233; DB 4; Length 564;
Best Local Similarity 22.9%; Pred. No. 2.1e-06;
RESULT 1393
ID ADE56670 standard; protein; 864 AA.
DE Rat Protein Q99372, SEQ ID NO 2524.
PD 27-FEB-2003.
PA (GEOH) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 9.9%; Score 233; DB 7; Length 864;
Best Local Similarity 26.0%; Pred. No. 3.1e-06;
RESULT 1394
ID AAB68065 standard; protein; 416 AA.

DE Amino acid sequence of a recombinant human gelatin.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 9.8%; Score 232.5; DB 4; Length 416;
Best Local Similarity 28.3%; Pred. No. 1.7e-06;
RESULT 1395
ID AAE02711 standard; protein; 416 AA.
DE Human alpha1(I) type I collagen helical domain (residues 615-1030).
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 9.8%; Score 232.5; DB 4; Length 416;
Best Local Similarity 28.3%; Pred. No. 1.7e-06;
RESULT 1396
ID ADB84298 standard; protein; 416 AA.
DE Recombinant gelatin #11.
PD 03-APR-2003.
PA (CHAN/) CHANG R C.
PA (KIVI/) KIVIRIKKO K I.
PA (NEFF/) NEFF T B.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
Query Match 9.8%; Score 232.5; DB 7; Length 416;
Best Local Similarity 28.3%; Pred. No. 1.7e-06;
RESULT 1397
ID ADP31594 standard; protein; 2542 AA.
DE Human secreted protein SEQ ID #2361.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 9.8%; Score 232.5; DB 8; Length 2542;
Best Local Similarity 25.1%; Pred. No. 9.5e-06;
RESULT 1398
ID AAB68057 standard; protein; 501 AA.
DE Amino acid sequence of a recombinant human gelatin.
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 9.8%; Score 232; DB 4; Length 501;
Best Local Similarity 29.7%; Pred. No. 2.2e-06;
RESULT 1399
ID AAE02703 standard; protein; 501 AA.
DE Human alpha1(I) type I collagen helical domain (residues 179-679).
PD 17-MAY-2001.
PA (FIBR-) FIBROGEN INC.
Query Match 9.8%; Score 232; DB 4; Length 501;
Best Local Similarity 29.7%; Pred. No. 2.2e-06;
RESULT 1400
ID ADB84290 standard; protein; 501 AA.
DE Recombinant gelatin #3.
PD 03-APR-2003.
PA (CHAN/) CHANG R C.
PA (KIVI/) KIVIRIKKO K I.
PA (NEFF/) NEFF T B.
PA (OLSE/) OLSEN D R.
PA (POLA/) POLAREK J W.
Query Match 9.8%; Score 232; DB 7; Length 501;
Best Local Similarity 29.7%; Pred. No. 2.2e-06;
RESULT 1401
ID ADQ39813 standard; protein; 1767 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1476.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.8%; Score 232; DB 8; Length 1767;
Best Local Similarity 24.5%; Pred. No. 7.2e-06;
RESULT 1402
ID ADQ39817 standard; protein; 1767 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1480.

PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1767;
Query Match Best Local Similarity 24.5%; Pred. No. 7.2e-06;
RESULT 1403
ID ADP65251 standard; protein; 1806 AA.
DE Human alpha 1 type XI collagen, isoform A preproprotein.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match Best Local Similarity 24.5%; Score 232; DB 7; Length 1806;
RESULT 1404
ID ADQ39816 standard; protein; 1806 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1479.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1806;
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;
RESULT 1405
ID ADQ39815 standard; protein; 1806 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1478.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1806;
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;
RESULT 1406
ID ADQ39812 standard; protein; 1818 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1475.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1818;
Query Match Best Local Similarity 24.5%; Pred. No. 7.4e-06;
RESULT 1407
ID ADQ39814 standard; protein; 1818 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1477.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1818;
Query Match Best Local Similarity 24.5%; Pred. No. 7.4e-06;
RESULT 1408
ID ADJ72165 standard; protein; 562 AA.
DE Elastic polypeptide copolymer sequence #11.
PN WO200309835-A1.
PD 04-DEC-2003.
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 562;
Query Match Best Local Similarity 29.8%; Pred. No. 2.6e-06;
RESULT 1409
ID ADO08545 standard; protein; 562 AA.
DE Elastomeric hydrophilic middle block protein SeqID 33.
PN EPI422242-A1.
PD 26-MAY-2004.
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 562;
Query Match Best Local Similarity 29.8%; Pred. No. 2.6e-06;
RESULT 1410
ID ADJ72166 standard; protein; 730 AA.
DE Elastic polypeptide copolymer sequence #12.
PN WO200309835-A1.
PD 04-DEC-2003.
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 730;
Query Match Best Local Similarity 29.8%; Pred. No. 3.3e-06;
RESULT 1411
ID ADO08547 standard; protein; 730 AA.
DE Elastomeric hydrophilic middle block protein SeqID 35.
PN EPI422242-A1.

PD 26-MAY-2004.
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 730;
Query Match Best Local Similarity 29.8%; Pred. No. 3.3e-06;
RESULT 1412
ID ADO08572 standard; protein; 1382 AA.
DE Multi-block copolymer PHP comprising elastic & plastic peptides SeqID 60.
PN EPI422242-A1.
PD 26-MAY-2004.
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 1382;
Query Match Best Local Similarity 29.8%; Pred. No. 6.1e-06;
RESULT 1413
ID ADO08565 standard; protein; 1550 AA.
DE Multi-block copolymer comprising elastomeric and plastic peptides Seq 54.
PN EPI422242-A1.
PD 26-MAY-2004.
PA (UYEM-) UNIV EMORY. 9.8%; Score 231.5; DB 8; Length 1550;
Query Match Best Local Similarity 29.8%; Pred. No. 6.8e-06;
RESULT 1414
ID ABG30822 standard; protein; 378 AA.
DE Chicken hnRNP1 protein.
PN US2002068321-A1.
PD 06-JUN-2002.
PA (NEWM/) NEWMAN S. A.
PA (BRON/) BRONSTEIN N. B. 9.8%; Score 230.5; DB 5; Length 378;
Query Match Best Local Similarity 33.5%; Pred. No. 2e-06;
RESULT 1415
ID AAM09221 standard; protein; 936 AA.
DE SELPOK-CS1 polymer.
PN WO9634618-A1.
PD 07-NOV-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 2; Length 936;
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;
RESULT 1416
ID AAY51891 standard; protein; 936 AA.
DE Plasmid pPT0370 protein fragment containing SELPOK-CS1 polymer units.
PN US6033654-A.
PD 07-MAR-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 3; Length 936;
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;
RESULT 1417
ID ABG31421 standard; protein; 936 AA.
DE SELPOK-CS1 protein encoded by plasmid pPT0370.
PN US6423333-B1.
PD 23-JUL-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 5; Length 936;
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;
RESULT 1418
ID ABW01637 standard; protein; 936 AA.
DE Plasmid pPT0370 SELPOK-CS1 polymer protein.
PN US2003104589-A1.
PD 05-JUN-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 7; Length 936;
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;
RESULT 1419
ID AAW3547 standard; protein; 937 AA.
DE Amino acid sequence of SELPOK-CS1 protein.
PN WO9810063-A1.
PD 12-MAR-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.8%; Score 230.5; DB 2; Length 937;
Query Match Best Local Similarity 27.5%; Pred. No. 4.8e-06;
RESULT 1420
ID AAE36928 standard; protein; 200 AA.
DE Araneus diadematus minor ampullate spidroin 1 consensus protein.
PN WO2003020916-A2.

PD 13-MAR-2003.
PA (UTWY-) UNIV WYOMING.
Query Match 9.7%; Score 230; DB 6; Length 200;
Best Local Similarity 29.2%; Pred. No. 1.2e-06;
RESULT 1421
ID ADP31572 standard; protein; 279 AA.
DE Human secreted protein SEQ ID #2339.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 9.7%; Score 229.5; DB 8; Length 279;
Best Local Similarity 26.1%; Pred. No. 1.8e-06;
RESULT 1422
ID ADC35283 standard; protein; 294 AA.
DE ADF-2 silk protein.
PN WO2003057727-A1.
PD 17-JUL-2003.
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.
Query Match 9.7%; Score 229.5; DB 7; Length 294;
Best Local Similarity 27.5%; Pred. No. 1.8e-06;
RESULT 1423
ID ABU19388 standard; protein; 827 AA.
DE Protein encoded by Prokaryotic essential gene #4915.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 9.7%; Score 229.5; DB 6; Length 827;
Best Local Similarity 28.7%; Pred. No. 5e-06;
RESULT 1424
ID AAY30680 standard; protein; 1574 AA.
DE Splice variant ZAP-1A protein of the human tumor suppressor gene ZAP-1.
PN WO9946276-A1.
PD 16-SEP-1999.
PA (GENO-) GENOS BIOSCIENCES INC.
Query Match 9.7%; Score 229.5; DB 2; Length 1574;
Best Local Similarity 27.9%; Pred. No. 9.2e-06;
RESULT 1425
ID ADL18527 standard; protein; 391 AA.
DE Wheat dehydrin protein SEQ ID NO:36.
PN WO2003027249-A2.
PD 03-APR-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 9.7%; Score 229; DB 7; Length 391;
Best Local Similarity 26.8%; Pred. No. 2.6e-06;
RESULT 1426
ID ADP31595 standard; protein; 3036 AA.
DE Human secreted protein SEQ ID #2362.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 9.7%; Score 229; DB 8; Length 3036;
Best Local Similarity 24.1%; Pred. No. 1.8e-05;
RESULT 1427
ID ABG93178 standard; protein; 430 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 314.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 9.7%; Score 228.5; DB 5; Length 430;
Best Local Similarity 22.8%; Pred. No. 3.1e-06;
RESULT 1428
ID ABU69145 standard; protein; 733 AA.
DE Human NOVX polypeptide #20.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.7%; Score 228.5; DB 6; Length 733;
Best Local Similarity 27.0%; Pred. No. 5.1e-06;
RESULT 1429
ID ABB63723 standard; protein; 5002 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17961.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 9.7%; Score 228.5; DB 4; Length 5002;
Best Local Similarity 27.3%; Pred. No. 3.2e-05;
RESULT 1430
ID AAG84989 standard; protein; 1389 AA.
DE Shrimp white spot Bacilliform virus (WSBV) protein 80.
PN WO200138351-A2.
PD 31-MAY-2001.
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
Query Match 9.6%; Score 228; DB 4; Length 1389;
Best Local Similarity 25.9%; Pred. No. 1e-05;
RESULT 1431
ID AAW65462 standard; protein; 485 AA.
DE Neocallimastix patriciarum endo-xylanase.
PN CA2190194-A.
PD 13-MAY-1998.
PA (LIUJ) LIU J H.
PA (SELI) SELINGER L B.
PA (MOLO) MOLONEY M M.
PA (FORS) FORSBERG C W.
PA (CHEN) CHENG K.
PA (HUYI) HU Y.
Query Match 9.6%; Score 227.5; DB 2; Length 485;
Best Local Similarity 28.4%; Pred. No. 3.9e-06;
RESULT 1432
ID AAY27283 standard; protein; 485 AA.
DE N. patriciarum xylanase.
PN US5948667-A.
PD 07-SEP-1999.
PA (MIAC) CANADA DEPT AGRICULTURE.
Query Match 9.6%; Score 227.5; DB 2; Length 485;
Best Local Similarity 28.4%; Pred. No. 3.9e-06;
RESULT 1433
ID AAB35588 standard; protein; 485 AA.
DE N. patriciarum endo-xylanase xynC.
PN US6137032-A.
PD 24-OCT-2000.
PA (MIAC) CANADA DEPT AGRICULTURE.
Query Match 9.6%; Score 227.5; DB 4; Length 485;
Best Local Similarity 28.4%; Pred. No. 3.9e-06;
RESULT 1434
ID ADJ72170 standard; protein; 528 AA.
DE Elastic polypeptide copolymer sequence #16.
PN WO2003099835-A1.
PD 04-DEC-2003.
PA (UYEM-) UNIV EMORY.
Query Match 9.6%; Score 227.5; DB 8; Length 528;
Best Local Similarity 29.7%; Pred. No. 4.3e-06;
RESULT 1435
ID ADO08555 standard; protein; 528 AA.
DE Elastomeric hydrophilic middle block protein SeqID 43.
PN EP142242-A1.
PD 26-MAY-2004.
PA (UYEM-) UNIV EMORY.
Query Match 9.6%; Score 227.5; DB 8; Length 528;
Best Local Similarity 29.7%; Pred. No. 4.3e-06;
RESULT 1436
ID ABP96315 standard; protein; 703 AA.
DE Human collagen protein SEQ ID NO:4.
PN WO2003016481-A2.
PD 27-FEB-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 9.6%; Score 227; DB 6; Length 703;
Best Local Similarity 26.8%; Pred. No. 6e-06;
RESULT 1437
ID ABP96314 standard; protein; 717 AA.
DE Human collagen protein SEQ ID NO:2.
PN WO2003016481-A2.
PD 27-FEB-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 9.6%; Score 227; DB 6; Length 717;

Best Local Similarity 26.8%; Pred. No. 6.2e-06;
RESULT 1438
ID ADF22968 standard; protein; 1181 AA.
DE PRO polypeptide SEQ ID NO:62.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 9.6%; Score 227; DB 8; Length 1181;
Best Local Similarity 26.8%; Pred. No. 9.9e-06;
RESULT 1439
ID ABP43711 standard; protein; 1497 AA.
DE Bullous pemphigoid autoantigen BP180 gene.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 9.6%; Score 227; DB 5; Length 1497;
Best Local Similarity 26.4%; Pred. No. 1.2e-05;
RESULT 1440
ID ADN24379 standard; protein; 1759 AA.
DE Bacterial polypeptide #7032.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 9.6%; Score 227; DB 8; Length 1759;
Best Local Similarity 27.9%; Pred. No. 1.5e-05;
RESULT 1441
ID ADQ39964 standard; protein; 2502 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1627.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.6%; Score 227; DB 8; Length 2502;
Best Local Similarity 26.8%; Pred. No. 2e-05;
RESULT 1442
ID ABB69041 standard; protein; 294 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33915.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.6%; Score 226.5; DB 4; Length 294;
Best Local Similarity 29.2%; Pred. No. 2.8e-06;
RESULT 1443
ID ADM16778 standard; protein; 448 AA.
DE N. patriciarum xylanase #1.
PN US2004053238-A1.
PD 18-MAR-2004.
PA (HSEU/) HSEU R.
PA (HUAN/) HUANG Y.
Query Match 9.6%; Score 226.5; DB 8; Length 448;
Best Local Similarity 28.5%; Pred. No. 4.2e-06;
RESULT 1444
ID AAB68959 standard; protein; 192 AA.
DE Zea mays root cap specific protein.
PN JP2000325081-A.
PD 28-NOV-2000.
PA (MITA) MITSUI CHEM INC.
Query Match 9.6%; Score 226; DB 4; Length 192;
Best Local Similarity 30.2%; Pred. No. 2e-06;
RESULT 1445
ID ABO52977 standard; protein; 379 AA.
DE Human spliceosome associated protein (SAP) #95.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 9.6%; Score 226; DB 6; Length 379;
Best Local Similarity 31.1%; Pred. No. 3.9e-06;
RESULT 1446
ID ADE61159 standard; protein; 379 AA.
DE Human Protein P51991, SEQ ID NO 7077.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 9.6%; Score 226; DB 7; Length 379;
Best Local Similarity 31.1%; Pred. No. 3.9e-06;
RESULT 1447
ID ABB60000 standard; protein; 945 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6792.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 9.6%; Score 226; DB 4; Length 945;
Best Local Similarity 22.1%; Pred. No. 9.2e-06;
RESULT 1448
ID ABB90760 standard; protein; 1669 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 252.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 9.6%; Score 226; DB 5; Length 1669;
Best Local Similarity 26.0%; Pred. No. 1.6e-05;
RESULT 1449
ID ABU54467 standard; protein; 1669 AA.
DE Human tumour endothelial marker TEM 31.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 9.6%; Score 226; DB 6; Length 1669;
Best Local Similarity 26.0%; Pred. No. 1.6e-05;
RESULT 1450
ID ADF90900 standard; protein; 1669 AA.
DE Human hepatic-fibrosis disease marker protein SEQ ID 362.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 9.6%; Score 226; DB 7; Length 1669;
Best Local Similarity 26.0%; Pred. No. 1.6e-05;
RESULT 1451
ID ADR87604 standard; protein; 1669 AA.
DE Human Type IV collagen alpha 1, SEQ ID 8.
PN WO2004075835-A2.
PD 10-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 9.6%; Score 226; DB 8; Length 1669;
Best Local Similarity 26.0%; Pred. No. 1.6e-05;
RESULT 1452
ID ADQ21326 standard; protein; 1678 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4146.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.6%; Score 226; DB 8; Length 1678;
Best Local Similarity 25.7%; Pred. No. 1.6e-05;
RESULT 1453
ID AAR05222 standard; protein; 2189 AA.
DE Antigen GX5401FL encoded by Eimeria tenella genomic DNA.
PN WO9000403-A.
PD 25-JAN-1990.
PA (GEMX) GENEX CORP.
Query Match 9.6%; Score 226; DB 2; Length 2189;
Best Local Similarity 27.0%; Pred. No. 2.1e-05;
RESULT 1454
ID ABR53293 standard; protein; 1113 AA.
DE Protein sequence #SEQ ID 1451.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZONE AG.
Query Match 9.5%; Score 225.5; DB 6; Length 1113;
Best Local Similarity 23.7%; Pred. No. 1.2e-05;
RESULT 1455
ID ADK63560 standard; protein; 1113 AA.

DE Disease treating protein complex-derived protein #873.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG. 9.5%; Score 225.5; DB 7; Length 1113;
Query Match
Best Local Similarity 23.7%; Pred. No. 1.2e-05;
RESULT 1456
ID A8M84430 standard; protein; 1476 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4679.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP. 9.5%; Score 225.5; DB 8; Length 1476;
Query Match
Best Local Similarity 25.4%; Pred. No. 1.5e-05;
RESULT 1457
ID AAE36930 standard; protein; 329 AA.
DE Nephila madagascariensis flagelliform (flag) consensus protein.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING. 9.5%; Score 225; DB 6; Length 329;
Query Match
Best Local Similarity 30.0%; Pred. No. 3.9e-06;
RESULT 1458
ID AAW53545 standard; protein; 378 AA.
DE Amino acid sequence of SELPOK peptide 3.
PN WO9810063-A1.
PD 12-MAR-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.5%; Score 225; DB 2; Length 378;
Query Match
Best Local Similarity 28.5%; Pred. No. 4.4e-06;
RESULT 1459
ID AAG39747 standard; protein; 174 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49227.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 29.9%; Pred. No. 2.3e-06;
RESULT 1460
ID AAM78619 standard; protein; 378 AA.
DE Human protein SEQ ID NO 1281.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC. 9.5%; Score 224.5; DB 4; Length 378;
Query Match
Best Local Similarity 30.3%; Pred. No. 4.7e-06;
RESULT 1461
ID ABE87046 standard; protein; 516 AA.
DE Human pancreatic cell protein sequence SeqID506.
PN WO2003060145-A2.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC. 9.5%; Score 224.5; DB 7; Length 516;
Query Match
Best Local Similarity 28.6%; Pred. No. 6.4e-06;
RESULT 1462
ID ADP31571 standard; protein; 252 AA.
DE Human secreted protein SEQ ID #2338.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC. 9.5%; Score 224; DB 8; Length 252;
Query Match
Best Local Similarity 27.3%; Pred. No. 3.5e-06;
RESULT 1463
ID ADA83846 standard; protein; 1497 AA.
DE Human COL17A1 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT. 9.5%; Score 224; DB 6; Length 1497;
Query Match
Best Local Similarity 26.4%; Pred. No. 1.9e-05;
RESULT 1464
ID ABB66232 standard; protein; 2309 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25488.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 9.5%; Score 224; DB 4; Length 2309;
Query Match
Best Local Similarity 23.8%; Pred. No. 2.9e-05;
RESULT 1465
ID ABO84587 standard; protein; 1475 AA.
DE Human cancer-associated protein HPI7-008.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC. 9.5%; Score 223.5; DB 8; Length 1475;
Query Match
Best Local Similarity 25.5%; Pred. No. 2e-05;
RESULT 1466
ID AAW09219 standard; protein; 378 AA.
DE SELPOK polymer.
PN WO9634618-A1.
PD 07-NOV-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 2; Length 378;
Query Match
Best Local Similarity 28.5%; Pred. No. 5.9e-06;
RESULT 1467
ID AAV51889 standard; protein; 378 AA.
DE Plasmid pPT0375 protein fragment containing SELPOK polymer units.
PN US6033654-A.
PD 07-MAR-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 3; Length 378;
Query Match
Best Local Similarity 28.5%; Pred. No. 5.9e-06;
RESULT 1468
ID ABG31419 standard; protein; 378 AA.
DE SELPOK protein encoded by plasmid pPT0375.
PN US6423333-B1.
PD 23-JUL-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 5; Length 378;
Query Match
Best Local Similarity 28.5%; Pred. No. 5.9e-06;
RESULT 1469
ID AEW01635 standard; protein; 378 AA.
DE Plasmid pPT0375 SELPOK polymer protein.
PN US2003104589-A1.
PD 05-JUN-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC. 9.4%; Score 223; DB 7; Length 378;
Query Match
Best Local Similarity 28.5%; Pred. No. 5.9e-06;
RESULT 1470
ID ADR28985 standard; protein; 976 AA.
DE Pseudomonas syringae antifreeze related protein SEQ ID NO:2.
PN WO2004072283-A1.
PD 26-AUG-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. 9.4%; Score 223; DB 8; Length 976;
Query Match
Best Local Similarity 24.8%; Pred. No. 1.5e-05;
RESULT 1471
ID ADR28997 standard; protein; 1200 AA.
DE Pseudomonas syringae antifreeze related protein SEQ ID NO:14.
PN WO2004072283-A1.
PD 26-AUG-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. 9.4%; Score 223; DB 8; Length 1200;
Query Match
Best Local Similarity 24.8%; Pred. No. 1.8e-05;
RESULT 1472
ID ADM48392 standard; protein; 821 AA.
DE Human recombinant gelatin-like polypeptide Hu-4.
PN EPI398324-A1.
PD 17-MAR-2004.
PA (FUJF) FUJI PHOTO FILM BV. 9.4%; Score 222.5; DB 8; Length 821;
Query Match
Best Local Similarity 24.3%; Pred. No. 1.3e-05;
RESULT 1473
ID AAW09223 standard; protein; 966 AA.
DE SELPOK-CS2 polymer.
PN WO9634618-A1.
PD 07-NOV-1996.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.4%; Score 222.5; DB 2; Length 966;
Best Local Similarity 26.3%; Pred. No. 1.5e-05;
RESULT 1474
ID AAY51893 standard; protein; 966 AA.
DE Plasmid pPT0373 crosslinking protein SELPOK-CS2 polymer unit.
PN US6033654-A.
PD 07-MAR-2000.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.4%; Score 222.5; DB 3; Length 966;
Best Local Similarity 26.3%; Pred. No. 1.5e-05;
RESULT 1475
ID ABG31423 standard; protein; 966 AA.
DE SELPOK-CS2 protein encoded by plasmid pPT0373.
PN US6423333-B1.
PD 23-JUL-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.4%; Score 222.5; DB 5; Length 966;
Best Local Similarity 26.3%; Pred. No. 1.5e-05;
RESULT 1476
ID ABW01639 standard; protein; 966 AA.
DE Plasmid pPT0373 SELPOK-CS2 polymer protein.
PN US2003104589-A1.
PD 05-JUN-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.4%; Score 222.5; DB 7; Length 966;
Best Local Similarity 26.3%; Pred. No. 1.5e-05;
RESULT 1477
ID ABB54168 standard; protein; 1063 AA.
DE Lactococcus lactis protein yihd.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 9.4%; Score 222.5; DB 5; Length 1063;
Best Local Similarity 24.8%; Pred. No. 1.7e-05;
RESULT 1478
ID ABO84590 standard; protein; 1472 AA.
DE Human cancer-associated protein HP17-008.5.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 9.4%; Score 222; DB 8; Length 1472;
Best Local Similarity 25.2%; Pred. No. 2.5e-05;
RESULT 1479
ID AAW40109 standard; protein; 1694 AA.
DE Human alpha-6(IV) collagen protein.
PN US5731192-A.
PD 24-MAR-1998.
PA (UYVA) UNIV YALE.
Query Match 9.4%; Score 222; DB 2; Length 1694;
Best Local Similarity 25.2%; Pred. No. 2.8e-05;
RESULT 1480
ID ABU19448 standard; protein; 979 AA.
DE Protein encoded by Prokaryotic essential gene #4975.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 9.4%; Score 221.5; DB 6; Length 979;
Best Local Similarity 26.3%; Pred. No. 1.8e-05;
RESULT 1481
ID AAB97070 standard; protein; 2058 AA.
DE Human polypeptide #3 expressed in intraabdominal adipose tissue.
PN JP2001008699-A.
PD 16-JAN-2001.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 9.4%; Score 221.5; DB 4; Length 2058;
Best Local Similarity 29.2%; Pred. No. 3.7e-05;
RESULT 1482
ID ABB69088 standard; protein; 181 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34056.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 9.3%; Score 220.5; DB 4; Length 181;
Best Local Similarity 32.9%; Pred. No. 4.1e-06;
RESULT 1483
ID ABP98825 standard; protein; 625 AA.
DE Human structural and cytoskeletal associated protein #16.
PN WO2003031940-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.3%; Score 220.5; DB 6; Length 625;
Best Local Similarity 41.2%; Pred. No. 1.4e-05;
RESULT 1484
ID ABG77177 standard; protein; 645 AA.
DE Prostate adenocarcinoma associated protein #12.
PN US2002119463-A1.
PD 29-AUG-2002.
PA (FARI/) FARIS M.
PA (TURN/) TURNER C M.
Query Match 9.3%; Score 220.5; DB 5; Length 645;
Best Local Similarity 41.2%; Pred. No. 1.4e-05;
RESULT 1485
ID ADN04309 standard; protein; 645 AA.
DE Antipsoriatic protein sequence #349.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 220.5; DB 8; Length 645;
Best Local Similarity 41.2%; Pred. No. 1.4e-05;
RESULT 1486
ID ABUS2683 standard; protein; 957 AA.
DE Human cell structure and mobility-associated protein from DKF2phfbr2_2b5.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 9.3%; Score 220; DB 4; Length 957;
Best Local Similarity 25.9%; Pred. No. 2.2e-05;
RESULT 1487
ID ADP31661 standard; protein; 1365 AA.
DE Human secreted protein SEQ ID #2428.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 9.3%; Score 220; DB 8; Length 1365;
Best Local Similarity 25.1%; Pred. No. 3.1e-05;
RESULT 1488
ID AAB37932 standard; protein; 1488 AA.
DE Human CGDD-21 protein.
PN WO2003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.3%; Score 220; DB 7; Length 1488;
Best Local Similarity 23.9%; Pred. No. 3.3e-05;
RESULT 1489
ID ADP31664 standard; protein; 1875 AA.
DE Human secreted protein SEQ ID #2431.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 9.3%; Score 220; DB 8; Length 1875;
Best Local Similarity 25.1%; Pred. No. 4.2e-05;
RESULT 1490
ID ADP31662 standard; protein; 1956 AA.
DE Human secreted protein SEQ ID #2429.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 9.3%; Score 220; DB 8; Length 1956;
Best Local Similarity 25.1%; Pred. No. 4.3e-05;
RESULT 1491
ID AAW26341 standard; protein; 168 AA.
DE Silk-like protein slpi dimer.
PN US5641648-A.
PD 24-JUN-1997.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 9.3%; Score 219.5; DB 2; Length 168;
Best Local Similarity 33.8%; Pred. No. 4.4e-06;
RESULT 1492
ID ABG69263 standard; protein; 168 AA.
DE Silk-like protein encoded by DNA clone PSY708 #2.
PN USG35776-B1.
PD 12-MAR-2002.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.3%; Score 219.5; DB 5; Length 168;
Best Local Similarity 33.8%; Pred. No. 4.4e-06;
RESULT 1493
ID ADE44947 standard; protein; 168 AA.
DE Silk fibroin protein repeating peptide related peptide 'seq id 52'.
PN US2003083464-A1.
PD 01-MAY-2003.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.3%; Score 219.5; DB 7; Length 168;
Best Local Similarity 33.8%; Pred. No. 4.4e-06;
RESULT 1494
ID ADM48391 standard; protein; 617 AA.
DE Human recombinant gelatin-like polypeptide Hu-3.
PN EP1398324-A1.
PD 17-MAR-2004.
PA (FUJF) FUJI PHOTO FILM BV.
Query Match 9.3%; Score 219.5; DB 8; Length 617;
Best Local Similarity 26.4%; Pred. No. 1.5e-05;
RESULT 1495
ID ADO26217 standard; protein; 617 AA.
DE Human gelatine-like polypeptide Hu-3.
PN WO2004056976-A2.
PD 08-JUL-2004.
PA (FUJF) FUJI PHOTO FILM BV.
Query Match 9.3%; Score 219.5; DB 8; Length 617;
Best Local Similarity 26.4%; Pred. No. 1.5e-05;
RESULT 1496
ID ADO08293 standard; protein; 733 AA.
DE Human NOVX polypeptide #20.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILT/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 9.3%; Score 219.5; DB 8; Length 733;
Best Local Similarity 26.5%; Pred. No. 1.8e-05;
RESULT 1497
ID AAR80334 standard; protein; 829 AA.
DE Protein polymeric adhesion substrate 1-F.

PN WO9523611-A1.
PD 08-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.3%; Score 219.5; DB 2; Length 829;
Best Local Similarity 29.4%; Pred. No. 2e-05;
RESULT 1498
ID AAW57673 standard; peptide; 829 AA.
DE Collagen-like polymer.
PN US5773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.3%; Score 219.5; DB 2; Length 829;
Best Local Similarity 29.4%; Pred. No. 2e-05;
RESULT 1499
ID AAW49723 standard; protein; 829 AA.
DE Protein polymer adhesive substrate PPASI-F.
PN US5773577-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 9.3%; Score 219.5; DB 2; Length 829;
Best Local Similarity 29.4%; Pred. No. 2e-05;
RESULT 1500
ID ADB70380 standard; protein; 1019 AA.
DE Collagen VI SEQ ID NO:72.
PN WO2003021229-A2.
PD 13-MAR-2003.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 9.3%; Score 219.5; DB 7; Length 1019;
Best Local Similarity 29.3%; Pred. No. 2.5e-05;

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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:03:25 ; Search time 44 Seconds
(without alignments)
746.491 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 2363

Sequence: 1 MKPQGPLACLLALLCLGSGE.....KLGFINDAINKQRRSRIP 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669	28.3	230	4	US-09-673-395A-256
2	402.5	17.0	1136	3	US-08-806-029-9
3	402.5	17.0	1177	1	US-07-609-716-31
4	402.5	17.0	1177	1	US-08-175-155-29
5	402.5	17.0	1177	1	US-08-477-509B-64
6	402.5	17.0	1177	2	US-08-707-237A-35
7	402.5	17.0	1177	3	US-08-482-085B-64
8	402.5	17.0	1177	3	US-08-475-411A-31
9	402.5	17.0	1177	3	US-08-478-029A-31
10	402.5	17.0	1177	3	US-09-444-791A-64
11	399	16.9	1059	2	US-08-175-155-48
12	399	16.9	1059	2	US-08-707-237A-54
13	399	16.9	1059	3	US-08-806-029-10
14	399	16.9	1101	1	US-08-477-509B-83
15	399	16.9	1101	3	US-08-482-085B-83
16	399	16.9	1101	3	US-09-444-791A-83
17	383	16.2	641	4	US-09-249-585A-3
18	383	16.2	641	4	US-09-410-399-4
19	376.5	15.9	1038	1	US-07-609-716-36
20	376.5	15.9	1038	3	US-08-475-411A-36
21	376.5	15.9	1038	3	US-08-478-029A-36
22	373	15.8	745	2	US-09-010-928B-28
23	373	15.8	870	2	US-09-010-928B-2
24	371	15.7	651	3	US-08-556-978B-19
25	371	15.7	651	3	US-09-247-806-1
26	371	15.7	651	3	US-09-863-859-1
27	371	15.7	718	1	US-08-425-069-2

Sequence 2, Appli	2	US-08-317-844B-2	718	15.7	371
Sequence 3, Appli	3	US-09-034-177-3	747	15.7	371
Sequence 94, Appli	1	US-08-477-509B-94	1011	15.5	367
Sequence 94, Appli	3	US-08-482-085B-94	1011	15.5	367
Sequence 94, Appli	3	US-09-444-791A-94	1011	15.5	367
Sequence 59, Appli	1	US-08-175-155-59	1170	15.5	367
Sequence 66, Appli	2	US-08-707-237A-66	1170	15.5	367
Sequence 53, Appli	1	US-08-175-155-53	766	15.5	366
Sequence 88, Appli	2	US-08-477-509B-88	766	15.5	366
Sequence 61, Appli	2	US-08-707-237A-61	766	15.5	366
Sequence 88, Appli	3	US-08-482-085B-88	766	15.5	366
Sequence 88, Appli	3	US-09-444-791A-88	766	15.5	366
Sequence 89, Appli	1	US-08-477-509B-89	979	15.5	366
Sequence 89, Appli	3	US-08-482-085B-89	979	15.5	366
Sequence 89, Appli	3	US-09-444-791A-89	979	15.5	366
Sequence 54, Appli	1	US-08-175-155-54	1050	15.5	366
Sequence 4, Appli	2	US-09-010-928B-4	907	15.4	364.5
Sequence 80, Appli	3	US-09-444-791A-80	2018	15.4	364.5
Sequence 80, Appli	3	US-08-477-509B-80	2100	15.4	364.5
Sequence 80, Appli	3	US-08-482-085B-80	2100	15.4	364.5
Sequence 49, Appli	1	US-07-609-716-49	649	15.4	364
Sequence 49, Appli	3	US-08-475-411A-49	649	15.4	364
Sequence 49, Appli	3	US-08-478-029A-49	649	15.4	364
Sequence 48, Appli	1	US-07-609-716-48	784	15.4	364
Sequence 48, Appli	3	US-08-475-411A-48	784	15.4	364
Sequence 11, Appli	1	US-08-089-862-11	1018	15.4	364
Sequence 18, Appli	1	US-08-587-333-18	1018	15.4	364
Sequence 15, Appli	5	PCT-US94-07776-16	1018	15.4	364
Sequence 45, Appli	1	US-08-175-155-45	2107	15.4	364
Sequence 51, Appli	2	US-08-707-237A-51	2107	15.4	364
Sequence 63, Appli	3	US-08-556-978B-63	604	15.3	362
Sequence 41, Appli	1	US-07-609-716-41	1332	15.3	362
Sequence 41, Appli	3	US-08-475-411A-41	1332	15.3	362
Sequence 41, Appli	3	US-08-478-029A-41	1332	15.3	362
Sequence 46, Appli	1	US-08-175-155-46	2055	15.2	358.5
Sequence 81, Appli	1	US-08-477-509B-81	2055	15.2	358.5
Sequence 52, Appli	2	US-08-707-237A-52	2055	15.2	358.5
Sequence 81, Appli	3	US-08-482-085B-81	2055	15.2	358.5
Sequence 81, Appli	3	US-09-444-791A-81	2055	15.2	358.5
Sequence 21, Appli	3	US-08-556-978B-21	606	15.2	358
Sequence 23, Appli	3	US-08-556-978B-23	606	15.2	358
Sequence 6, Appli	3	US-09-247-806-6	606	15.2	358
Sequence 8, Appli	3	US-09-247-806-8	606	15.2	358
Sequence 13, Appli	4	US-09-863-859-13	809	15.2	358
Sequence 22, Appli	4	US-09-863-859-22	818	15.2	358
Sequence 14, Appli	4	US-09-863-859-14	1617	15.2	358
Sequence 6, Appli	1	US-08-089-862-6	945	15.0	354
Sequence 11, Appli	1	US-08-587-333-13	945	15.0	354
Sequence 6, Appli	5	PCT-US94-07776-11	945	15.0	354
Sequence 29, Appli	1	US-08-212-237-6	1056	14.9	351.5
Sequence 6, Appli	3	US-08-806-029-29	1056	14.9	351.5
Sequence 47, Appli	5	PCT-US95-02772-6	1056	14.9	351.5
Sequence 82, Appli	1	US-08-175-155-47	2257	14.8	350.5
Sequence 53, Appli	2	US-08-477-509B-82	2257	14.8	350.5
Sequence 82, Appli	1	US-08-707-237A-53	2257	14.8	350.5
Sequence 82, Appli	3	US-08-482-085B-82	2257	14.8	350.5
Sequence 997, App	3	US-09-444-791A-82	2257	14.8	350.5
Sequence 8, Appli	4	US-09-538-092-997	316	14.8	350
Sequence 2, Appli	4	US-08-209-747-2	528	14.7	348
Sequence 2, Appli	4	US-08-458-298-2	832	14.7	348
Sequence 4, Appli	4	US-09-490-291-4	832	14.7	348
Sequence 6, Appli	4	US-09-490-291-6	691	14.5	343
Sequence 33, Appli	4	US-08-806-029-33	691	14.5	343
Sequence 728, App	3	US-09-060-756-728	1169	13.9	336
Sequence 728, App	3	US-09-670-314-728	334	13.9	327.5
Sequence 7, Appli	4	US-08-212-237-7	334	13.9	327.5
Sequence 30, Appli	1	US-08-806-029-30	972	13.6	322.5
Sequence 7, Appli	3	PCT-US95-02772-7	972	13.6	322.5
Sequence 727, App	3	US-09-060-756-727	318	13.5	319.5

101	319.5	13.5	318	4	US-09-670-314-727	Sequence 727, App	174	268	11.3	762	1	US-08-397-633A-31	Sequence 31, Appl
102	317.5	13.4	988	1	US-08-212-237-5	Sequence 5, Appl	175	267.5	11.3	1024	3	US-08-931-820-2	Sequence 2, Appl
103	317.5	13.4	988	3	US-08-806-029-28	Sequence 28, Appl	176	267.5	11.3	1366	3	US-08-963-825-19	Sequence 19, Appl
104	317.5	13.4	988	5	PCT-US95-02772-5	Sequence 5, Appl	177	267.5	11.3	1366	3	US-09-500-811-19	Sequence 19, Appl
105	309.5	13.1	200	4	US-09-989-981A-13	Sequence 13, Appl	178	267.5	11.3	1366	3	US-09-570-573-19	Sequence 19, Appl
106	309	13.1	201	3	US-09-052-995-1	Sequence 1, Appl	179	267.5	11.3	1366	3	US-09-548-608-19	Sequence 19, Appl
107	309	13.1	201	3	US-09-053-003-40	Sequence 40, Appl	180	264.5	11.2	1008	3	US-09-219-849-8	Sequence 8, Appl
108	309	13.1	201	4	US-09-054-281-22	Sequence 22, Appl	181	264.5	11.2	1065	1	US-08-642-255-80	Sequence 80, Appl
109	309	13.1	201	4	US-09-478-948-6	Sequence 6, Appl	182	264.5	11.2	1065	3	US-08-642-246-16	Sequence 16, Appl
110	309	13.1	201	4	US-09-818-094-40	Sequence 40, Appl	183	264.5	11.2	1065	3	US-09-451-206-16	Sequence 16, Appl
111	309	13.1	201	4	US-09-754-947-5	Sequence 5, Appl	184	264.5	11.2	1065	5	PCT-US96-06229-16	Sequence 16, Appl
112	308	13.0	235	2	US-08-829-190B-1	Sequence 1, Appl	185	264	11.2	269	1	US-08-452-531-4	Sequence 4, Appl
113	304.5	12.9	889	3	US-08-806-029-19	Sequence 19, Appl	186	264	11.2	269	2	US-08-460-746A-4	Sequence 4, Appl
114	302	12.8	714	3	US-08-556-978B-61	Sequence 61, Appl	187	264	11.2	269	2	US-08-460-555-4	Sequence 4, Appl
115	302	12.8	714	3	US-09-247-806-10	Sequence 10, Appl	188	264	11.2	269	3	US-08-460-066-4	Sequence 4, Appl
116	300.5	12.7	768	3	US-08-806-029-35	Sequence 35, Appl	189	257	10.9	633	1	US-08-642-255-73	Sequence 73, Appl
117	300.5	12.7	884	1	US-08-397-633A-68	Sequence 68, Appl	190	257	10.9	1065	3	US-08-642-255-72	Sequence 72, Appl
118	300.5	12.7	884	2	US-08-435-641-15	Sequence 15, Appl	191	254	10.7	1040	3	US-08-806-029-32	Sequence 32, Appl
119	300.5	12.7	884	2	US-08-707-237A-96	Sequence 96, Appl	192	254	10.7	1745	4	US-09-795-061-4	Sequence 4, Appl
120	300.5	12.7	884	3	US-08-642-246-15	Sequence 15, Appl	193	253	10.7	1060	3	US-08-931-820-3	Sequence 3, Appl
121	300.5	12.7	884	4	US-09-451-206-15	Sequence 15, Appl	194	253	10.7	1077	1	US-07-972-032-82	Sequence 82, Appl
122	300.5	12.7	884	5	PCT-US96-06229-15	Sequence 15, Appl	195	253	10.7	1077	1	US-08-642-255-95	Sequence 95, Appl
123	300	12.7	738	3	US-08-864-038A-3	Sequence 3, Appl	196	253	10.7	1418	3	US-08-963-825-20	Sequence 20, Appl
124	296.5	12.5	1024	1	US-08-212-237-8	Sequence 8, Appl	197	253	10.7	1418	3	US-09-010-999-1	Sequence 1, Appl
125	296.5	12.5	1024	3	US-08-806-029-31	Sequence 31, Appl	198	253	10.7	1418	3	US-09-500-811-20	Sequence 20, Appl
126	296.5	12.5	1024	5	PCT-US95-02772-8	Sequence 8, Appl	199	253	10.7	1418	3	US-09-570-573-20	Sequence 20, Appl
127	296	12.5	595	1	US-08-425-069-4	Sequence 4, Appl	200	253	10.7	1418	3	US-09-548-608-20	Sequence 20, Appl
128	296	12.5	595	2	US-08-317-844B-4	Sequence 4, Appl	201	251.5	10.6	462	4	US-09-919-039-324	Sequence 324, App
129	294.5	12.5	832	1	US-08-212-237-4	Sequence 4, Appl	202	248.5	10.5	1442	2	US-08-316-650-12	Sequence 12, Appl
130	294.5	12.5	832	3	US-08-806-029-27	Sequence 27, Appl	203	248.5	10.5	1442	5	PCT-US95-02251-12	Sequence 12, Appl
131	294.5	12.5	832	5	PCT-US95-02772-4	Sequence 4, Appl	204	247.5	10.5	419	4	US-09-270-767-41767	Sequence 41767, A
132	294	12.4	493	3	US-08-556-978B-59	Sequence 59, Appl	205	247.5	10.5	943	4	US-09-477-135A-131	Sequence 131, App
133	294	12.4	529	3	US-09-247-806-2	Sequence 2, Appl	206	247.5	10.5	1739	4	US-09-795-061-2	Sequence 2, Appl
134	294	12.4	674	1	US-08-317-522A-3	Sequence 3, Appl	207	247	10.5	975	4	US-09-328-352-4764	Sequence 4764, Ap
135	294	12.4	674	1	US-08-439-818A-3	Sequence 3, Appl	208	246.5	10.4	448	4	US-09-248-796A-19135	Sequence 19135, A
136	294	12.4	674	2	US-08-751-965-3	Sequence 3, Appl	209	246.5	10.4	556	4	US-09-248-796A-22338	Sequence 22338, A
137	294	12.4	674	2	US-08-738-975-3	Sequence 3, Appl	210	246.5	10.4	595	3	US-09-219-849-48	Sequence 48, Appl
138	294	12.4	674	2	US-08-728-626-3	Sequence 3, Appl	211	246.5	10.4	595	3	US-09-219-849-50	Sequence 50, Appl
139	294	12.4	674	3	US-08-808-599A-3	Sequence 3, Appl	212	246.5	10.4	822	3	US-09-219-849-49	Sequence 49, Appl
140	290.5	12.3	749	1	US-08-317-522A-2	Sequence 2, Appl	213	246.5	10.4	1057	3	US-08-931-820-1	Sequence 1, Appl
141	290.5	12.3	749	1	US-08-439-818A-2	Sequence 2, Appl	214	246.5	10.4	1341	3	US-08-963-825-18	Sequence 18, Appl
142	290.5	12.3	749	2	US-08-751-965-2	Sequence 2, Appl	215	246.5	10.4	1341	3	US-09-500-811-18	Sequence 18, Appl
143	290.5	12.3	749	2	US-08-738-975-2	Sequence 2, Appl	216	246.5	10.4	1341	3	US-09-570-573-18	Sequence 18, Appl
144	290.5	12.3	749	2	US-08-728-626-2	Sequence 2, Appl	217	246.5	10.4	1341	3	US-09-548-608-18	Sequence 18, Appl
145	290.5	12.3	749	3	US-08-808-599A-2	Sequence 2, Appl	218	246.5	10.4	1358	1	US-07-945-283-2	Sequence 2, Appl
146	288.5	12.2	877	1	US-08-397-633A-54	Sequence 54, Appl	219	245	10.4	907	4	US-09-949-016-9750	Sequence 9750, Ap
147	288.5	12.2	953	3	US-08-806-029-14	Sequence 14, Appl	220	245	10.4	907	4	US-09-949-016-9751	Sequence 9751, Ap
148	283.5	12.0	401	3	US-09-219-849-34	Sequence 34, Appl	221	244.5	10.3	492	4	US-08-468-996-11	Sequence 11, Appl
149	283.5	12.0	599	4	US-09-602-459-23	Sequence 23, Appl	222	244.5	10.3	1002	2	US-08-707-237A-103	Sequence 103, App
150	283.5	12.0	599	4	US-09-602-459-23	Sequence 23, Appl	223	244.5	10.3	1002	4	US-08-642-246-25	Sequence 25, Appl
151	283	12.0	1160	3	US-08-808-599A-24	Sequence 24, Appl	224	244.5	10.3	1002	4	US-09-451-206-25	Sequence 25, Appl
152	280	11.8	1057	3	US-08-931-820-4	Sequence 4, Appl	225	244.5	10.3	1002	5	PCT-US96-06229-25	Sequence 25, Appl
153	278.5	11.8	526	4	US-09-538-092-1080	Sequence 1080, Ap	226	244.5	10.3	1464	4	US-09-331-347C-21	Sequence 21, Appl
154	276	11.7	231	4	US-09-248-796A-14281	Sequence 14281, A	227	244	10.3	492	4	US-08-468-996-12	Sequence 12, Appl
155	276	11.7	1078	3	US-08-963-825-21	Sequence 21, Appl	228	243	10.3	1017	4	US-08-468-996-10	Sequence 10, Appl
156	276	11.7	1078	3	US-09-500-811-21	Sequence 21, Appl	229	242.5	10.3	955	4	US-09-949-016-8369	Sequence 8369, Ap
157	276	11.7	1078	3	US-09-570-573-21	Sequence 21, Appl	230	241.5	10.2	1461	4	US-09-585-887-9	Sequence 9, Appl
158	276	11.7	1078	3	US-09-548-608-21	Sequence 21, Appl	231	241.5	10.2	1461	4	US-09-289-578-9	Sequence 9, Appl
159	276	11.7	1366	4	US-09-585-887-10	Sequence 10, Appl	232	240.5	10.2	250	4	US-09-248-796A-22487	Sequence 22487, A
160	276	11.7	1366	4	US-09-289-578-10	Sequence 10, Appl	233	240.5	10.2	943	3	US-09-056-556-204	Sequence 204, App
161	276	11.7	1366	4	US-09-949-016-5882	Sequence 5882, Ap	234	240.5	10.2	943	4	US-09-072-596-199	Sequence 199, App
162	275	11.6	482	4	US-09-302-540-14708	Sequence 14708, A	235	240.5	10.2	943	4	US-09-072-967-204	Sequence 204, App
163	274	11.6	593	4	US-09-538-092-919	Sequence 919, App	236	239	10.1	960	3	US-09-219-849-6	Sequence 6, Appl
164	273	11.6	486	1	US-08-397-633A-77	Sequence 77, Appl	237	239	10.1	1806	4	US-09-919-497-56	Sequence 56, Appl
165	272.5	11.5	479	1	US-08-397-633A-78	Sequence 78, Appl	238	237.5	10.1	682	1	US-08-642-255-136	Sequence 136, App
166	272.5	11.5	619	4	US-09-252-991A-26352	Sequence 26352, A	239	237.5	10.1	682	1	US-08-397-633A-36	Sequence 36, Appl
167	272	11.5	291	4	US-09-490-291-2	Sequence 2, Appl	240	236.5	10.0	1413	2	US-08-175-155-39	Sequence 39, Appl
168	272	11.5	656	3	US-08-806-029-36	Sequence 36, Appl	241	236.5	10.0	1413	2	US-08-707-237A-45	Sequence 45, Appl
169	272	11.5	750	3	US-08-806-029-25	Sequence 25, Appl	242	236.5	10.0	1464	1	US-08-477-508B-74	Sequence 74, Appl
170	271	11.5	761	2	US-08-707-237A-84	Sequence 84, Appl	243	236.5	10.0	1464	3	US-08-482-085B-74	Sequence 74, Appl
171	271	11.5	762	1	US-08-642-255-114	Sequence 114, App	244	236.5	10.0	1465	3	US-09-444-791A-74	Sequence 74, Appl
172	271	11.5	762	1	US-08-397-633A-26	Sequence 26, Appl	245	236	10.0	508	4	US-09-270-767-46233	Sequence 46233, A
173	268	11.3	762	1	US-08-642-255-120	Sequence 120, App	246	236	10.0	552	3	US-09-219-849-7	Sequence 7, Appl

247	235.5	10.0	643	4	US-09-538-092-844	Sequence 844, App	320	206	8.7	417	1	US-08-477-509B-104	Sequence 104, App
248	234.5	9.9	936	1	US-08-212-237-3	Sequence 3, Appli	321	206	8.7	417	1	US-08-642-255-102	Sequence 102, App
249	234.5	9.9	936	2	US-08-806-029-26	Sequence 26, Appl	322	206	8.7	417	1	US-08-707-237A-76	Sequence 76, Appl
250	234.5	9.9	936	5	PCT-US95-02772-3	Sequence 3, Appli	323	206	8.7	417	3	US-08-482-085B-104	Sequence 104, App
251	232.5	9.8	536	1	US-09-270-767-43766	Sequence 43766, A	324	206	8.7	417	3	US-09-444-791A-104	Sequence 104, App
252	231.5	9.8	100	4	US-09-411-067C-4	Sequence 4, Appli	325	206	8.7	837	1	US-08-175-155-68	Sequence 68, Appl
253	231.5	9.8	2088	4	US-09-548-367D-13	Sequence 13, Appl	326	206	8.7	837	1	US-08-477-509B-103	Sequence 103, App
254	231.5	9.8	2088	4	US-09-548-367D-13	Sequence 13, Appl	327	206	8.7	837	1	US-08-642-255-101	Sequence 101, App
255	231.5	9.8	2088	4	US-09-551-853D-13	Sequence 13, Appl	328	206	8.7	837	3	US-08-707-237A-75	Sequence 75, Appl
256	231.5	9.8	2088	4	US-09-548-376D-13	Sequence 13, Appl	329	206	8.7	837	3	US-08-482-085B-103	Sequence 103, App
257	231.5	9.8	2088	4	US-09-548-373D-13	Sequence 13, Appl	330	206	8.7	837	3	US-08-482-085B-103	Sequence 103, App
258	231.5	9.8	2088	4	US-09-548-366P-13	Sequence 13, Appl	331	206	8.7	837	3	US-09-444-791A-103	Sequence 103, App
259	231.5	9.8	2088	4	US-09-548-368P-13	Sequence 13, Appl	332	206	8.7	837	3	US-08-397-633A-50	Sequence 50, Appl
260	230.5	9.8	936	2	US-08-707-237A-108	Sequence 108, App	333	205.5	8.7	1516	4	US-09-949-016-8209	Sequence 8209, Ap
261	230.5	9.8	936	3	US-08-642-246-30	Sequence 30, Appl	334	205.5	8.7	489	2	US-08-794-795-7	Sequence 7, Appli
262	230.5	9.8	936	4	US-09-451-206-30	Sequence 30, Appl	335	205.5	8.7	489	3	US-09-249-200-7	Sequence 2, Appli
263	230.5	9.8	936	5	PCT-US96-06229-30	Sequence 30, Appl	336	205.5	8.7	518	1	US-08-392-367B-2	Sequence 2, Appli
264	229.5	9.7	857	4	US-09-902-540-12312	Sequence 12312, A	337	205	8.7	518	3	US-08-893-467A-2	Sequence 4, Appli
265	227.5	9.6	485	2	US-08-749-391-2	Sequence 2, Appli	338	205	8.7	187	4	US-09-680-175-4	Sequence 4, Appli
266	227.5	9.6	485	3	US-09-390-200-2	Sequence 2, Appli	339	205	8.7	228	3	US-09-219-849-38	Sequence 38, Appl
267	224.5	9.5	748	3	US-09-219-849-10	Sequence 10, Appl	340	205	8.7	1415	4	US-09-252-991A-26438	Sequence 26438, A
268	223	9.4	378	2	US-08-707-237A-104	Sequence 104, App	341	203.5	8.6	1603	4	US-09-949-016-6136	Sequence 6136, A
269	223	9.4	378	3	US-08-642-246-26	Sequence 26, Appl	342	203	8.6	688	4	US-09-902-540-10297	Sequence 10297, A
270	223	9.4	378	4	US-09-451-206-26	Sequence 26, Appl	343	201.5	8.5	1259	4	US-09-949-016-10366	Sequence 10366, A
271	223	9.4	378	5	PCT-US96-06229-26	Sequence 26, Appl	344	201.5	8.5	123	4	US-09-072-596-243	Sequence 243, App
272	222.5	9.4	966	3	US-08-642-246-34	Sequence 34, Appl	345	201.5	8.5	123	4	US-09-072-596-248	Sequence 248, App
273	222.5	9.4	966	4	US-09-451-206-34	Sequence 34, Appl	346	201.5	8.5	312	3	US-08-806-029-34	Sequence 34, Appl
274	222.5	9.4	966	5	PCT-US96-06229-34	Sequence 34, Appl	347	201.5	8.5	433	4	US-09-524-101D-20	Sequence 20, Appl
275	222.5	9.4	1343	4	US-09-949-016-10641	Sequence 10641, A	348	201	8.5	684	4	US-09-949-016-8348	Sequence 8348, Ap
276	222	9.4	412	4	US-09-248-796A-26345	Sequence 26345, A	349	200.5	8.5	1712	4	US-09-961-403-9	Sequence 9, Appli
277	222	9.4	637	4	US-09-949-016-8152	Sequence 8152, Ap	350	200.5	8.5	341	2	US-08-538-711A-8	Sequence 8, Appli
278	222	9.4	1694	1	US-08-494-168-2	Sequence 2, Appli	351	200.5	8.5	341	3	US-08-725-027-8	Sequence 8, Appli
279	220.5	9.3	645	4	US-09-919-172-41	Sequence 41, Appl	352	200.5	8.5	341	4	US-09-542-552-8	Sequence 8, Appli
280	219.5	9.3	168	3	US-09-444-791A-52	Sequence 52, Appl	353	200.5	8.5	353	2	US-08-538-711A-7	Sequence 7, Appli
281	219.5	9.3	829	1	US-08-642-255-132	Sequence 132, App	354	200.5	8.5	353	4	US-08-725-027-7	Sequence 7, Appli
282	219.5	9.3	829	1	US-08-397-633A-53	Sequence 53, Appl	355	200.5	8.5	353	4	US-09-542-552-7	Sequence 7, Appli
283	219	9.3	274	4	US-09-976-594-417	Sequence 417, App	356	200.5	8.5	353	4	US-09-538-092-989	Sequence 989, App
284	218.5	9.2	378	4	US-10-164-595-2	Sequence 2, Appli	357	200.5	8.5	410	4	US-09-949-016-10345	Sequence 10345, A
285	217.5	9.2	495	2	US-08-794-795-2	Sequence 2, Appli	358	199	8.4	541	4	US-09-248-796A-26119	Sequence 26119, A
286	217.5	9.2	495	3	US-09-249-200-2	Sequence 2, Appli	359	199	8.4	599	4	US-09-949-016-8890	Sequence 8890, Ap
287	217	9.2	295	4	US-09-248-796A-25715	Sequence 25715, A	360	199	8.4	825	4	US-10-210-428-1	Sequence 1, Appli
288	216.5	9.2	595	4	US-09-370-838-187	Sequence 187, App	361	199	8.4	825	4	US-10-237-551-161	Sequence 161, App
289	216.5	9.2	595	4	US-09-854-133-187	Sequence 133, App	362	199	8.4	825	4	US-09-894-998A-47	Sequence 47, Appl
290	216.5	9.2	684	1	US-08-555-669-12	Sequence 12, Appl	363	199	8.4	826	4	US-10-237-551-47	Sequence 47, Appl
291	216.5	9.2	684	3	US-09-073-663-12	Sequence 12, Appl	364	198.5	8.4	547	1	US-08-494-168-7	Sequence 7, Appli
292	216.5	9.2	2090	4	US-09-538-092-1081	Sequence 1081, App	365	198	8.4	541	4	US-09-538-092-347	Sequence 347, App
293	216.5	9.2	2120	4	US-09-949-016-9768	Sequence 9768, Ap	366	197.5	8.4	464	4	US-09-252-991A-24883	Sequence 24883, A
294	215.5	9.1	520	2	US-08-794-795-6	Sequence 6, Appli	367	197	8.3	1078	4	US-09-949-016-11185	Sequence 11185, A
295	215.5	9.1	520	3	US-09-249-200-6	Sequence 6, Appli	368	197	8.3	1143	4	US-09-949-016-6137	Sequence 6137, Ap
296	215	9.1	390	1	US-08-106-981-4	Sequence 4, Appli	369	195.5	8.3	279	3	US-09-010-999-2	Sequence 2, Appli
297	215	9.1	479	3	US-09-177-349-3	Sequence 3, Appli	370	195	8.3	146	1	US-07-609-716-105	Sequence 105, App
298	215	9.1	479	4	US-09-918-951-3	Sequence 3, Appli	371	195	8.3	146	3	US-08-475-411A-105	Sequence 105, App
299	215	9.1	1218	4	US-09-949-016-7065	Sequence 7065, Ap	372	195	8.3	146	3	US-08-478-028A-105	Sequence 105, App
300	215	9.1	1319	4	US-09-538-092-1291	Sequence 1291, Ap	373	195	8.3	281	1	US-08-397-633A-75	Sequence 75, Appl
301	215	9.1	1690	4	US-09-949-016-5884	Sequence 5884, Ap	374	194.5	8.2	166	4	US-09-841-334A-21	Sequence 21, Appl
302	214	9.1	406	4	US-09-949-016-9243	Sequence 9243, Ap	375	194.5	8.2	166	4	US-09-837-969A-21	Sequence 21, Appl
303	213.5	9.0	310	3	US-09-219-849-47	Sequence 47, Appl	376	194.5	8.2	442	4	US-09-248-796A-21400	Sequence 21400, A
304	213.5	9.0	1670	4	US-09-949-016-5883	Sequence 5883, Ap	377	194.5	8.2	1268	4	US-09-949-016-7487	Sequence 7487, Ap
305	213	9.0	529	4	US-09-381-656-1	Sequence 1, Appli	378	193	8.2	359	4	US-09-270-767-43751	Sequence 43751, A
306	212.5	9.0	347	4	US-09-623-397-1	Sequence 5, Appli	379	192	8.1	623	3	US-09-029-348-3	Sequence 3, Appli
307	212	9.0	100	4	US-09-411-067C-5	Sequence 5, Appli	380	192	8.1	744	4	US-09-949-016-9607	Sequence 9607, Ap
308	211	8.9	371	4	US-09-538-092-884	Sequence 884, App	381	192	8.1	1345	2	US-08-977-767-3	Sequence 3, Appli
309	210.5	8.9	262	1	US-08-397-633A-73	Sequence 73, Appl	382	191.5	8.1	160	3	US-08-542-051-18	Sequence 18, Appl
310	210	8.9	1609	4	US-09-949-016-10910	Sequence 10910, A	383	191.5	8.1	644	4	US-09-919-039-121	Sequence 121, App
311	209.5	8.9	333	2	US-08-687-702-37	Sequence 37, Appl	384	191.5	8.1	847	4	US-09-373-157-4	Sequence 4, Appli
312	209.5	8.9	1034	4	US-09-252-991A-26658	Sequence 26658, A	385	191.5	8.1	875	4	US-09-949-016-8582	Sequence 8582, Ap
313	208.5	8.8	435	4	US-09-902-540-12731	Sequence 12731, A	386	190.5	8.1	637	4	US-09-248-796A-19134	Sequence 19134, A
314	208	8.8	689	4	US-09-949-016-11276	Sequence 11276, A	387	190.5	8.1	2870	4	US-09-479-467A-15	Sequence 15, Appl
315	208	8.8	1064	1	US-08-642-255-62	Sequence 62, Appl	388	190.5	8.1	3178	4	US-09-479-467A-4	Sequence 4, Appli
316	207	8.8	680	4	US-09-949-001-15	Sequence 15, Appl	389	190	8.0	276	3	US-08-506-553C-26	Sequence 26, Appli
317	207	8.8	680	4	US-09-949-001-20	Sequence 20, Appl	390	190	8.0	344	1	US-08-891-254-7	Sequence 7, Appli
318	206.5	8.7	938	4	US-09-949-016-9992	Sequence 9992, Ap	391	190	8.0	344	2	US-08-819-539-7	Sequence 7, Appli
319	206	8.7	417	1	US-08-175-155-69	Sequence 69, Appl	392	190	8.0	344	2	US-09-030-270A-7	Sequence 7, Appli

393	190	8.0	344	3	US-08-984-207-7	Sequence 7, Appli	466	171.5	7.3	1127	3	US-09-150-460B-11	Sequence 11, Appli
394	190	8.0	344	3	US-09-013-587-7	Sequence 7, Appli	467	171.5	7.3	2211	3	US-09-738-884-1	Sequence 1, Appli
395	190	8.0	344	4	US-09-086-118-27	Sequence 27, Appli	468	171.5	7.3	2211	4	US-10-096-961A-1	Sequence 1, Appli
396	190	8.0	344	4	US-09-431-614-15	Sequence 15, Appli	469	171.5	7.3	641	4	US-09-270-767-41562	Sequence 41562, A
397	190	8.0	344	5	PCT-US96-08819-7	Sequence 7, Appli	470	170.5	7.2	591	4	US-09-949-016-10914	Sequence 10914, A
398	190	8.0	626	3	US-09-029-348-2	Sequence 2, Appli	471	170.5	7.2	591	4	US-09-949-016-10915	Sequence 10915, A
399	189.5	8.0	549	1	US-08-494-168-8	Sequence 8, Appli	472	170.5	7.2	513	4	US-09-248-796A-25078	Sequence 25078, A
400	189.5	8.0	644	1	US-08-206-176-2	Sequence 2, Appli	473	170	7.2	513	3	US-09-453-702B-265	Sequence 265, App
401	189	8.0	643	2	US-08-551-356-4	Sequence 4, Appli	474	169.5	7.2	415	3	US-09-025-769B-280	Sequence 280, App
402	189	8.0	643	5	PCT-US93-12687-4	Sequence 4, Appli	475	169.5	7.2	415	4	US-09-490-070A-280	Sequence 280, App
403	189	8.0	1336	2	US-08-551-356-6	Sequence 6, Appli	476	169.5	7.2	415	4	US-09-490-153-280	Sequence 280, App
404	189	8.0	1336	5	PCT-US93-12687-6	Sequence 6, Appli	477	169.5	7.2	415	4	US-09-490-324-280	Sequence 280, App
405	188	8.0	287	1	US-08-397-633A-76	Sequence 76, Appli	478	168.5	7.1	208	5	US-08-212-237-9	Sequence 9, Appli
406	187.5	7.9	180	4	US-09-248-796A-22352	Sequence 22352, A	479	168.5	7.1	208	5	PCT-US95-02772-9	Sequence 9, Appli
407	187	7.9	252	1	US-08-642-255-61	Sequence 61, Appli	480	168.5	7.1	755	4	US-09-919-497-57	Sequence 57, Appli
408	186.5	7.9	532	1	US-08-494-168-9	Sequence 9, Appli	481	168	7.1	111	3	US-08-963-168C-15	Sequence 15, Appli
409	186.5	7.9	1566	4	US-09-581-472B-2	Sequence 2, Appli	482	168	7.1	131	3	US-08-963-168C-8	Sequence 8, Appli
410	186	7.9	251	1	US-08-397-633A-74	Sequence 74, Appli	483	168	7.1	136	3	US-08-963-168C-6	Sequence 6, Appli
411	186	7.9	336	4	US-09-767-44531	Sequence 44531, A	484	168	7.1	316	4	US-09-248-796A-26455	Sequence 26455, A
412	186	7.9	605	4	US-09-576-594-616	Sequence 616, App	485	168	7.1	345	4	US-09-657-013-112	Sequence 112, App
413	186	7.9	1581	3	US-09-110-517-2	Sequence 2, Appli	486	168	7.1	684	4	US-09-961-403-5	Sequence 5, Appli
414	185.5	7.9	673	4	US-09-107-532A-5134	Sequence 5134, Ap	487	167.5	7.1	357	1	US-07-609-716-66	Sequence 66, Appli
415	185	7.8	546	1	US-08-494-168-10	Sequence 10, Appli	488	167.5	7.1	357	1	US-08-642-255-33	Sequence 33, Appli
416	184.5	7.8	174	4	US-09-370-767-61801	Sequence 61801, A	489	167.5	7.1	357	3	US-08-475-411A-66	Sequence 66, Appli
417	184.5	7.8	216	3	US-08-506-553C-23	Sequence 23, Appli	490	167.5	7.1	357	3	US-08-478-029A-66	Sequence 66, Appli
418	184	7.8	159	1	US-07-609-716-104	Sequence 104, App	491	167.5	7.1	551	4	US-09-489-039A-3083	Sequence 3083, Ap
419	184	7.8	159	3	US-08-475-411A-104	Sequence 104, App	492	167.5	7.1	558	4	US-09-071-035-268	Sequence 268, App
420	184	7.8	159	3	US-08-478-029A-104	Sequence 104, App	493	167.5	7.1	1638	4	US-09-071-035-258	Sequence 258, App
421	182.5	7.7	472	4	US-09-538-092-312	Sequence 312, App	494	167.5	7.1	1638	4	US-09-071-035-262	Sequence 262, App
422	181	7.7	234	4	US-09-895-674A-1	Sequence 1, Appli	495	167.5	7.1	1638	4	US-09-071-035-266	Sequence 266, App
423	180	7.6	730	4	US-09-961-403-8	Sequence 8, Appli	496	167.5	7.1	1747	4	US-09-134-000C-5999	Sequence 5999, Ap
424	180	7.6	731	2	US-08-911-364-1	Sequence 1, Appli	497	166.5	7.0	1088	3	US-09-130-242-2	Sequence 2, Appli
425	180	7.6	733	3	US-08-464-700-2	Sequence 2, Appli	498	166.5	7.0	1088	4	US-09-583-610D-2	Sequence 2, Appli
426	180	7.6	792	2	US-08-678-039A-40	Sequence 40, Appli	499	166.5	7.0	1088	4	US-09-949-016-6935	Sequence 6935, Ap
427	179.5	7.6	960	3	US-09-219-849-5	Sequence 5, Appli	500	166.5	7.0	2504	4	US-09-328-352-5821	Sequence 5821, Ap
428	179	7.6	345	4	US-09-270-767-45883	Sequence 45883, A	501	165.5	7.0	116	3	US-08-963-168C-13	Sequence 13, Appli
429	178.5	7.6	216	4	US-09-248-796A-14221	Sequence 14221, A	502	165.5	7.0	132	3	US-08-963-168C-9	Sequence 9, Appli
430	178	7.5	889	3	US-09-336-447A-15	Sequence 15, Appli	503	165.5	7.0	416	4	US-09-902-540-11959	Sequence 11959, A
431	178	7.5	889	4	US-09-352-267B-15	Sequence 15, Appli	504	165	7.0	715	4	US-09-502-540-9752	Sequence 439, App
432	177.5	7.5	337	4	US-09-270-767-46550	Sequence 46550, A	505	165	7.0	823	4	US-09-538-092-4935	Sequence 439, App
433	177	7.5	190	2	US-08-560-398-8	Sequence 8, Appli	506	164.5	7.0	112	3	US-08-963-168C-16	Sequence 16206, A
434	177	7.5	731	4	US-09-340-736B-1	Sequence 1, Appli	507	164.5	7.0	356	4	US-09-252-991A-18206	Sequence 18206, A
435	177	7.5	731	4	US-09-964-662-1	Sequence 1, Appli	508	164.5	7.0	732	4	US-09-270-767-44652	Sequence 44652, A
436	177	7.5	232	4	US-09-086-436-30	Sequence 30, Appli	509	163.5	6.9	331	4	US-09-949-016-7015	Sequence 7015, Ap
437	176.5	7.5	571	3	US-09-134-001C-3865	Sequence 3865, Ap	510	163.5	6.9	335	4	US-09-949-016-7995	Sequence 7995, Ap
438	174.5	7.4	385	1	US-08-891-254-3	Sequence 3, Appli	511	163.5	6.9	414	1	US-08-343-682-1	Sequence 1, Appli
439	174.5	7.4	385	2	US-08-819-539-3	Sequence 3, Appli	512	163.5	6.9	414	2	US-08-705-660-26	Sequence 26, Appli
440	174.5	7.4	385	5	PCT-US96-08819-3	Sequence 3, Appli	513	163.5	6.9	414	4	US-08-989-045-26	Sequence 26, Appli
441	174.5	7.4	403	2	US-08-200-724A-2	Sequence 2, Appli	514	163.5	6.9	414	4	US-09-976-594-373	Sequence 373, App
442	174.5	7.4	403	2	US-09-030-270A-3	Sequence 2, Appli	515	163.5	6.9	414	4	US-09-315-355A-26	Sequence 26, Appli
443	174.5	7.4	403	3	US-08-851-376A-2	Sequence 2, Appli	516	163.5	6.9	666	2	US-08-737-716-14	Sequence 14, Appli
444	174.5	7.4	403	3	US-08-984-207-3	Sequence 3, Appli	517	163	6.9	384	4	US-09-949-016-11034	Sequence 11034, A
445	174.5	7.4	403	3	US-09-013-587-3	Sequence 3, Appli	518	163	6.9	535	3	US-09-029-348-1	Sequence 1, Appli
446	174.5	7.4	403	4	US-09-086-118-23	Sequence 23, Appli	519	163	6.9	537	3	US-09-029-348-4	Sequence 4, Appli
447	174.5	7.4	403	4	US-09-431-614-3	Sequence 3, Appli	520	163	6.9	920	4	US-09-538-092-1197	Sequence 1197, Ap
448	174.5	7.4	1261	3	US-09-208-742-4	Sequence 4, Appli	521	163	6.9	1216	4	US-09-134-000C-5130	Sequence 5130, Ap
449	174.5	7.4	1261	3	US-09-332-295-2	Sequence 2, Appli	522	163	6.9	1709	4	US-09-949-016-11345	Sequence 11345, A
450	174.5	7.4	1261	4	US-09-709-979-2	Sequence 2, Appli	523	162.5	6.9	878	4	US-09-540-236-3401	Sequence 3401, Ap
451	174.5	7.4	1261	4	US-10-147-268-2	Sequence 2, Appli	524	162	6.9	683	4	US-09-620-412C-357	Sequence 357, App
452	174	7.3	521	4	US-09-270-767-46291	Sequence 46291, A	525	162	6.9	683	4	US-09-598-419-357	Sequence 357, App
453	173.5	7.3	432	4	US-09-403-089A-1	Sequence 1, Appli	526	162	6.9	717	4	US-09-252-991A-31195	Sequence 31195, A
454	173.5	7.3	432	4	US-09-809-517A-25	Sequence 25, Appli	527	161.5	6.8	319	4	US-09-248-796A-18138	Sequence 18138, A
455	173.5	7.3	434	4	US-09-809-517A-23	Sequence 23, Appli	528	161.5	6.8	424	3	US-09-120-817-2	Sequence 2, Appli
456	173.5	7.3	434	4	US-09-809-517A-26	Sequence 26, Appli	529	161.5	6.8	424	4	US-09-431-614-14	Sequence 5, Appli
457	173.5	7.3	482	1	US-08-358-160-5	Sequence 5, Appli	530	161.5	6.8	534	3	US-09-029-348-5	Sequence 10, Appli
458	173.5	7.3	484	1	US-08-358-160-7	Sequence 7, Appli	531	161.5	6.8	557	3	US-09-320-095-10	Sequence 10, Appli
459	173	7.3	656	2	US-08-343-443B-2	Sequence 2, Appli	532	161.5	6.8	557	3	US-09-523-487-10	Sequence 52, Appli
460	173	7.3	656	3	US-09-214-564A-4	Sequence 4, Appli	533	161	6.8	503	3	US-08-845-258-52	Sequence 52, Appli
461	173	7.3	656	4	US-09-538-092-1250	Sequence 1250, Ap	534	161	6.8	503	3	US-08-990-571-52	Sequence 52, Appli
462	172.5	7.3	259	4	US-09-436-434-2	Sequence 2, Appli	535	161	6.8	503	4	US-09-528-784A-52	Sequence 52, Appli
463	172.5	7.3	385	5	PCT-US93-06243-2	Sequence 2, Appli	536	161	6.8	503	4	US-09-569-098A-52	Sequence 52, Appli
464	172	7.3	1268	4	US-09-270-767-45320	Sequence 45320, A	537	161	6.8	666	4	US-09-528-784A-85	Sequence 85, Appli
465	171.5	7.3	361	4	US-09-248-796A-20099	Sequence 20099, A	538	161	6.8	666	4	US-09-569-098A-85	Sequence 85, Appli

539	161	6.8	1091	4	US-09-949-016-8595	Sequence 8595, Ap	612	149	6.3	171	3	US-09-029-156-2	Sequence 2, Appli
540	161	6.8	1132	4	US-09-528-784A-87	Sequence 87, Appl	613	149	6.3	351	3	US-09-011-735-1	Sequence 1, Appli
541	161	6.8	1132	4	US-09-569-098A-87	Sequence 87, Appl	614	149	6.3	351	3	US-09-029-156-1	Sequence 1, Appli
542	161	6.8	1850	4	US-09-620-093A-5	Sequence 5, Appli	615	149	6.3	601	4	US-09-252-991A-27784	Sequence 27784, A
543	160.5	6.8	1850	4	US-09-252-991A-17984	Sequence 17984, A	616	148.5	6.3	266	4	US-09-495-880A-26	Sequence 26, Appl
544	160	6.8	300	3	US-08-765-856-2	Sequence 2, Appl	617	148.5	6.3	326	4	US-09-252-991A-17002	Sequence 17002, A
545	160	6.8	300	3	US-08-935-009A-2	Sequence 2, Appl	618	148.5	6.3	266	4	US-09-252-991A-30630	Sequence 30630, A
546	160	6.8	354	4	US-09-949-016-10178	Sequence 10178, A	619	148	6.3	657	4	US-09-248-796A-14517	Sequence 14517, A
547	160	6.8	396	4	US-09-640-211A-1055	Sequence 1055, Ap	620	148	6.3	447	3	US-09-120-927-2	Sequence 2, Appli
548	160	6.8	720	3	US-08-737-716-13	Sequence 13, Appl	621	148	6.3	447	3	US-09-431-614-6	Sequence 6, Appli
549	160	6.8	720	3	US-09-219-849-4	Sequence 4, Appli	622	147.5	6.2	1584	3	US-09-457-040B-27	Sequence 27, Appl
550	160	6.8	777	1	US-08-642-255-53	Sequence 53, Appl	623	147	6.2	97	1	US-08-175-155-15	Sequence 15, Appl
551	159	6.7	546	4	US-09-252-991A-18637	Sequence 18637, A	624	147	6.2	97	1	US-08-477-509B-50	Sequence 50, Appl
552	158	6.7	106	3	US-08-963-168C-14	Sequence 14, Appl	625	147	6.2	97	3	US-08-482-085B-50	Sequence 50, Appl
553	158	6.7	126	3	US-08-963-168C-7	Sequence 7, Appli	626	147	6.2	97	3	US-09-444-791A-50	Sequence 50, Appl
554	158	6.7	166	4	US-09-297-369-41	Sequence 41, Appl	627	147	6.2	98	2	US-08-707-237A-22	Sequence 22, Appl
555	158	6.7	435	4	US-09-270-767-43092	Sequence 43092, A	628	147	6.2	212	4	US-09-270-767-41907	Sequence 41907, A
556	157.5	6.7	430	2	US-08-945-848-8	Sequence 8, Appli	629	147	6.2	230	4	US-09-248-796A-28509	Sequence 28509, A
557	157.5	6.7	1032	4	US-09-270-767-44433	Sequence 44433, A	630	147	6.2	264	3	US-09-128-450-21	Sequence 21, Appl
558	157	6.6	272	4	US-09-949-016-9966	Sequence 9966, Ap	631	147	6.2	264	3	US-09-823-494-21	Sequence 21, Appl
559	157	6.6	272	4	US-09-949-016-9967	Sequence 9967, Ap	632	147	6.2	264	3	US-09-823-494-21	Sequence 21, Appl
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561	157	6.6	461	2	US-08-463-587A-26	Sequence 26, Appl	634	147	6.2	760	1	US-08-754-311B-2	Sequence 2, Appli
562	157	6.6	461	3	US-08-923-854-26	Sequence 4, Appli	634	147	6.2	908	4	US-08-714-741-44	Sequence 44, Appl
563	157	6.6	461	3	US-08-923-854-26	Sequence 26, Appl	635	146.5	6.2	385	4	US-09-270-767-46506	Sequence 46506, A
564	156.5	6.6	471	2	US-08-399-889-24	Sequence 24, Appl	636	146.5	6.2	388	4	US-09-248-796A-17306	Sequence 17306, A
565	156.5	6.6	471	2	US-09-167-364-24	Sequence 24, Appl	637	146.5	6.2	410	4	US-09-252-991A-25812	Sequence 25812, A
566	156.5	6.6	471	3	US-09-439-897-2	Sequence 2, Appli	638	146.5	6.2	717	3	US-08-910-925-1	Sequence 1, Appli
567	156	6.6	238	4	US-09-439-897-2	Sequence 2, Appli	639	146.5	6.2	918	3	US-09-041-886-11	Sequence 11, Appl
568	156	6.6	238	4	US-09-439-897-2	Sequence 2, Appl	640	146	6.2	84	1	US-08-175-155-17	Sequence 17, Appl
569	155.5	6.6	634	4	US-09-949-016-7117	Sequence 7117, Ap	641	146	6.2	84	1	US-08-477-509B-52	Sequence 52, Appl
570	155.5	6.6	187	4	US-09-634-238-414	Sequence 414, App	642	146	6.2	84	2	US-08-707-237A-23	Sequence 23, Appl
571	155.5	6.6	746	3	US-09-134-001C-3214	Sequence 3214, Ap	643	146	6.2	84	3	US-08-482-085B-52	Sequence 52, Appl
572	154.5	6.5	196	4	US-09-252-991A-27666	Sequence 27666, A	644	146	6.2	219	4	US-09-380-015B-2	Sequence 2, Appli
573	154.5	6.5	302	3	US-08-765-856-4	Sequence 23071, A	645	146	6.2	415	4	US-09-328-352-6430	Sequence 6430, Ap
574	154.5	6.5	302	3	US-08-765-856-4	Sequence 4, Appli	646	146	6.2	467	4	US-09-949-016-7778	Sequence 7778, Ap
575	154	6.5	1461	4	US-10-142-231-86	Sequence 4, Appl	647	146	6.2	467	4	US-09-949-016-7779	Sequence 7779, Ap
576	153	6.5	561	1	US-08-642-255-52	Sequence 86, Appl	648	145.5	6.2	99	4	US-09-072-596-255	Sequence 255, App
577	152.5	6.5	166	4	US-09-270-767-41190	Sequence 41190, A	649	145.5	6.2	99	4	US-09-072-596-260	Sequence 260, App
578	152.5	6.5	166	4	US-09-270-767-56406	Sequence 56406, A	650	145.5	6.2	743	3	US-08-910-925-3	Sequence 3, Appli
579	152.5	6.5	195	4	US-09-270-767-44458	Sequence 44458, A	651	145.5	6.2	743	4	US-09-949-016-6261	Sequence 6261, Ap
580	152.5	6.5	284	4	US-09-431-887-24	Sequence 24, Appl	652	145.5	6.2	970	4	US-09-270-767-42741	Sequence 42741, A
581	152.5	6.5	326	4	US-09-270-767-43241	Sequence 43241, A	653	145	6.1	264	4	US-09-431-887-27	Sequence 27, Appl
582	152.5	6.5	335	4	US-09-821-687-11	Sequence 11, Appl	654	145	6.1	328	1	US-08-229-287-4	Sequence 4, Appli
583	152.5	6.5	504	3	US-09-219-849-3	Sequence 3, Appli	655	145	6.1	553	3	US-09-083-351-2	Sequence 2, Appli
584	152.5	6.5	790	4	US-09-328-352-4283	Sequence 4283, Ap	656	145	6.1	553	3	US-09-083-352-2	Sequence 2, Appli
585	152.5	6.5	1395	4	US-09-252-991A-30345	Sequence 30345, A	657	145	6.1	553	4	US-09-612-809B-2	Sequence 2, Appli
586	152	6.4	1010	4	US-09-248-796A-16379	Sequence 16379, A	658	145	6.1	572	4	US-09-489-039A-11826	Sequence 11826, A
587	152	6.4	1417	3	US-08-900-230-3	Sequence 3, Appli	659	145	6.1	633	4	US-09-976-594-282	Sequence 282, App
588	151.5	6.4	461	1	US-08-186-222-2	Sequence 2, Appli	660	145	6.1	633	4	US-09-821-687-10	Sequence 10, Appl
589	151	6.4	313	4	US-09-949-016-9265	Sequence 9265, Ap	661	145	6.1	792	4	US-09-252-991A-25823	Sequence 25823, A
590	150.5	6.4	162	3	US-09-575-574-4	Sequence 4, Appli	662	145	6.1	919	4	US-09-538-092-895	Sequence 895, App
591	150.5	6.4	251	1	US-08-458-298-8	Sequence 8, Appli	663	145	6.1	923	4	US-09-497-822C-19	Sequence 19, Appl
592	150.5	6.4	251	1	US-08-458-298-8	Sequence 8, Appli	664	145	6.1	1186	2	US-08-861-464-8	Sequence 8, Appli
593	150.5	6.4	447	4	US-09-916-109-5	Sequence 5, Appli	665	145	6.1	1186	2	US-08-396-001-8	Sequence 8, Appli
594	150.5	6.4	447	4	US-10-211-412B-5	Sequence 5, Appli	666	145	6.1	1186	3	US-09-323-433A-8	Sequence 8, Appli
595	150.5	6.4	483	4	US-09-916-109-4	Sequence 4, Appli	667	145	6.1	1186	4	US-09-826-752-8	Sequence 8, Appli
596	150.5	6.4	483	4	US-10-211-412B-4	Sequence 4, Appli	668	145	6.1	2314	3	US-09-268-347-49	Sequence 49, Appl
597	150.5	6.4	483	4	US-09-538-092-1162	Sequence 1162, Ap	669	145	6.1	2763	3	US-08-496-944-2	Sequence 2, Appli
598	150	6.3	72	4	US-09-513-999C-5563	Sequence 5563, Ap	670	144.5	6.1	258	4	US-09-248-796A-23723	Sequence 23723, A
599	150	6.3	72	4	US-09-513-999C-5563	Sequence 5563, Ap	671	144.5	6.1	302	4	US-09-657-013-49	Sequence 49, Appl
600	150	6.3	207	4	US-09-513-999C-5564	Sequence 5564, Ap	672	144.5	6.1	302	4	US-09-949-016-6893	Sequence 6893, Ap
601	150	6.3	423	1	US-08-383-744-2	Sequence 2, Appli	673	144.5	6.1	411	4	US-09-657-013-57	Sequence 57, Appl
602	150	6.3	423	2	US-08-999-336-2	Sequence 2, Appli	674	144.5	6.1	411	4	US-09-949-016-6439	Sequence 6439, Ap
603	150	6.3	423	5	PCT-US96-01427-2	Sequence 2, Appli	675	144.5	6.1	477	4	US-09-863-901-5	Sequence 5, Appli
604	149.5	6.3	121	4	US-09-072-596-253	Sequence 253, App	676	144.5	6.1	906	4	US-09-863-901-6	Sequence 6, Appli
605	149.5	6.3	121	4	US-09-072-596-258	Sequence 258, App	677	144	6.1	91	4	US-09-270-767-39789	Sequence 39789, A
606	149.5	6.3	445	4	US-09-252-991A-24354	Sequence 24354, A	678	144	6.1	123	1	US-09-270-767-55006	Sequence 55006, A
607	149.5	6.3	1060	3	US-08-911-393-2	Sequence 2, Appli	679	144	6.1	91	4	US-07-609-716-103	Sequence 103, App
608	149.5	6.3	1060	4	US-09-955-509-2	Sequence 2, Appli	680	144	6.1	123	3	US-08-475-411A-103	Sequence 103, App
609	149	6.3	60	4	US-09-832-297A-12	Sequence 12, Appl	681	144	6.1	123	3	US-08-478-029A-103	Sequence 103, App
610	149	6.3	124	4	US-09-540-236-3076	Sequence 3076, Ap	682	144	6.1	375	4	US-09-600-932-29	Sequence 29, Appl
611	149	6.3	171	3	US-09-011-735-2	Sequence 2, Appli	683	144	6.1	391	4	US-09-395-017B-2	Sequence 2, Appli
							684	144	6.1	402	4	US-09-252-991A-20683	Sequence 20683, A

685	144	6.1	1475	4	US-09-538-092-1160	Sequence 1160, Ap	758	140	5.9	101	3	US-09-247-806-5	Sequence 5, Appli
686	144	6.1	1712	4	US-08-949-016-9450	Sequence 9450, Ap	759	140	5.9	101	3	US-09-247-806-7	Sequence 7, Appli
687	144	6.1	1833	4	US-08-621-944D-4	Sequence 4, Appli	760	140	5.9	101	4	US-09-863-858-11	Sequence 11, Appli
688	144	6.1	1833	4	US-08-945-567D-4	Sequence 4, Appli	761	140	5.9	148	4	US-09-248-796A-26837	Sequence 26837, A
689	144	6.1	1992	4	US-08-621-944D-3	Sequence 3, Appli	762	140	5.9	234	1	US-08-642-255-51	Sequence 51, Appli
690	144	6.1	1992	4	US-08-945-567D-3	Sequence 3, Appli	763	140	5.9	705	4	US-09-252-991A-30792	Sequence 30792, A
691	144	6.1	2123	3	US-08-968-685A-10	Sequence 10, Appl	764	140	5.9	892	3	US-09-336-447A-5	Sequence 5, Appli
692	143.5	6.1	482	4	US-08-509-031-16	Sequence 16, Appl	765	140	5.9	892	4	US-09-952-267B-5	Sequence 5, Appli
693	143.5	6.1	563	4	US-09-949-016-1053	Sequence 10153, A	766	140	5.9	956	4	US-09-949-016-8159	Sequence 8159, Ap
694	143.5	6.1	2142	4	US-09-540-236-3459	Sequence 3459, Ap	767	139.5	5.9	219	4	US-09-809-517A-24	Sequence 24, Appli
695	143	6.1	165	4	US-09-270-767-59895	Sequence 59895, A	768	139.5	5.9	219	4	US-09-809-517A-27	Sequence 27, Appli
696	143	6.1	263	1	US-08-242-188-3	Sequence 3, Appli	769	139.5	5.9	253	4	US-09-252-991A-20659	Sequence 20659, A
697	143	6.1	263	1	US-08-509-261A-3	Sequence 3, Appli	770	139.5	5.9	449	2	US-08-927-394-2	Sequence 2, Appli
698	143	6.1	263	1	US-08-660-626-9	Sequence 9, Appli	771	139.5	5.9	449	4	US-09-538-092-1372	Sequence 1372, Ap
699	143	6.1	263	1	US-08-592-892-3	Sequence 3, Appli	772	139.5	5.9	449	4	US-09-949-016-6004	Sequence 6604, Ap
700	143	6.1	263	2	US-08-713-939A-3	Sequence 3, Appli	773	139.5	5.9	467	4	US-09-252-991A-31427	Sequence 31427, A
701	143	6.1	263	2	US-08-868-162A-23	Sequence 23, Appl	774	139.5	5.9	489	4	US-09-366-009-8	Sequence 8, Appli
702	143	6.1	263	3	US-09-031-168-9	Sequence 9, Appli	775	139.5	5.9	489	4	US-08-809-156B-8	Sequence 8, Appli
703	143	6.1	263	3	US-09-036-579-3	Sequence 3, Appli	776	139.5	5.9	537	4	US-09-252-991A-27024	Sequence 27024, A
704	143	6.1	263	3	US-08-550-374-3	Sequence 3, Appli	777	139.5	5.9	653	4	US-09-345-473B-50	Sequence 50, Appl
705	143	6.1	263	3	US-09-943-906-3	Sequence 3, Appli	778	139.5	5.9	743	4	US-09-252-991A-28327	Sequence 28327, A
706	143	6.1	263	4	US-09-669-516C-9	Sequence 9, Appli	779	139.5	5.9	2291	4	US-09-252-991A-21854	Sequence 21854, A
707	143	6.1	264	4	US-09-627-218B-11	Sequence 11, Appl	780	139	5.9	393	4	US-09-252-991A-30202	Sequence 30202, A
708	143	6.1	544	4	US-09-538-092-1262	Sequence 12138, Ap	781	139	5.9	481	4	US-09-252-991A-16955	Sequence 16955, A
709	142.5	6.0	3969	4	US-08-270-767-56792	Sequence 56792, A	782	138.5	5.9	415	4	US-09-252-991A-27669	Sequence 27669, A
710	142	6.0	137	4	US-09-538-092-412	Sequence 412, App	783	138.5	5.9	421	4	US-09-252-991A-32326	Sequence 32326, A
711	142	6.0	289	4	US-09-252-991A-16628	Sequence 16628, A	784	138.5	5.9	437	4	US-09-921-099A-17	Sequence 17, Appl
712	142	6.0	367	4	US-09-252-991A-22945	Sequence 22945, A	785	138.5	5.9	1261	4	US-09-473-716-2	Sequence 2, Appli
713	142	6.0	413	4	US-09-294-298A-21	Sequence 21, Appl	786	138.5	5.9	1497	4	US-10-175-158-2	Sequence 2, Appli
714	142	6.0	1335	4	US-09-294-298A-6	Sequence 6, Appli	787	138	5.8	1497	4	US-09-060-854B-2	Sequence 3, Appli
715	142	6.0	1325	4	US-09-294-298A-6	Sequence 6, Appli	788	138	5.8	1497	4	US-09-529-904-3	Sequence 42654, A
716	142	6.0	1376	4	US-09-386-962C-14	Sequence 14, Appl	789	138	5.8	1815	4	US-09-270-767-42654	Sequence 38, Appl
717	142	6.0	1423	4	US-09-394-298A-2	Sequence 2, Appli	790	138	5.8	745	4	US-09-837-969A-38	Sequence 38, Appl
718	141.5	6.0	233	2	US-08-458-568A-4	Sequence 4, Appli	791	137.5	5.8	1805	1	US-07-853-913-2	Sequence 2, Appli
719	141.5	6.0	474	4	US-09-702-705-1812	Sequence 1812, Ap	798	137	5.8	867	4	US-09-540-236-2676	Sequence 2676, Ap
720	141.5	6.0	474	4	US-09-736-457-1812	Sequence 1812, Ap	799	137	5.8	995	4	US-09-252-991A-22297	Sequence 22297, A
721	141.5	6.0	474	4	US-09-671-325-1812	Sequence 1812, Ap	800	136.5	5.8	223	4	US-09-248-796A-27735	Sequence 27735, A
722	141.5	6.0	474	4	US-09-538-092-1279	Sequence 1279, Ap	801	136.5	5.8	464	2	US-08-836-854-19	Sequence 19, Appl
723	141.5	6.0	487	4	US-09-386-962C-14	Sequence 14, Appl	802	136.5	5.8	464	4	US-09-366-009-7	Sequence 7, Appli
724	141.5	6.0	487	4	US-09-386-959-65	Sequence 65, Appl	803	136.5	5.8	464	4	US-08-809-158B-7	Sequence 4, Appli
725	141	6.0	211	1	US-08-276-852-34	Sequence 34, Appl	804	136.5	5.8	703	3	US-08-910-923-4	Sequence 2, Appli
726	141	6.0	211	1	US-08-133-011-16	Sequence 16, Appl	805	136.5	5.8	850	4	US-09-129-603-2	Sequence 2, Appli
727	141	6.0	211	1	US-08-322-730A-16	Sequence 16, Appl	806	136.5	5.8	1113	4	US-09-252-991A-24385	Sequence 24385, A
728	141	6.0	211	1	US-08-387-874-16	Sequence 16, Appl	807	136.5	5.8	1290	3	US-09-150-460B-6	Sequence 6, Appli
729	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	808	136.5	5.8	1376	4	US-09-252-991A-30344	Sequence 30344, A
730	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	809	136.5	5.8	1388	4	US-09-463-048A-6	Sequence 6, Appli
731	141	6.0	211	3	US-08-907-739-16	Sequence 16, Appl	810	136	5.8	50	4	US-09-863-901-22	Sequence 22, Appl
732	141	6.0	211	3	US-08-907-739-16	Sequence 16, Appl	811	136	5.8	199	3	US-08-506-553C-8	Sequence 8, Appli
733	141	6.0	211	5	PCT-US93-08364-16	Sequence 16, Appl	812	136	5.8	247	4	US-09-252-991A-21412	Sequence 21412, A
734	141	6.0	211	5	PCT-US94-05669A-4	Sequence 4, Appli	813	136	5.8	339	4	US-09-252-991A-32096	Sequence 32096, A
735	141	6.0	211	5	PCT-US94-05669A-6	Sequence 6, Appli	814	135.5	5.7	260	4	US-09-431-887-6	Sequence 6, Appli
736	141	6.0	293	3	US-09-395-017B-1	Sequence 1, Appli	815	135.5	5.7	400	3	US-09-086-010-2	Sequence 19127, A
737	141	6.0	378	4	US-09-270-767-61286	Sequence 61286, A	816	135.5	5.7	590	4	US-09-252-991A-19127	Sequence 68, Appl
738	141	6.0	434	4	US-09-923-240A-9	Sequence 9, Appli	817	135	5.7	139	4	US-08-893-853-3	Sequence 3, Appli
739	141	6.0	609	4	US-09-270-767-45764	Sequence 45764, A	818	135	5.7	302	2	US-09-113-921-3	Sequence 3, Appli
740	141	6.0	1059	4	US-09-252-991A-22547	Sequence 22547, A	819	135	5.7	302	3	US-09-451-067-3	Sequence 19, Appl
741	140.5	5.9	456	4	US-09-252-991A-19417	Sequence 19417, A	820	135	5.7	310	3	US-08-845-258-19	Sequence 19, Appl
742	140.5	5.9	462	4	US-09-242-913B-17	Sequence 17, Appl	821	135	5.7	310	3	US-08-990-571-19	Sequence 19, Appl
743	140.5	5.9	484	4	US-09-949-016-11518	Sequence 11518, A	822	135	5.7	310	3	US-08-723-142A-19	Sequence 19, Appl
744	140.5	5.9	506	4	US-09-252-991A-24513	Sequence 24513, A	823	135	5.7	310	4	US-09-528-784A-19	Sequence 19, Appl
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747	140.5	5.9	1776	4	US-09-620-412C-179	Sequence 179, App	826	135	5.7	558	3	US-09-199-637A-277	Sequence 277, App
748	140.5	5.9	1776	4	US-09-598-419-179	Sequence 5, Appli	827	135	5.7	2516	3	US-08-374-077C-2	Sequence 2, Appli
749	140.5	5.9	3969	3	US-08-061-376-5	Sequence 22, Appl	828	135	5.7	2516	3	US-08-895-590-2	Sequence 2, Appli
750	140	5.9	101	3	US-08-556-978B-22	Sequence 62, Appl	829	135	5.7	2516	4	US-09-539-879A-2	Sequence 2, Appli
751	140	5.9	101	3	US-08-556-978B-62	Sequence 62, Appl	830	135	5.7	2516	4	US-09-539-879A-2	Sequence 2, Appli

831	134.5	5.7	101	3	US-08-556-978B-20	Sequence 20, Appl	904	130.5	5.5	72	3	US-09-444-791A-87	Sequence 87, Appl
832	134.5	5.7	101	3	US-09-247-806-3	Sequence 30, Appl	905	130.5	5.5	128	3	US-08-806-029-13	Sequence 13, Appl
833	134.5	5.7	101	4	US-09-863-859-10	Sequence 10, Appl	906	130.5	5.5	223	4	US-09-248-796A-24067	Sequence 24067, A
834	134.5	5.7	168	3	US-09-512-342-20	Sequence 20, Appl	907	130.5	5.5	301	4	US-09-252-991A-28663	Sequence 28663, A
835	134.5	5.7	339	4	US-09-252-991A-21715	Sequence 21715, A	908	130.5	5.5	362	4	US-09-252-991A-17884	Sequence 17884, A
836	134.5	5.7	634	4	US-09-248-796A-19513	Sequence 19513, A	909	130.5	5.5	365	4	US-09-252-991A-30166	Sequence 30166, A
837	134.5	5.7	984	1	US-08-257-073-3	Sequence 3, Appl	910	130.5	5.5	803	4	US-09-252-991A-23614	Sequence 23614, A
838	134.5	5.7	984	2	US-08-184-009-120	Sequence 120, App	911	130.5	5.5	858	4	US-09-627-650B-7	Sequence 7, Appl
839	134.5	5.7	984	2	US-08-458-356-120	Sequence 120, App	912	130.5	5.5	2508	4	US-09-436-063C-7	Sequence 7, Appl
840	134.5	5.7	984	3	US-08-460-736-120	Sequence 120, App	913	130.5	5.5	2544	4	US-09-627-650B-3	Sequence 3, Appl
841	134.5	5.7	984	4	US-09-535-370-120	Sequence 120, App	914	130.5	5.5	2544	4	US-09-436-063C-3	Sequence 3, Appl
842	134.5	5.7	984	4	US-09-663-667-120	Sequence 120, App	915	130.5	5.5	2601	4	US-09-627-650B-9	Sequence 9, Appl
843	134.5	5.7	2703	1	US-08-185-432-19	Sequence 19, Appl	916	130.5	5.5	2601	4	US-09-436-063C-9	Sequence 9, Appl
844	134.5	5.7	2703	4	US-08-899-232-4	Sequence 4, Appl	917	130	5.5	176	4	US-09-252-991A-28622	Sequence 28622, A
845	134.5	5.7	2703	4	US-09-121-457-4	Sequence 4, Appl	918	130	5.5	177	4	US-09-328-352-6964	Sequence 6964, Ap
846	134	5.7	104	3	US-09-219-849-33	Sequence 33, Appl	919	130	5.5	223	3	US-09-206-676C-1	Sequence 1, Appl
847	134	5.7	387	4	US-09-252-991A-23334	Sequence 23334, A	920	130	5.5	223	4	US-09-431-887-16	Sequence 16, Appl
848	134	5.7	1043	4	US-08-851-567B-61	Sequence 61, Appl	921	130	5.5	253	4	US-09-431-887-18	Sequence 18, Appl
849	134	5.7	1298	4	US-09-252-991A-30579	Sequence 30579, A	922	130	5.5	278	3	US-09-260-283-2	Sequence 2, Appl
850	134	5.7	2048	3	US-09-268-347-48	Sequence 48, Appl	923	130	5.5	425	4	US-09-252-991A-22321	Sequence 22321, A
851	133.5	5.6	148	1	US-08-207-904-15	Sequence 15, Appl	924	130	5.5	441	4	US-09-252-991A-24396	Sequence 24396, A
852	133.5	5.6	378	6	5171843-9	Patent No. 5171843	925	130	5.5	510	4	US-09-252-991A-17695	Sequence 17695, A
853	133.5	5.6	378	6	5171843-9	Patent No. 5171843	926	130	5.5	514	4	US-09-252-991A-18306	Sequence 18306, A
854	133.5	5.6	442	4	US-09-538-092-1123	Sequence 1123, Ap	927	130	5.5	635	4	US-09-252-991A-33100	Sequence 33100, A
855	133	5.6	141	4	US-09-252-991A-23427	Sequence 23427, A	928	130	5.5	941	3	US-09-336-447A-9	Sequence 9, Appl
856	133	5.6	486	4	US-09-710-279-788	Sequence 788, App	929	130	5.5	941	1	US-09-952-267B-9	Sequence 9, Appl
857	133	5.6	513	4	US-09-252-991A-18177	Sequence 18177, A	930	130	5.5	1618	1	US-07-853-913-4	Sequence 4, Appl
858	133	5.6	855	4	US-09-902-540-14518	Sequence 14518, A	931	130	5.5	1618	4	US-09-538-092-1143	Sequence 1143, Ap
859	132.5	5.6	80	4	US-09-248-796A-23892	Sequence 23892, A	932	129.5	5.5	103	1	US-08-209-747-4	Sequence 4, Appl
860	132.5	5.6	182	4	US-09-489-039A-8301	Sequence 8301, Ap	933	129.5	5.5	103	1	US-08-458-298-4	Sequence 4, Appl
861	132.5	5.6	247	3	US-09-199-637A-363	Sequence 363, App	934	129.5	5.5	119	3	US-08-556-978B-60	Sequence 60, Appl
862	132.5	5.6	301	3	US-09-469-318-142	Sequence 142, App	935	129.5	5.5	119	3	US-09-247-806-9	Sequence 9, Appl
863	132.5	5.6	301	3	US-08-468-609A-142	Sequence 142, App	936	129.5	5.5	368	3	US-08-591-685-13	Sequence 13, Appl
864	132.5	5.6	301	3	US-08-446-872A-142	Sequence 142, App	937	129.5	5.5	423	4	US-09-252-991A-27333	Sequence 27333, A
865	132.5	5.6	301	4	US-08-762-227A-142	Sequence 142, App	938	129.5	5.5	584	4	US-09-949-016-6628	Sequence 6628, Ap
866	132.5	5.6	301	5	FCT-US95-01185-142	Sequence 142, App	939	129.5	5.5	589	4	US-09-949-016-11035	Sequence 11035, A
867	132.5	5.6	466	3	US-09-134-001C-4749	Sequence 4749, Ap	940	129.5	5.5	577	4	US-09-252-991A-25632	Sequence 25632, A
868	132.5	5.6	468	4	US-09-252-991A-24394	Sequence 24394, A	941	129.5	5.5	865	4	US-09-252-991A-18683	Sequence 18683, A
869	132.5	5.6	706	4	US-09-270-767-40994	Sequence 40994, A	942	129.5	5.5	873	3	US-09-336-447A-13	Sequence 13, Appl
870	132.5	5.6	706	4	US-09-270-767-56210	Sequence 56210, A	943	129.5	5.5	873	4	US-09-952-267B-13	Sequence 13, Appl
871	132	5.6	186	4	US-09-366-009-6	Sequence 6, Appl	944	129.5	5.5	1705	3	US-08-669-785-4	Sequence 4, Appl
872	132	5.6	186	4	US-08-809-156B-6	Sequence 6, Appl	945	129.5	5.5	1794	6	5183745-6	Patent No. 5183745
873	132	5.6	430	4	US-09-252-991A-22599	Sequence 22599, A	946	129.5	5.5	1794	6	5183745-6	Patent No. 5183745
874	132	5.6	455	4	US-09-270-767-45531	Sequence 45531, A	947	129	5.5	45	4	US-09-863-901-25	Sequence 25, Appl
875	132	5.6	580	4	US-09-252-991A-29979	Sequence 29979, A	948	129	5.5	122	3	US-08-956-307B-19	Sequence 19, Appl
876	132	5.6	615	4	US-09-252-991A-23203	Sequence 23203, A	949	129	5.5	256	3	US-09-128-450-22	Sequence 22, Appl
877	132	5.6	929	4	US-09-252-991A-19203	Sequence 19203, A	950	129	5.5	256	3	US-09-823-494-22	Sequence 22, Appl
878	131.5	5.6	136	4	US-09-270-767-46188	Sequence 46188, A	951	129	5.5	334	4	US-09-949-016-11006	Sequence 11006, A
879	131.5	5.6	256	4	US-09-431-887-31	Sequence 31, Appl	952	129	5.5	456	4	US-09-919-172-31	Sequence 31, Appl
880	131.5	5.6	257	4	US-09-431-887-30	Sequence 30, Appl	953	129	5.5	707	4	US-09-919-039-278	Sequence 278, App
881	131.5	5.6	268	3	US-08-961-083-140	Sequence 140, App	954	129	5.5	707	4	US-09-538-092-993	Sequence 993, App
882	131.5	5.6	268	4	US-09-536-784-140	Sequence 140, App	955	129	5.5	729	4	US-09-949-016-10790	Sequence 10790, A
883	131.5	5.6	268	4	US-09-232-991A-25667	Sequence 25667, A	956	129	5.5	729	4	US-09-949-016-10791	Sequence 10791, A
884	131.5	5.6	388	4	US-09-252-991A-30608	Sequence 30608, A	957	128.5	5.4	226	3	US-09-206-676C-2	Sequence 2, Appl
885	131.5	5.6	647	2	US-08-770-761A-8	Sequence 8, Appl	958	128.5	5.4	247	4	US-09-252-991A-29972	Sequence 29972, A
886	131.5	5.6	705	4	US-08-770-761A-7	Sequence 7, Appl	959	128.5	5.4	365	4	US-09-252-991A-32327	Sequence 32327, A
887	131.5	5.6	709	4	US-09-702-705-335	Sequence 335, App	960	128.5	5.4	441	4	US-09-794-422-4	Sequence 4, Appl
888	131.5	5.6	709	4	US-09-736-457-335	Sequence 335, App	961	128.5	5.4	487	4	US-09-270-767-57297	Sequence 57297, A
889	131.5	5.6	709	4	US-09-614-124B-335	Sequence 335, App	962	128.5	5.4	569	4	US-09-349-016-11036	Sequence 11036, A
890	131.5	5.6	709	4	US-09-671-325-335	Sequence 335, App	963	128.5	5.4	975	4	US-09-270-767-42040	Sequence 42040, A
891	131.5	5.6	709	4	US-09-589-184-335	Sequence 335, App	964	128	5.4	297	4	US-09-252-991A-27909	Sequence 27909, A
892	131.5	5.6	709	4	US-09-658-824-335	Sequence 335, App	965	128	5.4	376	3	US-09-056-556-202	Sequence 202, App
893	131.5	5.6	945	4	US-09-252-991A-30699	Sequence 30699, A	966	128	5.4	376	4	US-09-072-596-197	Sequence 197, App
894	131.5	5.6	1706	3	US-08-669-785-2	Sequence 2, Appl	967	128	5.4	376	4	US-09-072-967-202	Sequence 202, App
895	131	5.5	302	4	US-09-252-991A-23166	Sequence 23166, A	968	128	5.4	499	4	US-09-252-991A-28010	Sequence 28010, A
896	131	5.5	456	4	US-09-495-880A-11	Sequence 11, Appl	969	128	5.4	555	4	US-09-252-991A-28734	Sequence 28734, A
897	130.5	5.5	72	1	US-07-609-716-35	Sequence 35, Appl	970	128	5.4	1164	4	US-09-502-540-12627	Sequence 12627, A
898	130.5	5.5	72	1	US-08-175-155-52	Sequence 52, Appl	971	128	5.4	1970	4	US-09-538-092-1005	Sequence 1005, Ap
899	130.5	5.5	72	1	US-08-477-509B-87	Sequence 87, Appl	972	127.5	5.4	192	4	US-09-902-540-10307	Sequence 10307, A
900	130.5	5.5	72	2	US-08-707-237A-60	Sequence 60, Appl	973	127.5	5.4	324	4	US-09-107-433-4143	Sequence 4143, Ap
901	130.5	5.5	72	3	US-08-482-085B-87	Sequence 87, Appl	974	127.5	5.4	375	4	US-09-252-991A-31128	Sequence 31128, A
902	130.5	5.5	72	3	US-08-475-411A-35	Sequence 35, Appl	975	127.5	5.4	391	4	US-09-538-092-1097	Sequence 1097, Ap
903	130.5	5.5	72	3	US-08-478-029A-35	Sequence 35, Appl	976	127.5	5.4	394	4	US-09-949-016-9912	Sequence 9912, Ap

977	127.5	5.4	406	4	US-09-949-016-8507	Sequence 8507, Ap	1050	125	5.3	254	3	US-09-823-494-26	Sequence 26, Appl
978	127.5	5.4	630	4	US-09-252-991A-19702	Sequence 19702, A	1051	125	5.3	349	3	US-08-469-318-151	Sequence 151, App
979	127.5	5.4	878	3	US-08-653-648A-15	Sequence 15, Appl	1052	125	5.3	349	3	US-08-468-609A-151	Sequence 151, App
980	127.5	5.4	878	4	US-09-564-418-8	Sequence 8, Appl	1053	125	5.3	349	3	US-08-446-872A-151	Sequence 151, App
981	127	5.4	253	1	US-08-242-188-2	Sequence 2, Appl	1054	125	5.3	349	4	US-08-762-227A-151	Sequence 151, App
982	127	5.4	253	1	US-08-509-261A-2	Sequence 2, Appl	1055	125	5.3	349	5	PCT-US95-01185-151	Sequence 151, App
983	127	5.4	253	1	US-08-660-626-8	Sequence 8, Appl	1056	125	5.3	432	4	US-09-248-796A-16450	Sequence 16450, A
984	127	5.4	253	1	US-08-692-892-2	Sequence 2, Appl	1057	125	5.3	712	4	US-09-248-796A-16474	Sequence 16474, A
985	127	5.4	253	2	US-08-713-939A-2	Sequence 2, Appl	1058	125	5.3	716	4	US-09-107-532A-5208	Sequence 5208, Ap
986	127	5.4	253	3	US-08-868-162A-22	Sequence 22, Appl	1059	124.5	5.3	60	3	US-08-469-318-195	Sequence 195, App
987	127	5.4	253	3	US-09-031-168-8	Sequence 8, Appl	1060	124.5	5.3	60	3	US-08-468-609A-195	Sequence 195, App
988	127	5.4	253	3	US-09-128-450-20	Sequence 20, Appl	1061	124.5	5.3	60	3	US-08-446-872A-195	Sequence 195, App
989	127	5.4	253	3	US-09-036-579-2	Sequence 2, Appl	1062	124.5	5.3	60	4	US-08-762-227A-195	Sequence 195, App
990	127	5.4	253	3	US-08-823-494-20	Sequence 20, Appl	1063	124.5	5.3	60	5	PCT-US95-01185-195	Sequence 195, App
991	127	5.4	253	3	US-09-350-374-2	Sequence 2, Appl	1064	124.5	5.3	184	4	US-09-270-767-5165	Sequence 5165, A
992	127	5.4	253	4	US-09-431-887-1	Sequence 1, Appl	1065	124.5	5.3	281	4	US-09-252-991A-18173	Sequence 18173, A
993	127	5.4	253	4	US-09-431-887-2	Sequence 2, Appl	1066	124.5	5.3	294	4	US-09-270-767-43772	Sequence 43772, A
994	127	5.4	253	4	US-09-431-887-3	Sequence 3, Appl	1067	124.5	5.3	349	3	US-08-469-318-139	Sequence 139, App
995	127	5.4	253	4	US-09-431-887-4	Sequence 4, Appl	1068	124.5	5.3	349	3	US-08-468-609A-139	Sequence 139, App
996	127	5.4	253	4	US-08-431-887-8	Sequence 8, Appl	1069	124.5	5.3	349	3	US-08-446-872A-139	Sequence 139, App
997	127	5.4	253	4	US-09-431-887-19	Sequence 19, Appl	1070	124.5	5.3	349	4	US-08-762-227A-139	Sequence 139, App
998	127	5.4	253	4	US-09-943-906-2	Sequence 2, Appl	1071	124.5	5.3	349	5	PCT-US95-01185-139	Sequence 139, App
999	127	5.4	253	4	US-09-669-516C-8	Sequence 8, Appl	1072	124.5	5.3	383	4	US-09-252-991A-24223	Sequence 24223, A
1000	127	5.4	253	4	US-09-904-987-3	Sequence 3, Appl	1073	124.5	5.3	425	4	US-09-252-991A-19054	Sequence 19054, A
1001	127	5.4	257	4	US-09-431-887-29	Sequence 29, Appl	1074	124.5	5.3	510	4	US-09-252-991A-33084	Sequence 33084, A
1002	127	5.4	258	3	US-08-122-458D-11	Sequence 11, Appl	1075	124.5	5.3	534	4	US-09-252-991A-20468	Sequence 20468, A
1003	127	5.4	331	4	US-09-270-767-45830	Sequence 45830, A	1076	124.5	5.3	757	4	US-09-252-991A-23569	Sequence 23569, A
1004	127	5.4	374	4	US-09-248-796A-17283	Sequence 17283, A	1077	124.5	5.3	1261	4	US-09-248-796A-16620	Sequence 16620, A
1005	127	5.4	886	4	US-09-252-991A-24378	Sequence 24378, A	1078	124.5	5.3	1665	4	US-09-858-664A-2	Sequence 2, Appl
1006	127	5.4	1004	3	US-09-368-347-30	Sequence 30, Appl	1079	124.5	5.3	1665	4	US-10-274-978-2	Sequence 2, Appl
1007	126.5	5.4	217	4	US-09-270-767-31877	Sequence 31877, A	1080	124	5.2	76	1	US-10-697-263-2	Sequence 2, Appl
1008	126.5	5.4	219	4	US-08-270-767-47094	Sequence 47094, A	1081	124	5.2	76	1	US-08-089-863-10	Sequence 10, Appl
1009	126.5	5.4	219	4	US-09-248-796A-23661	Sequence 23661, A	1082	124	5.2	76	1	US-08-587-333-17	Sequence 17, Appl
1010	126.5	5.4	256	4	US-09-431-887-25	Sequence 25, Appl	1083	124	5.2	76	5	PCT-US94-07776-15	Sequence 15, Appl
1011	126.5	5.4	256	4	US-09-431-887-28	Sequence 28, Appl	1084	124	5.2	155	4	US-09-252-991A-27532	Sequence 27532, A
1012	126.5	5.4	351	4	US-09-352-991A-29678	Sequence 29678, A	1085	124	5.2	212	4	US-09-252-991A-24512	Sequence 24512, A
1013	126.5	5.4	405	4	US-09-166-265-1	Sequence 1, Appl	1086	124	5.2	212	4	US-09-252-991A-37887	Sequence 27887, A
1014	126.5	5.4	427	4	US-09-270-767-45426	Sequence 45426, A	1087	124	5.2	469	4	US-09-252-991A-26584	Sequence 26584, A
1015	126.5	5.4	439	4	US-09-252-991A-16736	Sequence 16736, A	1088	124	5.2	482	4	US-09-270-767-43292	Sequence 43292, A
1016	126.5	5.4	451	4	US-09-252-991A-25804	Sequence 25804, A	1089	124	5.2	586	4	US-09-252-991A-24514	Sequence 24514, A
1017	126.5	5.4	476	4	US-09-252-991A-17887	Sequence 17887, A	1090	123.5	5.2	229	4	US-09-248-796A-24831	Sequence 24831, A
1018	126.5	5.4	650	4	US-09-252-991A-23546	Sequence 23546, A	1091	123.5	5.2	325	4	US-09-902-540-13678	Sequence 13678, A
1019	126.5	5.4	834	4	US-09-252-991A-28145	Sequence 28145, A	1092	123.5	5.2	501	4	US-09-252-991A-19191	Sequence 19191, A
1020	126.5	5.4	1011	4	US-09-252-991A-32419	Sequence 32419, A	1093	123.5	5.2	704	4	US-09-270-767-46362	Sequence 46362, A
1021	126.5	5.4	2142	4	US-09-338-092-1142	Sequence 1142, Ap	1094	123.5	5.2	742	4	US-09-949-016-7729	Sequence 7729, Ap
1022	126.5	5.4	2442	3	US-09-514-247A-10	Sequence 10, Appl	1095	123.5	5.2	783	4	US-09-252-991A-18035	Sequence 18035, A
1023	126.5	5.4	2442	3	US-09-538-092-1370	Sequence 1370, Ap	1096	123.5	5.2	1403	2	US-08-387-942C-3	Sequence 3, Appl
1024	126	5.3	97	1	US-07-609-716-99	Sequence 99, Appl	1097	123	5.2	179	4	US-09-270-767-57837	Sequence 57837, A
1025	126	5.3	97	3	US-08-475-411A-99	Sequence 99, Appl	1098	123	5.2	208	4	US-09-252-991A-37661	Sequence 37661, A
1026	126	5.3	97	3	US-08-478-029A-99	Sequence 99, Appl	1099	123	5.2	252	4	US-09-431-887-17	Sequence 17, Appl
1027	126	5.3	208	3	US-09-128-450-18	Sequence 18, Appl	1100	123	5.2	321	3	US-08-485-511A-4	Sequence 4, Appl
1028	126	5.3	208	3	US-09-823-494-18	Sequence 18, Appl	1101	123	5.2	321	3	US-09-538-092-1096	Sequence 1096, Ap
1029	126	5.3	253	4	US-09-919-172-57	Sequence 57, Appl	1102	123	5.2	524	4	US-09-252-991A-23901	Sequence 23901, A
1030	126	5.3	253	4	US-09-976-594-72	Sequence 72, Appl	1103	123	5.2	588	4	US-09-252-991A-18578	Sequence 18578, A
1031	126	5.3	374	4	US-09-949-016-7191	Sequence 7191, Ap	1104	123	5.2	801	1	US-07-906-349A-6	Sequence 6, Appl
1032	126	5.3	383	4	US-09-352-991A-22283	Sequence 22283, A	1105	123	5.2	1620	1	US-08-542-363-2	Sequence 2, Appl
1033	126	5.3	584	4	US-09-252-991A-21071	Sequence 21071, A	1106	123	5.2	1620	3	US-09-100-089-2	Sequence 2, Appl
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1035	126	5.3	891	4	US-09-949-016-7798	Sequence 7798, Ap	1108	123	5.2	1620	4	US-09-827-949-2	Sequence 2, Appl
1036	126	5.3	1394	4	US-09-902-540-16497	Sequence 16497, A	1109	122.5	5.2	155	1	US-08-458-298-15	Sequence 15, Appl
1037	126	5.3	1400	3	US-08-630-915A-37	Sequence 37, Appl	1110	122.5	5.2	155	1	US-08-209-747-15	Sequence 15, Appl
1038	126	5.3	1400	4	US-09-879-957-37	Sequence 37, Appl	1111	122.5	5.2	189	4	US-09-710-279-2692	Sequence 2692, Ap
1039	125.5	5.3	232	6	517843-7	Patent No. 517843	1112	122.5	5.2	203	4	US-09-270-767-35326	Sequence 35326, A
1040	125.5	5.3	232	6	517843-7	Patent No. 517843	1113	122.5	5.2	203	4	US-09-270-767-35326	Sequence 35326, A
1041	125.5	5.3	334	1	US-08-712-948-1	Sequence 1, Appl	1114	122.5	5.2	226	4	US-09-252-991A-23893	Sequence 23893, A
1042	125.5	5.3	344	1	US-07-941-523-24	Sequence 24, Appl	1115	122.5	5.2	528	4	US-09-270-767-42914	Sequence 42914, A
1043	125.5	5.3	556	4	US-09-352-991A-27601	Sequence 27601, A	1116	122.5	5.2	601	4	US-09-252-991A-22594	Sequence 22594, A
1044	125.5	5.3	757	4	US-09-252-991A-25918	Sequence 25918, A	1117	122.5	5.2	606	4	US-09-248-796A-14276	Sequence 14276, A
1045	125.5	5.3	933	3	US-08-293-728-2	Sequence 2, Appl	1118	122.5	5.2	763	4	US-09-252-991A-30146	Sequence 30146, A
1046	125.5	5.3	933	3	US-09-421-868-2	Sequence 2, Appl	1119	122.5	5.2	930	4	US-09-198-452A-470	Sequence 470, App
1047	125.5	5.3	936	4	US-08-956-171B-5249	Sequence 5249, Ap	1120	122.5	5.2	938	4	US-09-438-185A-448	Sequence 448, App
1048	125.5	5.3	936	4	US-08-781-986A-5249	Sequence 5249, Ap	1121	122.5	5.2	1085	4	US-09-841-334A-39	Sequence 39, Appl
1049	125	5.3	254	3	US-09-128-450-26	Sequence 26, Appl	1122	122.5	5.2	1085	4	US-09-837-969A-39	Sequence 39, Appl

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1124	122	5.2	253	4	US-09-431-887-7	Sequence 7, Appli	1197	121	5.1	2104	2	US-08-808-793-4	Sequence 4, Appli
1125	122	5.2	253	4	US-09-431-887-9	Sequence 9, Appli	1198	121	5.1	2104	3	US-08-772-512A-4	Sequence 4, Appli
1126	122	5.2	253	4	US-09-431-887-10	Sequence 10, Appl	1199	121	5.1	2104	4	US-09-428-371-4	Sequence 4, Appli
1127	122	5.2	253	4	US-09-431-887-11	Sequence 11, Appl	1200	120.5	5.1	83	1	US-07-609-716-101	Sequence 101, App
1128	122	5.2	253	4	US-09-431-887-12	Sequence 12, Appl	1201	120.5	5.1	83	3	US-08-475-411A-101	Sequence 101, App
1129	122	5.2	253	4	US-09-431-887-13	Sequence 13, Appl	1202	120.5	5.1	83	3	US-08-478-029A-101	Sequence 101, App
1130	122	5.2	256	4	US-09-431-887-14	Sequence 14, Appl	1203	120.5	5.1	88	4	US-09-248-796A-27988	Sequence 27988, A
1131	122	5.2	302	4	US-10-029-180-18	Sequence 18, Appl	1204	120.5	5.1	119	4	US-09-902-540-10158	Sequence 10158, A
1132	122	5.2	304	4	US-09-252-991A-23016	Sequence 23016, A	1205	120.5	5.1	133	4	US-09-270-767-39893	Sequence 39893, A
1133	122	5.2	311	4	US-09-949-016-8142	Sequence 8142, Ap	1206	120.5	5.1	133	4	US-09-270-767-55110	Sequence 55110, A
1134	122	5.2	380	4	US-09-270-767-43626	Sequence 43626, A	1207	120.5	5.1	240	4	US-09-252-991A-21852	Sequence 21852, A
1135	122	5.2	392	4	US-09-949-016-6078	Sequence 6078, Ap	1208	120.5	5.1	252	4	US-09-431-887-32	Sequence 32, Appl
1136	122	5.2	466	3	US-09-215-221-24	Sequence 24, Appl	1209	120.5	5.1	308	4	US-09-252-991A-217249	Sequence 217249, A
1137	122	5.2	471	4	US-09-538-092-837	Sequence 837, App	1210	120.5	5.1	374	4	US-09-252-991A-28527	Sequence 28527, A
1138	122	5.2	476	4	US-09-248-796A-18994	Sequence 18994, A	1211	120.5	5.1	394	4	US-09-252-991A-28148	Sequence 28148, A
1139	122	5.2	551	2	US-09-033-537A-1	Sequence 1, Appli	1212	120.5	5.1	408	4	US-09-543-681A-6442	Sequence 6442, Ap
1140	122	5.2	552	4	US-09-252-991A-25589	Sequence 25589, A	1213	120.5	5.1	43	4	US-09-252-991A-30036	Sequence 30036, A
1141	122	5.2	639	4	US-09-232-991A-28453	Sequence 28453, A	1214	120.5	5.1	474	4	US-09-252-991A-28084	Sequence 28084, A
1142	122	5.2	735	4	US-09-949-016-10120	Sequence 10120, A	1215	120.5	5.1	491	4	US-09-252-991A-22394	Sequence 22394, A
1143	122	5.2	989	3	US-08-213-419B-2	Sequence 2, Appli	1216	120.5	5.1	863	4	US-09-252-991A-26099	Sequence 26099, A
1144	122	5.2	989	3	US-08-213-419B-4	Sequence 4, Appli	1217	120.5	5.1	918	4	US-09-300-650B-1	Sequence 1, Appli
1145	122	5.2	1239	2	US-08-937-931-2	Sequence 2, Appli	1218	120.5	5.1	1591	4	US-09-270-767-45698	Sequence 45698, A
1146	122	5.2	1239	3	US-09-285-502-2	Sequence 2, Appli	1219	120	5.1	72	1	US-07-609-716-44	Sequence 44, Appl
1147	122	5.2	1239	3	US-09-709-126-2	Sequence 2, Appli	1220	120	5.1	72	3	US-08-475-411A-44	Sequence 44, Appl
1148	122	5.2	1239	3	US-09-871-385A-2	Sequence 2, Appli	1221	120	5.1	72	3	US-08-478-029A-44	Sequence 44, Appl
1149	121.5	5.1	75	1	US-07-609-716-39	Sequence 39, Appl	1222	120	5.1	171	4	US-09-489-039A-8235	Sequence 8235, Ap
1150	121.5	5.1	75	3	US-08-475-411A-39	Sequence 39, Appl	1223	120	5.1	262	4	US-09-949-016-7209	Sequence 7209, Ap
1151	121.5	5.1	75	3	US-08-478-029A-39	Sequence 39, Appl	1224	120	5.1	269	3	US-09-134-001C-3461	Sequence 3461, Ap
1152	121.5	5.1	86	1	US-07-609-716-102	Sequence 102, App	1225	120	5.1	271	4	US-09-252-991A-17292	Sequence 17292, A
1153	121.5	5.1	86	3	US-08-475-411A-102	Sequence 102, App	1226	120	5.1	337	3	US-08-469-318-148	Sequence 148, App
1154	121.5	5.1	86	3	US-08-478-029A-102	Sequence 102, App	1227	120	5.1	337	3	US-08-468-609A-148	Sequence 148, App
1155	121.5	5.1	180	4	US-10-029-180-38	Sequence 38, Appl	1228	120	5.1	337	3	US-08-446-872A-148	Sequence 148, App
1156	121.5	5.1	207	4	US-09-248-796A-21137	Sequence 21137, A	1229	120	5.1	337	4	US-08-762-227A-148	Sequence 148, App
1157	121.5	5.1	236	4	US-09-248-796A-22126	Sequence 22126, A	1230	120	5.1	337	5	PCT-US95-01185-148	Sequence 148, App
1158	121.5	5.1	256	4	US-09-252-991A-25670	Sequence 25670, A	1231	120	5.1	382	3	US-08-213-419B-19	Sequence 19, Appl
1159	121.5	5.1	330	2	US-08-712-948-2	Sequence 2, Appli	1232	120	5.1	468	4	US-09-863-901-4	Sequence 4, Appl
1160	121.5	5.1	330	4	US-09-949-016-6621	Sequence 7988, Ap	1233	120	5.1	477	4	US-09-252-991A-19831	Sequence 19831, A
1161	121.5	5.1	334	4	US-09-949-016-7988	Sequence 7988, Ap	1234	120	5.1	508	4	US-09-949-016-6316	Sequence 6316, Ap
1162	121.5	5.1	464	4	US-09-270-767-61287	Sequence 61287, A	1235	120	5.1	508	4	US-09-902-540-10562	Sequence 10562, A
1163	121.5	5.1	495	3	US-08-828-7A1B-4	Sequence 4, Appli	1236	120	5.1	518	4	US-09-949-016-11589	Sequence 11589, A
1164	121.5	5.1	495	3	US-09-160-567-4	Sequence 4, Appli	1237	120	5.1	518	2	US-08-818-024-4	Sequence 4, Appli
1165	121.5	5.1	495	4	US-09-710-299-4	Sequence 4, Appli	1238	120	5.1	539	3	US-09-334-775A-4	Sequence 4, Appli
1166	121.5	5.1	495	4	US-09-509-031-4	Sequence 4, Appli	1239	120	5.1	539	3	US-08-789-275-6	Sequence 6, Appli
1167	121.5	5.1	514	3	US-08-796-899-25	Sequence 25, Appl	1240	119.5	5.1	213	4	US-09-489-039A-11130	Sequence 11130, A
1168	121.5	5.1	635	4	US-09-252-991A-17122	Sequence 17122, A	1241	119.5	5.1	354	4	US-09-949-016-11550	Sequence 11550, A
1169	121.5	5.1	683	4	US-09-949-016-11117	Sequence 11117, A	1242	119.5	5.1	420	2	US-08-845-998-8	Sequence 8, Appli
1170	121.5	5.1	718	4	US-09-902-540-14365	Sequence 14365, A	1243	119.5	5.1	420	3	US-09-206-537-8	Sequence 8, Appli
1171	121	5.1	191	4	US-09-252-991A-18626	Sequence 18626, A	1244	119.5	5.1	420	3	US-09-430-854-8	Sequence 8, Appli
1172	121	5.1	194	4	US-09-431-887-13	Sequence 13, Appl	1245	119.5	5.1	464	4	US-09-949-016-9828	Sequence 9828, Ap
1173	121	5.1	252	4	US-09-431-887-13	Sequence 13, Appl	1246	119.5	5.1	531	4	US-09-252-991A-31109	Sequence 31109, A
1174	121	5.1	283	4	US-09-270-767-46301	Sequence 46301, A	1247	119.5	5.1	690	4	US-09-248-796A-19169	Sequence 19169, A
1175	121	5.1	330	1	US-08-642-255-32	Sequence 32, Appl	1248	119.5	5.1	1427	4	US-09-252-991A-20577	Sequence 20577, A
1176	121	5.1	335	3	US-08-469-318-143	Sequence 143, App	1249	119.5	5.1	1548	4	US-09-252-991A-22301	Sequence 22301, A
1177	121	5.1	335	3	US-08-468-609A-143	Sequence 143, App	1250	119	5.0	163	4	US-09-270-767-39871	Sequence 39871, A
1178	121	5.1	335	3	US-08-446-872A-143	Sequence 143, App	1251	119	5.0	163	4	US-09-270-767-55088	Sequence 55088, A
1179	121	5.1	335	4	US-08-762-227A-143	Sequence 143, App	1252	119	5.0	213	4	US-09-252-991A-16621	Sequence 16621, A
1180	121	5.1	335	5	PCT-US95-01185-143	Sequence 143, App	1253	119	5.0	255	1	US-08-242-188-4	Sequence 4, Appli
1181	121	5.1	337	4	US-09-270-767-45762	Sequence 45762, A	1254	119	5.0	255	1	US-08-509-261A-4	Sequence 4, Appli
1182	121	5.1	367	3	US-08-213-419B-15	Sequence 15, Appl	1255	119	5.0	255	1	US-08-660-626-10	Sequence 10, Appl
1183	121	5.1	408	1	US-07-609-716-65	Sequence 65, Appl	1256	119	5.0	255	1	US-08-692-892-4	Sequence 4, Appli
1184	121	5.1	408	3	US-08-475-411A-65	Sequence 65, Appl	1257	119	5.0	255	2	US-08-713-939A-4	Sequence 4, Appli
1185	121	5.1	408	3	US-08-478-029A-65	Sequence 65, Appl	1258	119	5.0	255	2	US-08-868-162A-24	Sequence 24, Appl
1186	121	5.1	412	4	US-09-252-991A-26284	Sequence 26284, A	1259	119	5.0	255	3	US-09-031-168-10	Sequence 10, Appl
1187	121	5.1	444	4	US-09-252-991A-22448	Sequence 22448, A	1260	119	5.0	255	3	US-09-036-579-4	Sequence 4, Appli
1188	121	5.1	461	4	US-09-902-540-10506	Sequence 10506, A	1261	119	5.0	255	3	US-09-550-374-4	Sequence 4, Appli
1189	121	5.1	509	4	US-09-252-991A-32576	Sequence 32576, A	1262	119	5.0	255	4	US-09-943-906-4	Sequence 4, Appli
1190	121	5.1	546	2	US-09-067-351-1	Sequence 1, Appli	1263	119	5.0	255	4	US-09-669-516C-10	Sequence 10, Appl
1191	121	5.1	546	3	US-09-360-490-1	Sequence 1, Appli	1264	119	5.0	259	4	US-09-252-991A-21547	Sequence 21547, A
1192	121	5.1	642	4	US-09-252-991A-21889	Sequence 21889, A	1265	119	5.0	322	1	US-08-014-943A-2	Sequence 2, Appli
1193	121	5.1	686	4	US-09-252-991A-20509	Sequence 20509, A	1266	119	5.0	322	1	US-08-486-421-3	Sequence 3, Appli
1194	121	5.1	859	1	US-08-395-580-2	Sequence 2, Appli	1267	119	5.0	322	1	US-08-470-911-3	Sequence 3, Appli
1195	121	5.1	859	5	PCT-US95-02792-2	Sequence 2, Appli	1268	119	5.0	322	2	US-08-486-809-3	Sequence 3, Appli

1269	119	5.0	397	4	US-09-252-991A-24025	Sequence 24025, A	1342	117	5.0	691	1	US-08-066-167-4	Sequence 4, Appli
1270	119	5.0	407	4	US-09-252-991A-26060	Sequence 26060, A	1343	117	5.0	691	2	US-08-449-733-2	Sequence 2, Appli
1271	119	5.0	446	2	US-08-836-854-15	Sequence 15, Appl	1344	117	5.0	692	3	US-08-448-194-62	Sequence 62, Appl
1272	119	5.0	541	4	US-09-252-991A-24521	Sequence 24521, A	1345	117	5.0	692	3	US-08-867-921-62	Sequence 62, Appl
1273	119	5.0	616	4	US-09-252-991A-20777	Sequence 20777, A	1346	117	5.0	711	1	US-08-487-890A-98	Sequence 98, Appl
1274	119	5.0	654	4	US-09-620-412C-341	Sequence 341, App	1347	117	5.0	711	1	US-08-478-435-98	Sequence 98, Appl
1275	119	5.0	654	4	US-09-598-419-341	Sequence 341, App	1348	117	5.0	711	2	US-08-337-483-98	Sequence 98, Appl
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1277	119	5.0	1321	2	US-08-317-310A-64	Sequence 64, Appl	1350	117	5.0	711	3	US-08-474-671-98	Sequence 98, Appl
1278	119	5.0	2110	4	US-09-270-767-46547	Sequence 46547, A	1351	117	5.0	711	3	US-08-483-577A-98	Sequence 98, Appl
1279	118.5	5.0	74	1	US-07-609-716-63	Sequence 63, Appl	1352	117	5.0	711	3	US-08-448-194-8	Sequence 8, Appli
1280	118.5	5.0	74	3	US-08-475-411A-63	Sequence 63, Appl	1353	117	5.0	711	3	US-08-867-438-98	Sequence 98, Appl
1281	118.5	5.0	74	3	US-08-478-029A-63	Sequence 63, Appl	1354	117	5.0	711	3	US-08-867-921-8	Sequence 8, Appli
1282	118.5	5.0	309	4	US-09-270-767-44846	Sequence 44846, A	1355	117	5.0	711	3	US-08-637-654-98	Sequence 98, Appl
1283	118.5	5.0	310	4	US-09-248-796A-24630	Sequence 24630, A	1356	117	5.0	711	3	US-08-649-518-98	Sequence 98, Appl
1284	118.5	5.0	444	4	US-09-902-540-12378	Sequence 12378, A	1357	117	5.0	752	4	US-09-693-543-89	Sequence 89, Appl
1285	118.5	5.0	473	4	US-09-252-991A-16904	Sequence 16904, A	1358	117	5.0	785	4	US-09-538-092-872	Sequence 872, App
1286	118.5	5.0	489	4	US-09-252-991A-16940	Sequence 16940, A	1359	117	5.0	1266	4	US-09-949-016-8963	Sequence 8963, Ap
1287	118.5	5.0	508	4	US-09-270-767-43201	Sequence 43201, A	1360	116.5	4.9	258	4	US-09-252-991A-30969	Sequence 30969, A
1288	118.5	5.0	1234	2	US-08-317-310A-15	Sequence 15, Appl	1361	116.5	4.9	333	4	US-09-107-532A-6475	Sequence 6475, Ap
1289	118.5	5.0	1234	5	PCT-US95-13041-15	Sequence 15, Appl	1362	116.5	4.9	338	4	US-09-270-767-43629	Sequence 43629, A
1290	118	5.0	139	4	US-09-270-767-36667	Sequence 36667, A	1363	116.5	4.9	392	4	US-09-949-016-7351	Sequence 7351, Ap
1291	118	5.0	139	4	US-09-270-767-51884	Sequence 51884, A	1364	116.5	4.9	404	4	US-09-252-991A-25762	Sequence 25762, A
1292	118	5.0	331	4	US-09-949-016-6708	Sequence 6708, Ap	1365	116.5	4.9	407	4	US-09-949-016-6156	Sequence 6156, Ap
1293	118	5.0	437	2	US-08-935-450-8	Sequence 8, Appli	1366	116.5	4.9	460	4	US-09-252-991A-33082	Sequence 33082, A
1294	118	5.0	437	4	US-09-338-123-8	Sequence 8, Appli	1367	116.5	4.9	483	4	US-09-949-016-10171	Sequence 10171, A
1295	118	5.0	445	4	US-09-252-991A-28706	Sequence 28706, A	1368	116.5	4.9	557	4	US-09-902-540-14660	Sequence 14660, A
1296	118	5.0	460	4	US-09-252-991A-33090	Sequence 33090, A	1369	116.5	4.9	617	1	US-08-137-614A-26	Sequence 26, Appl
1297	118	5.0	478	4	US-09-252-991A-25191	Sequence 25191, A	1370	116.5	4.9	637	3	US-08-072-064-1	Sequence 1, Appli
1298	118	5.0	524	4	US-09-252-991A-19671	Sequence 19671, A	1371	116.5	4.9	637	3	US-08-072-064-4	Sequence 4, Appli
1299	118	5.0	551	4	US-09-252-991A-30116	Sequence 30116, A	1372	116.5	4.9	637	3	US-08-072-064-6	Sequence 6, Appli
1300	118	5.0	656	4	US-09-902-540-12404	Sequence 12404, A	1373	116.5	4.9	637	3	US-08-072-064-8	Sequence 8, Appli
1301	118	5.0	851	4	US-09-252-991A-30624	Sequence 30624, A	1374	116.5	4.9	637	5	PCT-US92-08558-1	Sequence 1, Appli
1302	118	5.0	1749	4	US-09-640-419C-28	Sequence 28, Appl	1375	116.5	4.9	728	4	US-09-252-991A-33613	Sequence 33613, A
1303	117.5	5.0	141	4	US-09-328-352-7100	Sequence 7100, Ap	1376	116.5	4.9	786	4	US-09-252-991A-30441	Sequence 30441, A
1304	117.5	5.0	142	1	US-07-609-716-100	Sequence 100, App	1377	116.5	4.9	990	4	US-09-252-991A-32469	Sequence 32469, A
1305	117.5	5.0	142	3	US-08-475-411A-100	Sequence 100, App	1378	116.5	4.9	1155	1	US-08-094-948A-29	Sequence 29, Appl
1306	117.5	5.0	142	3	US-08-478-029A-100	Sequence 100, App	1379	116.5	4.9	1155	5	PCT-US96-09319-29	Sequence 29, Appl
1307	117.5	5.0	163	4	US-09-248-796A-18929	Sequence 18929, A	1380	116	4.9	173	4	US-09-270-767-60931	Sequence 60931, A
1308	117.5	5.0	163	4	US-10-000-489-58	Sequence 58, Appl	1381	116	4.9	251	4	US-09-538-092-840	Sequence 840, App
1309	117.5	5.0	187	4	US-09-640-211A-1129	Sequence 1129, Ap	1382	116	4.9	314	4	US-09-736-457-1863	Sequence 1863, Ap
1310	117.5	5.0	249	4	US-09-270-767-44857	Sequence 44857, A	1383	116	4.9	326	4	US-09-252-991A-33000	Sequence 33000, A
1311	117.5	5.0	320	4	US-09-949-016-8196	Sequence 8196, Ap	1384	116	4.9	340	4	US-09-248-796A-18866	Sequence 18866, A
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1314	117.5	5.0	359	4	US-09-252-991A-18788	Sequence 18788, A	1387	116	4.9	569	4	US-09-252-991A-35582	Sequence 25582, A
1315	117.5	5.0	414	4	US-09-252-991A-31110	Sequence 31110, A	1388	116	4.9	580	4	US-09-922-364A-2	Sequence 2, Appli
1316	117.5	5.0	428	4	US-09-252-991A-20199	Sequence 20199, A	1389	116	4.9	580	4	US-10-115-415-2	Sequence 2, Appli
1317	117.5	5.0	444	1	US-07-881-075-3	Sequence 3, Appli	1390	116	4.9	580	4	US-10-115-415-2	Sequence 2, Appli
1318	117.5	5.0	444	1	US-08-120-827-3	Sequence 3, Appli	1391	116	4.9	580	4	US-10-115-671-2	Sequence 2, Appli
1319	117.5	5.0	444	1	US-08-478-675-3	Sequence 3, Appli	1392	116	4.9	580	4	US-10-115-671-2	Sequence 2, Appli
1320	117.5	5.0	447	4	US-09-252-991A-27755	Sequence 27755, A	1393	116	4.9	624	3	US-09-336-447A-7	Sequence 7, Appli
1321	117.5	5.0	513	2	US-08-676-166A-4	Sequence 4, Appli	1394	116	4.9	624	4	US-09-952-267B-7	Sequence 7, Appli
1322	117.5	5.0	521	4	US-09-270-767-44481	Sequence 44481, A	1395	116	4.9	634	4	US-09-949-016-7542	Sequence 7542, Ap
1323	117.5	5.0	718	4	US-09-252-991A-32743	Sequence 32743, A	1396	116	4.9	715	4	US-09-252-991A-32740	Sequence 32740, A
1324	117.5	5.0	1489	6	5183745-2	Patent No. 5183745	1397	116	4.9	979	4	US-09-538-092-990	Sequence 990, App
1325	117.5	5.0	1489	6	5183745-2	Patent No. 5183745	1398	116	4.9	997	2	US-08-387-942C-4	Sequence 4, Appli
1326	117	5.0	63	4	US-09-646-691B-10	Sequence 10, Appl	1399	116	4.9	1414	4	US-09-438-185A-446	Sequence 446, App
1327	117	5.0	144	1	US-08-642-255-49	Sequence 49, Appl	1400	116	4.9	1663	5	PCT-US93-07261-16	Sequence 16, Appl
1328	117	5.0	235	4	US-09-205-258-318	Sequence 318, App	1401	116	4.9	2441	1	US-08-194-468-2	Sequence 2, Appli
1329	117	5.0	235	4	US-09-205-258-738	Sequence 738, App	1402	116	4.9	2441	3	US-08-961-739-2	Sequence 2, Appli
1330	117	5.0	233	4	US-09-252-991A-32459	Sequence 32459, A	1403	116	4.9	2441	3	US-09-514-247A-8	Sequence 8, Appli
1331	117	5.0	234	4	US-09-431-887-20	Sequence 20, Appl	1404	116	4.9	2441	4	US-09-686-316-2	Sequence 2, Appli
1332	117	5.0	254	4	US-09-431-887-21	Sequence 21, Appl	1405	115.5	4.9	93	4	US-09-072-596-272	Sequence 272, App
1333	117	5.0	254	4	US-09-431-887-22	Sequence 22, Appl	1406	115.5	4.9	93	4	US-09-072-967-277	Sequence 277, App
1334	117	5.0	259	4	US-09-431-887-33	Sequence 33, Appl	1407	115.5	4.9	206	4	US-09-252-991A-31481	Sequence 31481, A
1335	117	5.0	314	4	US-09-949-016-6437	Sequence 6437, Ap	1408	115.5	4.9	215	4	US-09-252-991A-25666	Sequence 25666, A
1336	117	5.0	321	4	US-09-252-991A-24270	Sequence 24270, A	1409	115.5	4.9	245	4	US-09-949-016-8385	Sequence 8385, Ap
1337	117	5.0	343	4	US-09-252-991A-17876	Sequence 17876, A	1410	115.5	4.9	253	4	US-09-252-991A-29632	Sequence 29632, A
1338	117	5.0	344	4	US-09-949-016-9889	Sequence 9889, Ap	1411	115.5	4.9	271	4	US-10-237-551-74	Sequence 74, Appl
1339	117	5.0	356	4	US-09-252-991A-21526	Sequence 21526, A	1412	115.5	4.9	411	4	US-09-248-796A-4488	Sequence 14848, A
1340	117	5.0	662	4	US-09-252-991A-30943	Sequence 30943, A	1413	115.5	4.9	446	3	US-08-956-254-2	Sequence 2, Appli
1341	117	5.0	691	1	US-08-064-174-2	Sequence 2, Appli	1414	115.5	4.9	446	3	US-09-008-388-1	Sequence 1, Appli

COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1136 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-806-029-9

Query Match 17.0%; Score 402.5; DB 3; Length 1136;
Best Local Similarity 30.4%; Pred. No. 2.9e-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;

QY 17 GSGEAGPLQSGEESTGTNIGELHGLDLSRGVKAIGKEAGGAGSKVSEALQGGTR 76
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QY 77 EAVGTGVRO-VPGFGAADALGNRVGEAAHALGNTGHEIGRQAEADVIRHGADAVRGSWQGV 135
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DB 850 GSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 902
QY 194 GQG-GNGGPPNFTNTQGAQVAPQYGSVRAASQNEGCTNPPPSGGGGS-----SNSGGG 247
DB 903 GSGAGAGSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 962
QY 248 SGSQSGS-----SGSGNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSS 304
DB 963 SGAGAGSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1022
QY 305 GSSESSWSSSTGSSGNHNG---GSGGNGHKGPKCEKPGNEARGSGE-SGIQPRGQGVSSN 360
DB 1023 GAGAGSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1082
QY 361 MREISKEGNRLLGSGDNYRGQSSWGSWGSGGDAVGGVNTVNSSTSPGMFNTFTFW 415
DB 1083 AGAGSGAG-----AGSGAAGYAGAGSGAGAGSGAGAGAGAGAGAGAGAGAG 1133

RESULT 3

US-07-609-716-31
Sequence 31, Application US/07609716
Patent No. 5514581
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinant Protein Polymer
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
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CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-609-716-31

Query Match 17.0%; Score 402.5; DB 1; Length 1177;
Best Local Similarity 30.4%; Pred. No. 3e-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;

QY 17 GSGEAGPLQSGEESTGTNIGELHGLDLSRGVKAIGKEAGGAGSKVSEALQGGTR 76
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DB 831 AGSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 890
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DB 891 GSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 943
QY 194 GQG-GNGGPPNFTNTQGAQVAPQYGSVRAASQNEGCTNPPPSGGGGS-----SNSGGG 247
DB 944 GSGAGAGSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003
QY 248 SGSQSGS-----SGSGNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSS 304
DB 1004 SGAGAGSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1063
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DB 1064 GAGAGSGAGAGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1123
QY 361 MREISKEGNRLLGSGDNYRGQSSWGSWGSGGDAVGGVNTVNSSTSPGMFNTFTFW 415
DB 1124 AGAGSGAG-----AGSGAAGYAGAGSGAGAGSGAGAGAGAGAGAGAGAGAG 1174

RESULT 4

US-08-175-155-29
Sequence 29, Application US/08175155
Patent No. 5641648
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.

Db 1004 SGAGSGAGAGGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 1063
QY 305 GSBSWGSSTGSSSGNHG---GSGGGNGHKGPKCEKPNEARGSGB-SGIQGFRCQGVSSN 360
Db 1064 GAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGG 1123
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Db 1124 AGAGSGAG----AGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1174

RESULT 6
US-08-707-237A-35
; Sequence 35, Application US/08707237A
; Patent No. 5830713
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Capello, Joseph W.
; APPLICANT: Crissman, John W.
; APPLICANT: Dorman, Mary A.
; TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
; TITLE OF INVENTION: REPETITIVE DNA
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/707,237A
; FILING DATE: 03-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/609,716
; FILING DATE: 06-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/269,429
; FILING DATE: 09-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-10/WH/D
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1177 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-08-707-237A-35
Query Match 17.0%; Score 402.5; DB 2; Length 1177;
Best Local Similarity 30.4%; Pred. No. 38-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;
QY 17 GSSEAGPLQSGSEESTGTNTIGEAIGHGLGDALSEGVGKATGKEAGGAAGSKVSEALQGGTR 76
Db 771 GAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 830
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Db 831 AGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 890
QY 136 PGHSGAWETSGGHGI-FGSQGGILG-GQGQNGPGLGTWPWHGYPGNSAGSFGMNPQAPW 193
Db 891 GSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 943
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Db 1004 SGAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1063
QY 305 GSSEWSGSSTGSSSGNHG---GSGGGNGHKGPKCEKPNEARGSGB-SGIQGFRCQGVSSN 360
Db 1064 GAGAGSGAGAGSGAAGYGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1123
QY 361 MREISKEGNRLGGSDNYRGQSSWGSGGDDAVGGVNTVNSSETSPGMFNFDTFW 415
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RESULT 7
US-08-482-085B-64
; Sequence 64, Application US/08482085B
; Patent No. 6018030
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Richardson, Charles
; APPLICANT: Chambers, James
; APPLICANT: Causey, Stuart
; APPLICANT: Pollock, Thomas J.
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W.
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,085B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-6/RPT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-085B-64

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Best Local Similarity 30.4%; Pred. No. 3e-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;

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QY 77 EAVGTGVRO-VPGFGADALGNRVGEAAHALNGTGHIEIGRAEDVIRHGADAVRGSQGV 135
D 831 AGSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 890
QY 136 PGHSGAWETSGHGI-FGSGGGLG-GGCGNPGGLGTPVHGYPCNSAGSFGHNPQCAPW 193
D 891 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 943
QY 194 GQG-GNGGPPNFCTNTQGAQVAPQGYSVRASNQNEGCTNPPPSGGGGS-----SNSGGG 247
D 944 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003
QY 248 SGQSQGS---SGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSG 304
D 1004 SGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1063
QY 305 GSSESSWGSSSTGSSSGNHG---GSGCGNGHKPGCEKPCNEARSGE-SGIQGFROGVSSN 360
D 1064 GAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1123
QY 361 MREISKEGNRLGSGDNYRGQGSWGGGDAVGGVNTVNSSTSPGMFNFDTFW 415
D 1124 AGAGSGAG---AGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1174

RESULT 8
US-08-475-411A-31
; Sequence 31, Application US/08475411A
; Patent No. 6140072
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Functional Recombinantly Prepared
; TITLE OF INVENTION: Synthetic Protein Polymer
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,411A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 06-NOV-1990
; APPLICATION NUMBER: US 07/609,716
; PRIOR APPLICATION DATA:
; FILING DATE: 09-NOV-1988
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-9/RPT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-475-411A-31

Query Match 17.0%; Score 402.5; DB 3; Length 1177;
Best Local Similarity 30.4%; Pred. No. 3e-20;
Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;

QY 17 GSCEAGPLQSGEESTGTNIGELGHLGDLSEGVGKAIGKEAGGAAGSKVSEALGQTR 76
D 771 GAGSGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 830
QY 77 EAVGTGVRO-VPGFGADALGNRVGEAAHALNGTGHIEIGRAEDVIRHGADAVRGSQGV 135
D 831 AGSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 890
QY 136 PGHSGAWETSGHGI-FGSGGGLG-GGCGNPGGLGTPVHGYPCNSAGSFGHNPQCAPW 193
D 891 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 943
QY 194 GQG-GNGGPPNFCTNTQGAQVAPQGYSVRASNQNEGCTNPPPSGGGGS-----SNSGGG 247
D 944 GSGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003
QY 248 SGQSQGS---SGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSG 304
D 1004 SGAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1063
QY 305 GSSESSWGSSSTGSSSGNHG---GSGCGNGHKPGCEKPCNEARSGE-SGIQGFROGVSSN 360
D 1064 GAGAGSAAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1123
QY 361 MREISKEGNRLGSGDNYRGQGSWGGGDAVGGVNTVNSSTSPGMFNFDTFW 415
D 1124 AGAGSGAG---AGSGAAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1174

RESULT 9
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; Sequence 31, Application US/08478029A
; Patent No. 6184348
; GENERAL INFORMATION:
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; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-10/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-707-237A-54

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Best Local Similarity 30.4%; Pred. No. 4.7e-20;
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

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Db 896 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 955
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RESULT 13
US-08-806-029-10
; Sequence 10, Application US/08806029
; Patent No. 6380154
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Stedronsky, Erwin R.
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
; DELIVERY: Delivery and Tissue Augmentation
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806,029
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,237
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-806-029-10

Query Match 16.9%; Score 399; DB 3; Length 1059;
Best Local Similarity 30.4%; Pred. No. 4.7e-20;
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

QY 17 GSGEAGPLOSREESTGNIIEALGHLGDLALSGVGKAIKKEAGGAGSKVSEALQGQTR 76
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QY 77 EAVGTGVROPVPGFADALGNRVGEAAHALGNTGHEIGRQABDVIRHGADAVRGSWQGV 136
Db 725 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 784
QY 137 GHSAGMETSGHGIFGSGQLG-GGQGNPGLGTPVWHGYPGNSAGSGFMNPGAPWQ 195
Db 785 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGS 835
QY 196 GCGNGPPNPGTWTQGAQVPGYGSVRASNQNSGCTNPPPSGSGGS-SNSGGSGSGSGS 254
Db 836 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 895
QY 255 -SGSGGNDNNNGSSG-GSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS 312
Db 896 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 955
QY 313 STGSSGNHGGSGGNHKGPKCEKPGNEARSGE-SGICGFRGQGVSSNMREISKEGN 371
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QY 372 LGSGDNYRQGSWSGCGDAVGGVNTVNSSETSPGMFNFTFW 415
Db 1016 GAGAGS---GAGAGSGAGAGSGAGAGMDPGRYQLSAGRYHYQLVW 1056

RESULT 14
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; Sequence 83, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A
; APPLICANT: Cappello, Joseph
; APPLICANT: Crisman, John W
; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; UNITS OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESSES:

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Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:10:21 ; Search time 144 Seconds
(without alignments)
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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565	2363	100.0	440	14	US-10-223-084-150
566	2363	100.0	440	14	US-10-223-088-150
567	2363	100.0	440	14	US-10-223-090-150
573	2363	100.0	440	14	US-10-223-087-150
586	2363	100.0	440	14	US-10-223-085-150
592	2363	100.0	440	14	US-10-223-089-150
618	2363	100.0	440	14	US-10-174-587-202
688	2363	100.0	440	14	US-10-063-742-52
764	2363	100.0	440	14	US-10-013-909A-52
769	2363	100.0	440	14	US-10-223-081-150
807	2363	100.0	440	14	US-10-223-082-150

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848	2363	100.0	440	15	US-10-081-056-150	Sequence 150, App
859	2363	100.0	440	17	US-10-972-317-52	Sequence 52, Appl
860	2030	85.9	386	14	US-10-050-704-100	Sequence 100, App
861	2030	85.9	386	16	US-10-798-512-100	Sequence 100, App
862	450.5	19.1	1079	10	US-09-820-843A-20	Sequence 20, Appl
863	439.5	18.6	1306	15	US-10-282-122A-64405	Sequence 64405, A
864	415.5	17.6	1381	15	US-10-282-122A-64895	Sequence 64895, A
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870	402.5	17.0	1177	14	US-10-096-986-64	Sequence 64, Appl
871	399	16.9	1059	8	US-08-806-029-10	Sequence 10, Appl
872	399	16.9	1101	14	US-10-096-986-83	Sequence 83, Appl
873	392.5	16.6	923	15	US-10-282-122A-64474	Sequence 64474, A
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875	383	16.2	641	14	US-10-138-098-52	Sequence 52, Appl
876	383	16.2	641	14	US-10-294-804-4	Sequence 4, Appli
877	383	16.2	641	15	US-10-225-838B-22	Sequence 22, Appl
878	383	16.2	641	16	US-10-732-694-11	Sequence 11, Appl
879	383	16.2	641	17	US-10-476-615-52	Sequence 52, Appl
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885	373.5	15.8	584	15	US-10-282-122A-64903	Sequence 64903, A
886	373.5	15.8	667	15	US-10-282-122A-64494	Sequence 64494, A
887	372	15.7	694	15	US-10-282-122A-64726	Sequence 64726, A
888	371	15.7	615	15	US-10-282-122A-64786	Sequence 64786, A
889	371	15.7	651	9	US-09-861-597-1	Sequence 1, Appli
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891	371	15.7	651	17	US-10-887-100-1	Sequence 1, Appli
892	370.5	15.7	491	15	US-10-282-122A-64558	Sequence 64558, A
893	368	15.6	420	16	US-10-437-963-201378	Sequence 201378, A
894	367	15.5	1011	14	US-10-096-986-94	Sequence 94, Appl
895	367	15.5	691	17	US-10-488-056-48	Sequence 48, Appl
896	366	15.5	766	14	US-10-096-986-88	Sequence 88, Appl
897	366	15.5	799	14	US-10-096-986-89	Sequence 89, Appl
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907	358.5	15.2	486	16	US-10-437-963-117435	Sequence 117435, A
908	358.5	15.2	2055	14	US-10-096-986-81	Sequence 81, Appl
909	358	15.2	606	9	US-09-861-597-4	Sequence 4, Appli
910	358	15.2	606	9	US-09-861-597-6	Sequence 6, Appli
911	358	15.2	606	9	US-09-861-597-8	Sequence 8, Appli
912	358	15.2	606	17	US-10-887-100-4	Sequence 4, Appli
913	358	15.2	606	17	US-10-887-100-6	Sequence 6, Appli
914	358	15.2	606	17	US-10-887-100-8	Sequence 8, Appli
915	358	15.2	809	14	US-10-414-760-13	Sequence 13, Appl
916	358	15.2	818	14	US-10-414-760-22	Sequence 22, Appl
917	358	15.2	1617	14	US-10-414-760-14	Sequence 14, Appl
918	358	15.2	1626	14	US-10-414-760-24	Sequence 24, Appl
919	353	14.9	505	15	US-10-282-122A-62341	Sequence 62341, A
920	352	14.9	603	15	US-10-282-122A-64537	Sequence 64537, A
921	351.5	14.9	1056	8	US-08-806-029-29	Sequence 29, Appl
922	351	14.9	957	15	US-10-282-122A-64361	Sequence 64361, A
923	350.5	14.8	461	15	US-10-282-122A-64750	Sequence 64750, A
924	350.5	14.8	2257	14	US-10-096-986-82	Sequence 82, Appl
925	349	14.6	618	15	US-10-282-122A-64608	Sequence 64608, A
926	346	14.6	648	17	US-10-488-056-30	Sequence 30, Appl
927	344	14.6	283	9	US-09-864-761-36720	Sequence 36720, A
928	344	14.6	525	15	US-10-282-122A-64763	Sequence 64763, A
929	344	14.6	651	17	US-10-488-056-45	Sequence 45, Appl

930	342.5	14.5	629	16	US-10-406-832-29	Sequence 29, Appl	1027	302	12.8	714	17	US-10-887-100-10	Sequence 10, Appl
931	342.5	14.5	629	17	US-10-893-588-29	Sequence 29, Appl	1028	301.5	12.8	285	16	US-10-437-963-187773	Sequence 187773
932	342.5	14.5	629	18	US-10-282-122A-64613	Sequence 29, Appl	1029	300.5	12.7	768	14	US-08-806-023-35	Sequence 35, Appl
933	339.5	14.4	515	15	US-10-282-122A-64347	Sequence 64347, A	1030	300.5	12.7	884	14	US-10-117-931-15	Sequence 15, Appl
934	337	14.3	487	15	US-10-488-056-46	Sequence 46, Appl	1031	299	12.7	373	17	US-10-488-056-40	Sequence 40, Appl
935	336	14.2	1169	8	US-08-806-029-33	Sequence 33, Appl	1032	297.5	12.6	270	16	US-10-437-963-122263	Sequence 122263
936	334	14.1	498	15	US-10-225-838B-21	Sequence 21, Appl	1033	296.5	12.5	1024	8	US-08-806-029-31	Sequence 31, Appl
937	334	14.1	498	15	US-10-282-122A-64610	Sequence 64610, A	1034	294.5	12.5	832	8	US-08-806-029-27	Sequence 27, Appl
938	330	14.0	447	17	US-10-488-056-29	Sequence 29, Appl	1035	294	12.4	529	9	US-09-861-597-2	Sequence 2, Appl
939	329	13.9	780	15	US-10-441-965-19	Sequence 19, Appl	1036	294	12.4	529	17	US-10-887-100-2	Sequence 2, Appl
940	329	13.9	780	16	US-10-800-179-19	Sequence 19, Appl	1037	294	12.4	821	15	US-10-292-798-1370	Sequence 1370, Ap
941	327.5	13.9	334	14	US-10-259-678-728	Sequence 728, App	1038	293.5	12.4	611	14	US-10-086-510-4	Sequence 4, Appl
942	326	13.8	422	16	US-10-437-963-121579	Sequence 121579, A	1039	293	12.4	256	10	US-09-820-843A-18	Sequence 18, Appl
943	325.5	13.8	439	15	US-10-282-122A-64905	Sequence 64905, A	1040	292	12.4	912	17	US-10-488-056-50	Sequence 50, Appl
944	324	13.7	1038	16	US-10-800-179-30	Sequence 30, Appl	1041	290.5	12.3	406	14	US-10-156-761-14828	Sequence 14828, A
945	322.5	13.6	972	8	US-08-806-029-30	Sequence 30, Appl	1042	290.5	12.3	805	14	US-10-029-386-34042	Sequence 34042, A
946	320.5	13.5	263	15	US-10-425-114-49960	Sequence 49960, A	1043	289	12.2	295	11	US-09-855-604-902	Sequence 902, App
947	320	13.5	594	15	US-10-283-122A-64397	Sequence 64397, A	1044	289	12.2	627	16	US-10-406-832-28	Sequence 28, Appl
948	320	13.5	1953	17	US-10-488-056-42	Sequence 42, Appl	1045	289	12.2	627	17	US-10-893-598-28	Sequence 28, Appl
949	319.5	13.5	318	14	US-10-259-678-727	Sequence 727, App	1046	288.5	12.2	953	8	US-08-806-029-14	Sequence 14, Appl
950	318	13.5	884	16	US-10-800-179-25	Sequence 25, Appl	1047	286	12.1	454	16	US-10-767-701-45105	Sequence 45105, A
951	317.5	13.4	988	8	US-08-806-029-28	Sequence 28, Appl	1048	286	12.1	563	17	US-10-488-056-43	Sequence 43, Appl
952	315.5	13.4	965	16	US-10-800-179-31	Sequence 31, Appl	1049	285.5	12.1	234	16	US-10-767-701-45603	Sequence 45603, A
953	314.5	13.3	1968	14	US-10-123-155-163	Sequence 163, App	1050	283.5	12.0	401	15	US-10-342-331-34	Sequence 34, Appl
956	314	13.3	116	10	US-09-764-891-2877	Sequence 2877, App	1051	283	12.0	764	15	US-10-424-599-143917	Sequence 143917, A
967	312	13.2	242	15	US-10-425-114-61520	Sequence 61520, A	1052	281.5	11.9	185	16	US-10-437-963-126075	Sequence 126075, A
968	309.5	13.1	200	9	US-09-798-584-18	Sequence 18, Appl	1053	281	11.9	223	15	US-10-424-599-244310	Sequence 244310, A
969	309.5	13.1	200	9	US-09-967-624-19	Sequence 19, Appl	1054	280	11.8	444	17	US-10-488-056-37	Sequence 37, Appl
970	309.5	13.1	200	9	US-09-998-667-18	Sequence 18, Appl	1055	280	11.8	1466	14	US-09-918-715-226	Sequence 226, App
971	309.5	13.1	200	10	US-09-921-159-34	Sequence 34, Appl	1056	280	11.8	1466	14	US-10-177-293-68	Sequence 68, Appl
972	309.5	13.1	200	10	US-09-990-940-21	Sequence 21, Appl	1057	280	11.8	1466	14	US-10-301-822-33	Sequence 33, Appl
973	309.5	13.1	200	10	US-09-989-981A-13	Sequence 13, Appl	1058	280	11.8	1466	15	US-10-257-021-72	Sequence 72, Appl
974	309.5	13.1	200	10	US-09-850-948-29	Sequence 29, Appl	1059	280	11.8	1466	16	US-10-357-851-3	Sequence 3, Appl
975	309.5	13.1	200	14	US-10-160-354-4	Sequence 4, Appl	1060	280	11.8	1466	16	US-10-358-024-3	Sequence 3, Appl
976	309.5	13.1	200	14	US-10-026-331B-21	Sequence 21, Appl	1061	280	11.8	1466	16	US-10-734-564-103	Sequence 103, App
977	309.5	13.1	200	14	US-10-026-021-8	Sequence 8, Appl	1062	279	11.8	1096	17	US-10-741-849-7179	Sequence 7179, Ap
978	309.5	13.1	200	14	US-10-161-165-3	Sequence 3, Appl	1063	277.5	11.7	230	16	US-10-437-963-122258	Sequence 122258, A
979	309.5	13.1	200	14	US-10-160-663-3	Sequence 3, Appl	1064	277.5	11.7	332	15	US-10-437-963-137540	Sequence 137540, A
980	309.5	13.1	200	14	US-10-071-838-15	Sequence 15, Appl	1065	277	11.7	237	15	US-10-282-122A-68044	Sequence 68044, A
981	309.5	13.1	200	14	US-10-094-417-25	Sequence 25, Appl	1066	276	11.7	1040	15	US-10-104-889-30	Sequence 30, Appl
982	309.5	13.1	200	14	US-10-188-405-13	Sequence 13, Appl	1067	276	11.7	1040	15	US-10-104-889-32	Sequence 32, Appl
983	309.5	13.1	200	14	US-10-273-575-29	Sequence 29, Appl	1068	276	11.7	1078	14	US-10-058-124-21	Sequence 21, Appl
984	309.5	13.1	200	14	US-10-233-098-5	Sequence 5, Appl	1069	276	11.7	1366	10	US-09-918-715-214	Sequence 214, App
985	309.5	13.1	200	14	US-10-245-850-3	Sequence 3, Appl	1070	276	11.7	1366	10	US-09-918-715-234	Sequence 234, App
986	309.5	13.1	200	14	US-10-293-582-27	Sequence 27, Appl	1071	276	11.7	1366	10	US-09-918-715-265	Sequence 265, App
987	309.5	13.1	200	14	US-10-100-818-14	Sequence 14, Appl	1072	276	11.7	1366	14	US-10-171-311-36	Sequence 38, Appl
988	309.5	13.1	200	14	US-10-237-467-18	Sequence 18, Appl	1073	276	11.7	1366	14	US-10-301-822-31	Sequence 31, Appl
989	309.5	13.1	200	14	US-10-321-204-54	Sequence 54, Appl	1074	276	11.7	1366	16	US-10-734-564-95	Sequence 95, Appl
990	309.5	13.1	200	14	US-10-179-766-12	Sequence 12, Appl	1075	275	11.6	208	14	US-10-029-386-33055	Sequence 33055, A
991	309.5	13.1	200	14	US-10-123-568-4	Sequence 4, Appl	1076	275	11.6	525	16	US-10-755-889-650	Sequence 650, App
992	309.5	13.1	200	14	US-10-123-731-10	Sequence 10, Appl	1077	274	11.6	593	15	US-10-435-696-50	Sequence 50, Appl
993	309.5	13.1	200	15	US-10-308-393-53	Sequence 53, Appl	1078	272.5	11.5	696	15	US-10-441-965-21	Sequence 21, Appl
994	309.5	13.1	200	15	US-10-352-724-5	Sequence 5, Appl	1079	272	11.5	696	8	US-08-806-029-36	Sequence 36, Appl
995	309.5	13.1	200	15	US-10-328-916-57	Sequence 57, Appl	1080	272	11.5	696	15	US-10-441-965-23	Sequence 23, Appl
996	309.5	13.1	200	15	US-10-452-015-3	Sequence 3, Appl	1081	272	11.5	750	8	US-08-806-029-25	Sequence 25, Appl
997	309.5	13.1	200	15	US-10-364-861-94	Sequence 94, Appl	1082	271.5	11.5	370	15	US-10-282-122A-64566	Sequence 64566, A
998	309.5	13.1	200	15	US-10-231-956A-521	Sequence 521, App	1083	271.5	11.5	2338	14	US-10-023-386-31982	Sequence 31982, A
999	309.5	13.1	200	15	US-10-255-775-3	Sequence 3, Appl	1084	270.5	11.4	1368	16	US-10-437-963-108730	Sequence 2, Appl
1000	309.5	13.1	200	15	US-10-459-190-24	Sequence 24, Appl	1085	270.5	11.4	1366	16	US-10-357-851-2	Sequence 2, Appl
1001	309.5	13.1	200	15	US-10-339-744-4	Sequence 4, Appl	1086	270.5	11.4	1366	16	US-10-358-024-2	Sequence 2, Appl
1002	309.5	13.1	200	16	US-10-649-400-7	Sequence 7, Appl	1087	270.5	11.4	1366	16	US-10-788-792-153	Sequence 153, App
1003	309.5	13.1	200	16	US-10-620-052A-78	Sequence 78, Appl	1088	270	11.4	920	15	US-10-292-798-1514	Sequence 1514, Ap
1004	309.5	13.1	200	17	US-10-616-403-7	Sequence 7, Appl	1089	270	11.4	1466	15	US-10-402-089-12	Sequence 12, Appl
1005	309	13.1	201	9	US-09-918-094-40	Sequence 40, Appl	1090	270	11.4	1466	15	US-10-402-072A-12	Sequence 12, Appl
1006	309	13.1	201	9	US-09-948-990-22	Sequence 22, Appl	1091	269.5	11.4	360	17	US-10-488-056-31	Sequence 31, Appl
1007	309	13.1	201	9	US-09-760-364-14	Sequence 14, Appl	1092	268.5	11.4	278	15	US-10-425-114-54522	Sequence 54522, A
1008	309	13.1	201	11	US-09-754-947-5	Sequence 5, Appl	1093	268.5	11.4	287	16	US-10-437-963-161543	Sequence 161543, A
1009	309	13.1	201	15	US-10-338-744-5	Sequence 5, Appl	1094	268.5	11.4	1027	15	US-10-360-101-221	Sequence 221, App
1010	307.5	13.0	1670	14	US-10-123-155-325	Sequence 325, App	1095	267.5	11.3	1366	14	US-10-058-124-19	Sequence 19, Appl
1023	305	12.9	242	16	US-10-471-587A-1	Sequence 1, Appl	1096	267.5	11.3	1366	15	US-10-257-021-76	Sequence 76, Appl
1024	304.5	12.9	889	8	US-08-806-029-19	Sequence 19, Appl	1097	266	11.3	1088	16	US-10-437-963-158455	Sequence 158455, A
1025	302	12.8	592	15	US-10-369-493-17534	Sequence 17534, A	1098	265.5	11.2	265	16	US-10-437-963-154907	Sequence 154907, A
1026	302	12.8	714	9	US-09-861-597-10	Sequence 10, Appl	1099	265.5	11.2	568	14	US-10-086-510-5	Sequence 5, Appl

1100	265.5	11.2	1366	15	US-10-402-089-10	Sequence 10, Appl	1185	244	10.3	492	16	US-10-639-286-12	Sequence 12, Appl
1101	265.5	11.2	1366	15	US-10-402-072A-10	Sequence 10, Appl	1186	244	10.3	591	14	US-10-233-553-23	Sequence 23, Appl
1102	265	11.2	343	14	US-10-148-306-21	Sequence 21, Appl	1187	243.5	10.3	1046	14	US-10-156-761-10088	Sequence 10088, A
1103	264.5	11.2	578	16	US-10-437-963-164510	Sequence 164510,	1190	243	10.3	449	15	US-10-424-593-285485	Sequence 285485,
1104	264.5	11.2	1008	15	US-10-342-331-8	Sequence 8, Appl	1191	243	10.3	714	14	US-10-233-885-44	Sequence 44, Appl
1105	264.5	11.2	1008	15	US-10-441-965-22	Sequence 22, Appl	1192	243	10.3	714	14	US-10-231-581-44	Sequence 44, Appl
1106	264.5	11.2	1063	16	US-10-800-179-29	Sequence 29, Appl	1193	243	10.3	714	15	US-10-326-508A-15	Sequence 15, Appl
1107	264.5	11.2	1065	14	US-10-117-931-16	Sequence 16, Appl	1194	243	10.3	1017	16	US-10-639-286-10	Sequence 10, Appl
1108	263.5	11.2	920	14	US-10-017-161-1858	Sequence 1858, Ap	1195	242.5	10.3	345	15	US-10-425-114-43660	Sequence 42660, A
1109	262.5	11.1	1466	15	US-10-402-089-4	Sequence 4, Appl	1196	242.5	10.3	940	15	US-10-291-174-363	Sequence 363, App
1110	262.5	11.1	1466	15	US-10-402-089-6	Sequence 6, Appl	1197	242.5	10.3	940	15	US-10-221-278-363	Sequence 363, App
1111	262.5	11.1	1466	15	US-10-402-072A-4	Sequence 4, Appl	1198	242.5	10.3	1014	17	US-10-901-816A-9	Sequence 9, Appl
1112	262.5	11.1	1466	15	US-10-402-072A-6	Sequence 6, Appl	1199	242.5	10.3	1014	17	US-10-901-816A-11	Sequence 11, Appl
1113	260.5	11.0	2498	14	US-10-123-155-483	Sequence 483, App	1200	242.5	10.3	1496	14	US-10-177-293-70	Sequence 70, Appl
1116	259.5	11.0	399	17	US-10-488-056-41	Sequence 41, Appl	1201	242.5	10.3	1496	14	US-10-301-822-35	Sequence 35, Appl
1127	258.5	10.9	478	15	US-10-425-114-58912	Sequence 58912, A	1202	242.5	10.3	1496	15	US-10-236-031B-74	Sequence 74, Appl
1128	258.5	10.9	480	15	US-10-425-114-61022	Sequence 61022, A	1203	242.5	10.3	1496	16	US-10-468-091-22	Sequence 22, Appl
1129	257	10.9	974	15	US-10-282-122A-44999	Sequence 44999, A	1204	242.5	10.3	1496	16	US-10-788-792-248	Sequence 248, App
1130	254	10.7	1040	8	US-08-806-029-32	Sequence 32, Appl	1205	242	10.2	193	16	US-10-437-963-148500	Sequence 148500,
1131	254	10.7	1745	10	US-09-795-061-4	Sequence 4, Appl	1206	242	10.2	319	15	US-10-282-122A-62423	Sequence 62423, A
1132	253	10.7	780	15	US-10-441-965-25	Sequence 25, Appl	1207	242	10.2	3721	14	US-10-123-155-543	Sequence 543, App
1133	253	10.7	1014	14	US-10-194-441A-1	Sequence 1, Appl	1220	241.5	10.2	185	16	US-10-437-963-182893	Sequence 182893,
1134	253	10.7	1217	14	US-10-311-406-2	Sequence 2, Appl	1221	241.5	10.2	988	15	US-10-291-172-739	Sequence 739, App
1135	253	10.7	1418	14	US-10-058-124-20	Sequence 20, Appl	1222	241.5	10.2	988	15	US-10-221-278-739	Sequence 739, App
1136	253	10.7	1418	14	US-10-468-091-5	Sequence 5, Appl	1226	241	10.2	342	17	US-10-488-056-39	Sequence 39, Appl
1137	252.5	10.7	455	15	US-10-425-114-65134	Sequence 65134, A	1227	241	10.2	1744	14	US-10-369-493-5832	Sequence 5832, Ap
1138	252.5	10.7	529	15	US-10-425-114-49406	Sequence 49406, A	1228	240.5	10.2	943	14	US-10-193-003-139	Sequence 199, App
1139	252.5	10.7	1047	16	US-10-901-816A-12	Sequence 12, Appl	1229	240.5	10.2	943	14	US-10-084-843-204	Sequence 204, App
1140	252	10.7	1497	16	US-10-468-091-23	Sequence 23, Appl	1230	240.5	10.2	1159	15	US-10-104-889-6	Sequence 6, Appl
1141	251.5	10.6	462	10	US-09-919-039-324	Sequence 324, App	1231	240.5	10.2	1637	16	US-10-437-963-180397	Sequence 180397,
1142	250.5	10.6	284	10	US-09-804-014A-24	Sequence 24, Appl	1232	240	10.2	678	15	US-10-282-122A-64573	Sequence 64573, A
1143	250.5	10.6	585	9	US-09-738-626-6032	Sequence 6032, Ap	1233	240	10.2	1212	15	US-10-331-496A-26	Sequence 26, Appl
1144	250	10.6	597	9	US-09-793-306-146	Sequence 146, App	1236	239.5	10.1	264	16	US-10-437-963-135092	Sequence 135092,
1145	249.5	10.6	669	15	US-10-282-122A-53462	Sequence 53462, A	1237	239.5	10.1	469	15	US-10-282-122A-45275	Sequence 45275, A
1146	247.5	10.5	943	9	US-09-996-634-131	Sequence 131, App	1238	239.5	10.1	653	14	US-10-156-761-9799	Sequence 9799, Ap
1147	247.5	10.5	943	10	US-09-997-182-131	Sequence 131, App	1239	239.5	10.1	1057	15	US-10-104-889-16	Sequence 16, Appl
1148	247.5	10.5	943	10	US-09-997-181-131	Sequence 131, App	1240	239.5	10.1	1464	15	US-09-918-715-261	Sequence 261, Appl
1149	247.5	10.5	1739	10	US-09-795-061-2	Sequence 2, Appl	1241	239.5	10.1	1464	14	US-10-060-036-159	Sequence 159, App
1150	247.5	10.5	3300	15	US-10-282-122A-64369	Sequence 64369, A	1242	239.5	10.1	1464	14	US-10-171-311-36	Sequence 36, Appl
1151	246.5	10.4	595	15	US-10-342-331-48	Sequence 48, Appl	1243	239.5	10.1	1464	14	US-10-149-352-2	Sequence 2, Appl
1152	246.5	10.4	595	15	US-10-342-331-50	Sequence 50, Appl	1244	239.5	10.1	1464	14	US-10-177-293-65	Sequence 65, Appl
1153	246.5	10.4	822	15	US-10-342-331-49	Sequence 49, Appl	1245	239.5	10.1	1464	14	US-10-301-822-28	Sequence 28, Appl
1154	246.5	10.4	1341	14	US-10-058-124-18	Sequence 18, Appl	1246	239.5	10.1	1464	16	US-10-734-564-79	Sequence 79, Appl
1155	246.5	10.4	1431	16	US-10-468-091-26	Sequence 26, Appl	1247	239	10.1	584	15	US-10-282-122A-50604	Sequence 50604, A
1156	245.5	10.4	185	16	US-10-437-963-122260	Sequence 122260,	1248	239	10.1	662	14	US-10-232-175-33	Sequence 33, Appl
1157	245.5	10.4	354	10	US-09-820-843A-21	Sequence 21, Appl	1249	239	10.1	960	15	US-10-342-331-6	Sequence 6, Appl
1158	245.5	10.4	1014	14	US-10-194-441A-48	Sequence 48, Appl	1250	239	10.1	1463	15	US-10-402-089-2	Sequence 2, Appl
1159	245.5	10.4	1449	15	US-10-402-089-8	Sequence 8, Appl	1251	239	10.1	1463	15	US-09-919-497-56	Sequence 56, Appl
1160	245.5	10.4	1449	15	US-10-402-072A-8	Sequence 8, Appl	1252	239	10.1	1806	9	US-10-058-270A-122	Sequence 122, App
1161	245.5	10.4	1487	16	US-10-468-091-6	Sequence 6, Appl	1253	239	10.1	1806	15	US-10-123-155-281	Sequence 121, App
1162	245	10.4	894	14	US-10-233-553-11	Sequence 11, Appl	1254	238.5	10.1	1471	14	US-10-901-816A-1	Sequence 1, Appl
1163	245	10.4	1684	16	US-10-408-765A-811	Sequence 811, App	1267	238	10.1	498	17	US-10-901-816A-1	Sequence 1, Appl
1164	244.5	10.3	492	16	US-10-639-286-11	Sequence 11, Appl	1268	238	10.1	500	14	US-10-232-175-22	Sequence 22, Appl
1165	244.5	10.3	660	17	US-10-901-816A-3	Sequence 3, Appl	1269	238	10.1	2380	16	US-10-239-399A-19	Sequence 19, Appl
1166	244.5	10.3	660	17	US-10-901-816A-4	Sequence 4, Appl	1270	237.5	10.1	185	16	US-10-437-963-121283	Sequence 121283,
1167	244.5	10.3	1002	14	US-10-117-931-25	Sequence 25, Appl	1271	237.5	10.1	349	17	US-10-488-056-36	Sequence 36, Appl
1168	244.5	10.3	1014	17	US-10-901-816A-5	Sequence 5, Appl	1272	237	10.0	628	16	US-10-437-963-158059	Sequence 158059,
1169	244.5	10.3	1014	17	US-10-901-816A-6	Sequence 6, Appl	1273	236.5	10.0	498	17	US-10-901-816A-2	Sequence 2, Appl
1170	244.5	10.3	1014	17	US-10-901-816A-7	Sequence 7, Appl	1274	236.5	10.0	1465	14	US-10-096-986-74	Sequence 74, Appl
1171	244.5	10.3	1014	17	US-10-901-816A-8	Sequence 8, Appl	1275	236	10.0	552	15	US-10-342-331-7	Sequence 7, Appl
1172	244.5	10.3	1014	17	US-10-901-816A-9	Sequence 9, Appl	1276	236	10.0	887	15	US-10-425-114-68923	Sequence 68923, A
1173	244.5	10.3	1014	17	US-10-901-816A-13	Sequence 13, Appl	1277	235	9.9	251	16	US-10-767-701-32417	Sequence 32417, A
1174	244.5	10.3	1057	15	US-10-104-889-20	Sequence 20, Appl	1278	235	9.9	847	16	US-10-437-963-142796	Sequence 142796,
1175	244.5	10.3	1107	15	US-10-104-889-11	Sequence 11, Appl	1279	234.5	9.9	510	14	US-10-232-175-26	Sequence 26, Appl
1176	244.5	10.3	1171	15	US-10-104-889-8	Sequence 8, Appl	1280	234.5	9.9	236	17	US-08-806-029-26	Sequence 26, Appl
1177	244.5	10.3	1388	15	US-10-104-889-10	Sequence 10, Appl	1281	234.5	9.9	344	8	US-10-741-600-1629	Sequence 1629, Ap
1178	244.5	10.3	1461	16	US-10-468-091-25	Sequence 25, Appl	1282	234.5	9.9	3507	15	US-10-369-493-5784	Sequence 5784, Ap
1179	244.5	10.3	1464	14	US-10-216-705-21	Sequence 21, Appl	1283	234	9.9	1626	14	US-10-202-167-2	Sequence 2, Appl
1180	244.5	10.3	1464	15	US-10-291-265-243	Sequence 243, App	1284	233	9.9	655	16	US-10-437-963-157893	Sequence 157893,
1181	244.5	10.3	1464	16	US-10-357-851-1	Sequence 1, Appl	1285	232.5	9.8	253	16	US-10-437-963-114193	Sequence 114193,
1182	244.5	10.3	1464	16	US-10-358-024-1	Sequence 1, Appl	1286	232.5	9.8	416	14	US-10-234-175-25	Sequence 25, Appl
1183	244.5	10.3	1464	16	US-10-788-792-150	Sequence 150, App	1289	232	9.8	391	15	US-10-425-114-56680	Sequence 56680, A
1184	244	10.3	266	14	US-10-148-306-20	Sequence 20, Appl	1290	232	9.8	501	14	US-10-232-175-17	Sequence 17, Appl

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1291	232	9.8	1767	17	US-10-741-600-1476	Sequence 1476, Ap
1292	232	9.8	1767	17	US-10-741-600-1480	Sequence 1480, Ap
1293	232	9.8	1806	17	US-10-741-600-1478	Sequence 1478, Ap
1294	232	9.8	1806	17	US-10-741-600-1479	Sequence 1479, Ap
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1296	232	9.8	1818	17	US-10-741-600-1477	Sequence 1477, Ap
1297	231.5	9.8	562	16	US-10-720-025-33	Sequence 33, Appl
1298	231.5	9.8	730	16	US-10-720-025-35	Sequence 35, Appl
1299	231.5	9.8	1382	16	US-10-720-025-60	Sequence 60, Appl
1300	231.5	9.8	1550	16	US-10-720-025-54	Sequence 54, Appl
1301	230.5	9.8	378	9	US-09-849-967A-2	Sequence 2, Appl
1302	230.5	9.8	936	14	US-10-117-931-30	Sequence 30, Appl
1303	229.5	9.7	140	16	US-10-437-963-191576	Sequence 191576, A
1304	229.5	9.7	827	15	US-10-282-122A-47312	Sequence 47312, A
1305	228.5	9.7	152	15	US-10-424-593-202771	Sequence 202771, A
1306	228.5	9.7	430	16	US-10-451-467A-314	Sequence 314, App
1307	228.5	9.7	733	15	US-10-138-588-40	Sequence 40, Appl
1308	228	9.6	189	16	US-10-437-963-170736	Sequence 170736, A
1309	227.5	9.6	166	16	US-10-437-963-112933	Sequence 112933, A
1310	227.5	9.6	528	16	US-10-720-025-43	Sequence 43, Appl
1311	227.5	9.6	726	14	US-10-156-761-12539	Sequence 12539, A
1312	227.5	9.6	2800	15	US-10-417-426-15	Sequence 15, Appl
1313	227.5	9.6	4038	15	US-10-417-426-14	Sequence 14, Appl
1314	227	9.6	703	14	US-10-219-449-4	Sequence 4, Appl
1315	227	9.6	717	14	US-10-219-449-2	Sequence 2, Appl
1316	227	9.6	1621	14	US-10-185-990-10	Sequence 10, Appl
1317	227	9.6	1626	14	US-10-185-990-11	Sequence 11, Appl
1318	227	9.6	1759	15	US-10-369-493-7032	Sequence 7032, Ap
1319	227	9.6	2502	17	US-10-741-600-1627	Sequence 1627, Ap
1320	226.5	9.6	448	15	US-10-244-596-14	Sequence 14, Appl
1321	226	9.6	189	16	US-10-437-963-125315	Sequence 125315, A
1322	226	9.6	1669	10	US-09-918-715-252	Sequence 252, App
1323	226	9.6	1669	15	US-10-372-683-8	Sequence 8, Appl
1324	225.5	9.5	308	15	US-10-424-599-247149	Sequence 247149, A
1325	225	9.5	2368	14	US-10-123-155-423	Sequence 423, App
1326	224.5	9.5	197	15	US-10-425-114-67750	Sequence 67750, A
1327	224.5	9.5	748	15	US-10-342-331-10	Sequence 10, Appl
1328	224	9.5	1497	14	US-10-157-031-128	Sequence 128, App
1329	223	9.4	378	14	US-10-117-931-26	Sequence 26, Appl
1330	222.5	9.4	966	14	US-10-117-931-34	Sequence 34, Appl
1331	221.5	9.4	326	16	US-10-437-963-201447	Sequence 201447, A
1332	221.5	9.4	979	15	US-10-282-122A-47372	Sequence 47372, A
1333	221	9.4	214	16	US-10-437-963-119143	Sequence 119143, A
1334	220.5	9.3	645	9	US-09-919-172-41	Sequence 41, Appl
1335	220.5	9.3	192	16	US-10-437-963-143943	Sequence 143943, A
1336	220	9.3	1838	14	US-10-123-155-289	Sequence 289, App
1337	219.5	9.3	168	14	US-10-096-986-52	Sequence 52, Appl
1338	219.5	9.3	1019	15	US-10-236-031B-72	Sequence 72, Appl
1339	219.5	9.3	2276	14	US-10-123-155-9	Sequence 9, Appl
1340	219	9.3	716	14	US-10-156-761-15050	Sequence 15050, A
1341	219	9.3	775	14	US-10-156-761-12824	Sequence 12824, A
1342	218.5	9.2	684	14	US-10-157-031-62	Sequence 62, Appl
1343	218	9.2	202	16	US-10-437-963-133505	Sequence 133505, A
1344	218	9.2	215	15	US-10-425-114-68305	Sequence 68305, A
1345	218	9.2	284	17	US-10-488-056-34	Sequence 34, Appl
1346	218	9.2	360	16	US-10-437-963-118547	Sequence 118547, A
1347	216.5	9.2	595	9	US-09-738-973-187	Sequence 187, App
1348	216.5	9.2	595	9	US-09-854-133-187	Sequence 187, App
1349	216.5	9.2	595	14	US-10-144-649A-187	Sequence 187, App
1350	216.5	9.2	828	16	US-10-789-378-24	Sequence 24, Appl
1351	216.5	9.2	863	15	US-10-112-944-366	Sequence 366, App
1352	216.5	9.2	999	17	US-10-486-678-14	Sequence 14, Appl
1353	216.5	9.2	1019	17	US-10-486-678-13	Sequence 13, Appl
1354	216.5	9.2	2956	14	US-10-123-155-15	Sequence 15, Appl
1355	216	9.1	195	16	US-10-437-963-157867	Sequence 157867, A
1356	216	9.1	446	16	US-10-437-963-142366	Sequence 142366, A
1357	216	9.1	638	13	US-10-001-887-108	Sequence 108, App
1358	216	9.1	638	17	US-10-958-863-108	Sequence 108, App
1359	215.5	9.1	494	9	US-09-925-302-690	Sequence 690, App
1360	215.5	9.1	494	10	US-09-925-302-690	Sequence 690, App

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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:06:41 ; Search time 46 Seconds
(without alignments)
920.334 Million cell updates/sec

Title: US-10-063-561-52
Perfect score: 2363
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450.5	19.1	1079	2 B70807	hypothetical glyci
2	439.5	18.6	1306	2 A70934	hypothetical glyci
3	423	17.9	396	2 T49109	glycine-rich prote
4	415.5	17.6	1381	2 F70806	hypothetical glyci
5	412.5	17.5	484	2 G70846	hypothetical glyci
6	406	17.2	1901	2 F70806	hypothetical glyci
7	404.5	17.1	532	2 F70580	hypothetical glyci
8	403	17.1	1489	2 D70807	hypothetical glyci
9	400.5	16.9	1538	2 H70846	hypothetical glyci
10	399.5	16.9	853	2 A70896	hypothetical glyci
11	395	16.7	714	2 A70807	hypothetical glyci
12	395	16.7	1660	2 A70869	hypothetical glyci
13	392.5	16.6	923	2 E70820	hypothetical glyci
14	392	16.6	731	2 C70974	hypothetical glyci
15	392	16.6	1329	2 E70917	hypothetical glyci
16	386	16.3	778	2 F70895	hypothetical glyci
17	383.5	16.2	767	2 E70895	hypothetical glyci
18	383	16.2	641	1 Q0B831	nuclear antigen BB
19	381.5	16.1	741	2 G70917	hypothetical glyci
20	380.5	16.1	837	2 E70835	hypothetical glyci
21	379	16.0	465	1 S01820	glycine-rich cell
22	378	16.0	588	2 F70971	hypothetical glyci
23	376.5	15.9	749	2 A70812	hypothetical glyci
24	375	15.9	914	2 H70892	hypothetical glyci
25	373.5	15.8	584	2 G70804	hypothetical glyci
26	373.5	15.8	667	2 A70893	hypothetical glyci
27	372	15.7	694	2 F70868	hypothetical glyci
28	371	15.7	615	2 H70589	hypothetical glyci
29	371	15.7	718	2 A36068	major ampullate fi

30	370.5	15.7	491	2 D70916	hypothetical glyci
31	369.5	15.6	1428	2 T08852	lustrin A - Califo
32	366	15.5	408	2 S57483	glycin-rich protei
33	365.5	15.5	496	2 H70839	hypothetical glyci
34	365	15.4	576	2 A70900	hypothetical glyci
35	365	15.4	591	2 B70523	hypothetical glyci
36	364.5	15.4	801	2 F70824	hypothetical glyci
37	364	15.4	606	2 H70816	hypothetical glyci
38	363	15.4	481	2 A35628	hypothetical glyci
39	363	15.4	639	2 D70931	hypothetical glyci
40	360	15.2	562	2 B70953	hypothetical glyci
41	359.5	15.2	1011	2 F70820	hypothetical glyci
42	359	15.2	463	2 B70893	hypothetical glyci
43	358.5	15.2	338	1 K0MU	hypothetical glyci
44	355	15.0	291	1 S31415	glycine-rich cell
45	352.5	14.9	384	1 A26099	glycine-rich prote
46	352	14.9	274	2 T25404	hypothetical glyci
47	352	14.9	603	2 A70770	hypothetical glyci
48	351	14.9	957	2 D70835	hypothetical glyci
49	350.5	14.8	461	2 F70571	hypothetical glyci
50	350	14.8	316	1 A38743	hypothetical glyci
51	349	14.8	618	2 A70989	hypothetical glyci
52	349	14.8	882	2 B70812	hypothetical glyci
53	345	14.6	713	1 UMMS	period clock prote
54	345	14.6	966	2 A33626	fibrinogen alpha c
55	344	14.6	525	2 D70878	hypothetical glyci
56	344	14.6	783	2 E70824	hypothetical glyci
57	342	14.5	515	2 H70663	hypothetical glyci
58	339.5	14.4	487	2 E70983	hypothetical glyci
59	339	14.3	937	2 S58135	hypally regulated
60	335	14.2	434	2 E70768	hypothetical glyci
61	334	14.1	255	2 B84777	hypothetical prote
62	334	14.1	498	2 C70720	hypothetical glyci
63	329	13.9	549	2 T20720	hypothetical prote
64	325.5	13.8	439	2 D70954	hypothetical glyci
65	322	13.6	1207	2 T23754	hypothetical glyci
66	320	13.5	594	2 G70545	hypothetical glyci
67	315	13.3	302	2 C84470	hypothetical glyci
68	314.5	13.3	543	2 F70726	hypothetical glyci
69	312.5	13.2	252	1 S01821	glycine-rich prote
70	308.5	13.1	2639	2 T31328	fibroin - Chinese
71	308	13.0	271	2 S34666	glycine-rich prote
72	306.5	13.0	419	1 OZZQAM	circumsporozoite p
73	306	12.9	284	2 T23158	hypothetical prote
74	302	12.8	592	2 E82759	endo-1,4-beta-gluc
75	301	12.7	485	2 A60610	circumsporozoite p
76	300.5	12.7	622	2 I37984	keratin 9, type I
77	299.5	12.7	3198	2 A43426	collagen alpha 2 f
78	298.5	12.6	210	2 JQ1060	glycine-rich prote
79	298.5	12.6	2174	2 E95965	hypothetical glyci
80	296.5	12.5	1585	2 T31611	hypothetical prote
81	296	12.5	627	2 A4112	spidroin 2, dragli
82	293.5	12.4	794	2 T10519	pre-pro-legumin -
83	293	12.4	256	2 A70514	hypothetical glyci
84	290.5	12.3	749	2 I38488	trophinin - human
85	290	12.3	543	2 S19333	glycine-rich prote
86	290	12.3	751	2 S64741	cuticle collagen -
87	289	12.2	1414	1 S23809	collagen alpha 2(I
88	288.5	12.2	528	2 G02127	fus-like protein -
89	287	12.1	13288	2 T03099	muclin, submaxillar
90	286	12.1	286	2 C61615	muclin MG-2 - gre
91	283	12.0	1051	2 A35763	collagen alpha 2 c
92	282	11.9	543	2 T49892	glycine-rich prote
93	280	11.8	1466	1 CGHU7L	collagen alpha 1(I
94	278.5	11.8	526	1 S33799	RNA-binding protei
95	278	11.8	220	2 T14441	glycine-rich prote
96	278	11.8	270	2 A60830	keratin, 70k type
97	277	11.7	256	2 T03371	glycine-rich prote
98	276.5	11.7	682	2 T28899	hypothetical prote
99	275	11.6	1172	2 T32759	hypothetical prote
100	274	11.6	593	1 KRHU0	keratin 10, type I
101	274	11.6	730	2 F96559	hypothetical prote
102	274	11.6	3016	2 S77300	hypothetical prote

103	273.5	11.6	183	2	PN0109	keratin-like prote	176	240	10.2	170	2	JC2213	hypothetical 14.7K
104	272.5	11.5	1373	1	A43291	collagen alpha 2(I	177	240	10.2	678	2	A70762	probable PPE prote
105	272.5	11.5	1492	2	A03333	collagen alpha 1(I	178	239.5	10.1	812	2	S31521	collagen COLF1 - f
106	272	11.5	375	2	JS0427	S-antigen precursor	179	239.5	10.1	1869	1	CGMS4B	collagen alpha 1(I
107	272	11.5	1156	2	T43326	germline RNA helic	180	239	10.1	1806	1	CGHU1E	eggshell protein 1(X
108	271.5	11.5	370	2	G70872	hypothetical glyci	181	238.5	10.1	212	2	A44994	hypothetical prote
109	271	11.5	681	2	AB2155	hypothetical prote	182	238.5	10.1	387	2	C41156	circumsporozoite p
110	270.5	11.4	1049	2	S28774	collagen alpha cha	183	238.5	10.1	387	2	D41156	circumsporozoite p
111	270	11.4	1844	2	T51890	related to Nup98-N	184	237	10.0	570	2	S07330	keratin, epidermal
112	269	11.4	361	2	G70682	hypothetical glyci	185	236.5	10.0	220	2	A44805	eggshell protein p
113	269	11.4	1366	1	CGHU2S	collagen alpha 2(I	186	236.5	10.0	1733	1	B45344	probable nuclear a
114	268.5	11.4	259	2	T15126	hypothetical prote	187	236	10.0	888	2	S28791	collagen alpha 1(X
115	268	11.3	183	1	KNR2G2	glycine-rich cell	188	235	9.9	839	2	F75518	hypothetical prote
116	266	11.3	683	2	A82704	1,4-beta-cellobios	189	234.5	9.9	207	2	B44994	eggshell protein 2
117	265.5	11.2	568	2	JC7210	molluscan shell ma	190	234.5	9.9	419	2	T14448	oleosin homolog pc
118	265.5	11.2	615	2	E70663	probable PPE prote	191	234.5	9.9	438	2	SS3787	collagen alpha cha
119	263	11.1	435	2	T15143	hypothetical prote	192	234.5	9.9	2109	1	I50421	aggreccan precursor
120	263	11.1	1752	2	A45407	collagen alpha 3(I	193	234.5	9.9	2944	2	A54849	collagen alpha 1(V
121	262.5	11.1	645	2	F70825	probable PPE prote	194	234.5	9.9	3507	2	T34513	hypothetical prote
122	262.5	11.1	1049	1	CGH07S	collagen alpha 1(I	195	234	9.9	227	2	B41342	circumsporozoite p
123	262.5	11.1	2038	2	A43742	female sterile hom	196	234	9.9	1655	2	T13998	gene mastermind pr
124	262	11.1	1549	2	I48103	type VII collagen	197	233.5	9.9	165	1	KNRZG1	glycine-rich cell
125	260	11.0	730	2	A36226	collagen alpha 1 c	198	233.5	9.9	171	2	H84709	probable glycine-r
126	260	11.0	1486	1	B40333	collagen alpha 1(I	199	233.5	9.9	180	2	T28938	hypothetical prote
127	258	10.9	462	4	S33798	FUS/CHOP mutant fu	200	233	9.9	783	2	T35389	probable serine-th
128	257.5	10.9	386	1	S22315	snRNP-associated p	201	233	9.9	864	1	EART	elastin precursor
129	257.5	10.9	581	1	KRMS2	keratin, type II c	202	232.5	9.8	290	2	T23416	hypothetical prote
130	257.5	10.9	1464	2	SS9856	collagen alpha 1(I	203	232.5	9.8	643	1	KRHU2	keratin I, type II
131	255.5	10.8	589	2	S71954	RNA/ssDNA-binding	204	231.5	9.8	244	2	T49893	glycine-rich prote
132	255	10.8	632	2	S42731	collagen alpha-1 c	205	231	9.8	221	2	T04592	glycine-rich cell
133	254	10.7	1747	2	A54121	collagen alpha-4 c	206	231	9.8	413	2	E70661	probable PPE protei
134	253.5	10.7	401	1	OZZQAC	circumsporozoite p	207	231	9.8	1758	2	T29350	hypothetical prote
135	253.5	10.7	539	2	T28770	hypothetical prote	208	230.5	9.8	1300	2	T03166	probable PPE prote
136	253	10.7	1217	2	SS2714	sericinB - silkwo	209	230.5	9.8	3157	2	B70969	probable PPE prote
137	253	10.7	1487	1	CGHU6C	collagen alpha 1(I	210	230	9.7	115	2	D61615	sericin MG-1 - gre
138	252.5	10.7	404	2	S54729	RNA-binding protei	211	230	9.7	1778	2	T50074	probable nucleopor
139	252	10.7	582	2	F70675	probable PPE prote	212	229.5	9.7	569	1	KRMSE1	keratin, 59K type
140	252	10.7	149607	2	I49607	procollagen type V	213	229	9.7	162	2	C85356	glycine-rich prote
141	251.5	10.6	490	2	T05444	hypothetical prote	214	229	9.7	391	2	T08224	COR39 protein - wh
142	251.5	10.6	860	1	EMAS	elastin precursor	215	228.5	9.7	190	2	B48571	circumsporozoite p
143	251	10.6	429	2	A45504	circumsporozoite p	216	228.5	9.7	430	1	HHBYD8	heat shock protein
144	251	10.6	671	1	CGRT1S	collagen alpha 1(I	217	228.5	9.7	555	2	S70791	vsaB protein - Myc
145	249.5	10.6	395	2	A41156	circumsporozoite p	218	228.5	9.7	561	2	A31994	keratin 10, type I
146	249.5	10.6	940	2	JE0291	FB19 protein - hum	219	228	9.6	373	2	A40777	heterogeneous ribo
147	249	10.5	590	2	E70946	probable PPE prote	220	228	9.6	920	2	B34493	collagen alpha 1(I
148	248.5	10.5	1032	2	G89427	protein T08D2.3 [i	221	227.5	9.6	180	2	T49530	related to glycine
149	248	10.5	343	2	T05221	hypothetical prote	222	227	9.6	371	2	E88633	protein F5683.1 [i
150	248	10.5	395	2	S40778	ribonucleoprotein	223	227	9.6	402	1	CGH02S	collagen alpha 2(I
151	247.5	10.5	1418	2	T45467	collagen alpha 1(I	224	227	9.6	1210	2	A25547	ice nucleation pro
152	247.5	10.5	3300	2	D70575	probable PPE prote	225	227	9.6	1759	2	T29351	collagen alpha 2(I
153	246.5	10.4	1453	2	S21626	collagen alpha 1(I	226	226.5	9.6	326	2	A41732	heterogeneous ribo
154	246.5	10.4	1464	1	CGHU1S	collagen alpha 1(I	227	226.5	9.6	469	2	T06987	dehydrin homolog W
155	246.5	10.4	1958	2	B40505	hypothetical prote	228	226.5	9.6	641	2	T30076	hypothetical prote
156	245.5	10.4	354	2	B70663	probable PPE prote	229	226.5	9.6	918	2	S23377	collagen alpha 2(V
157	245.5	10.4	636	2	S41067	collagen alpha 1(I	230	226.5	9.6	1022	2	S04111	collagen alpha 2(V
158	245.5	10.4	1419	2	A41182	collagen alpha 1(I	231	226	9.6	1669	1	CGHU4B	collagen alpha 1(I
159	245.5	10.4	1487	2	B41182	collagen alpha 1(I	232	225.5	9.5	1113	2	S28925	nuclear pore compl
160	245	10.4	886	2	I50694	collagen alpha 1(I	233	224	9.5	167	2	S21359	keratin, type I, c
161	245	10.4	1684	2	T02367	hypothetical prote	234	224	9.5	404	2	B84745	probable RNA-bind
162	243	10.3	424	2	T08093	oleosin homolog ST	235	224	9.5	447	2	T42987	hypothetical prote
163	243	10.3	1236	2	T04045	hypothetical prote	236	224	9.5	1532	2	A61262	collagen alpha 1(X
164	242.5	10.3	2305	2	T07959	probable cell wall	237	223.5	9.5	572	2	T08509	trbl protein - Ent
165	242.5	10.3	1496	1	CGHU2V	collagen alpha 2(V	238	223	9.4	545	2	T15667	hypothetical prote
166	242.5	10.3	1775	2	A31893	collagen alpha 1(I	239	223	9.4	1200	1	SNFSO	ice nucleation pro
167	242	10.2	385	2	T20410	hypothetical prote	240	222.5	9.4	1063	2	D86731	hypothetical prote
168	242	10.2	779	1	CGH01S	collagen alpha 1(I	241	222.5	9.4	1761	2	T13990	collagen type IV a
169	241.5	10.2	608	2	T05442	glycine-rich prote	242	222.5	9.4	2523	2	F70846	probable PPE prote
170	241.5	10.2	1042	1	CGCH1S	collagen alpha 1(I	243	222	9.4	365	2	A34840	heterogeneous ribo
171	241	10.2	380	2	A48295	collagen 1 - marin	244	222	9.4	552	2	CGRH0A	probable PPE prote
172	241	10.2	964	1	CGCH2S	collagen alpha 2(I	245	222	9.4	1691	1	CGRH0B	collagen alpha 6(I
173	241	10.2	1546	1	CGHU2E	collagen alpha 2(X	246	221.5	9.4	173	2	JQ1064	glycine-rich prote
174	241	10.2	1744	2	S40991	collagen alpha 1(I	247	221	9.4	310	2	I50696	collagen alpha 1(I
175	240.5	10.2	673	1	CGH06C	collagen alpha 1(I	248	221	9.4	575	2	T52420	dehydrin 5 [import

249	221	9.4	575	2	S35327	protein kinase egg	322	204.5	8.7	770	2	S59623	tropolaetin - she
250	220.5	9.3	316	2	H20497	hypothetical prote	323	204.5	8.7	1019	1	A32856	collagen alpha 1(V
251	220.5	9.3	618	2	H70552	probable PPG prote	324	204	8.6	177	2	A31204	eggshell protein p
252	220.5	9.3	645	2	A44861	keratin, 67K type	325	204	8.6	228	2	S19932	glycine-rich prote
253	220	9.3	917	2	S09646	collagen alpha 2(V	326	204	8.6	547	2	A36046	collagen alpha cha
254	220	9.3	1018	1	CGHU2A	collagen alpha 2(V	327	204	8.6	1146	2	A38587	collagen, cornea-s
255	219.5	9.3	207	2	T07381	glycine-rich prote	328	203	8.6	223	2	B96506	hypothetical prote
256	219.5	9.3	2248	2	A35938	profilaggrin - hum	329	203	8.6	680	2	T08080	probable myrosinase
257	218	9.2	287	2	A60643	antigen 5401 - Bim	330	203	8.6	825	2	JC4163	DNA-binding protei
258	217.5	9.2	1880	2	T18531	tractin - medicina	331	203	8.6	1034	2	JC2143	ice nucleation act
259	217	9.2	575	2	S27761	dehydrin Dhn5 - ba	332	203	8.6	2327	2	T42630	aggreacan - bovine
260	216.5	9.2	674	2	S13301	collagen alpha 1(X	333	202.5	8.6	351	2	B34840	heterogeneous ribo
261	216.5	9.2	2090	2	S26058	probable transform	334	202.5	8.6	677	2	S23296	collagen alpha 2(I
262	216	9.1	409	2	T20847	hypothetical prote	335	202.5	8.6	1028	1	CGHU1A	collagen alpha 1(V
263	215.5	9.1	2132	1	A55182	aggreacan precursor	336	202.5	8.6	3176	2	CGHU3A	collagen alpha 3(V
264	215	9.1	200	2	S10334	glycine-rich prote	337	202	8.5	430	2	S22700	NUP42 protein - Ye
265	215	9.1	479	2	F70573	hypothetical prote	338	201.5	8.5	393	2	T20268	hypothetical prote
266	215	9.1	1029	1	S21369	collagen alpha 2(V	339	201	8.5	1712	1	CGHU2B	collagen alpha 2(I
267	215	9.1	1567	2	S11672	ice nucleation pro	340	200.5	8.5	312	2	T25048	hypothetical prote
268	215	9.1	1690	1	CGHU1B	collagen alpha 4(I	341	200.5	8.5	353	2	B34504	heterogeneous nucl
269	215	9.1	1838	1	CGHU1V	collagen alpha 1(V	342	200.5	8.5	623	1	S33167	gene pointed prote
270	215	9.1	1843	2	S18803	collagen alpha 1(V	343	200.5	8.5	675	2	S20819	collagen alpha 3(I
271	214.5	9.1	290	2	A32249	collagen - sea urc	344	200.5	8.5	2232	2	T34434	hypothetical prote
272	214.5	9.1	388	2	T29173	hypothetical prote	345	200	8.5	1096	2	H86237	protein F14N23.29
273	214.5	9.1	465	2	F75524	hypothetical prote	346	200	8.5	1258	2	J00188	ice nucleation pro
274	214.5	9.1	1018	2	H83135	probable adhesin P	347	200	8.5	3716	2	E70969	probable PPG prote
275	214	9.1	1024	2	S18251	collagen alpha 1(X	348	199.5	8.4	214	1	KNNT2S	glycine-rich prote
276	214	9.1	1275	2	T33369	hypothetical prote	349	199.5	8.4	670	2	T49510	fibroin-3 related
277	213.5	9.0	245	2	F70787	hypothetical glyci	350	199.5	8.4	707	2	A48686	probable RNA helic
278	213.5	9.0	695	2	T24950	hypothetical prote	351	199.5	8.4	1022	2	T44663	hypothetical prote
279	213.5	9.0	959	2	B44402	nuclear pore compl	352	199	8.4	825	1	EDBEXD	immediate-early pr
280	213.5	9.0	1670	1	CGHU3B	collagen alpha 3(I	353	198.5	8.4	191	2	A42844	oleosin homolog pc
281	213.5	9.0	2415	1	A39086	aggreacan precursor	354	198.5	8.4	920	2	T14447	oleosin alpha 1(I
282	212.5	9.0	1804	2	H96597	hypothetical prote	355	198.5	8.4	381	2	S40495	oleosin homolog pc
283	212.5	9.0	2551	2	B98047	hypothetical prote	356	198.5	8.4	1433	2	A46053	bullous pemphigoid
284	212	9.0	330	2	S27766	WCS120 protein - w	357	198.5	8.4	1691	1	S22917	collagen alpha 5(I
285	212	9.0	635	2	A57131	collagen alpha 2(V	358	198	8.4	346	2	S40775	ribonucleoprotein
286	212	9.0	907	2	A45560	sporozoite surface	359	198	8.4	541	2	S51799	nucleoporin NUP57
287	211.5	9.0	488	2	A27353	collagen alpha 1(I	360	198	8.4	1213	2	S16356	ovo protein - frui
288	211	8.9	967	2	S66852	hypothetical prote	361	197.5	8.4	744	2	S15435	oleosin homolog gb
289	210.5	8.9	471	2	T33997	hypothetical prote	362	197	8.3	361	2	T14460	collagen alpha 1(X
290	210.5	8.9	3190	2	T13828	CREB-binding prote	363	197	8.3	1142	2	JX0369	collagen alpha 1(X
291	209.5	8.9	688	2	A53330	collagen alpha 2(I	364	196.5	8.3	571	1	UMFF	period clock prote
292	209.5	8.9	920	2	A45748	collagen alpha 1(V	365	196.5	8.3	754	2	A55267	collagen alpha 5(I
293	209	8.8	680	2	S31216	collagen alpha 1(X	366	196	8.3	136	2	T29282	hypothetical prote
294	209	8.8	1707	2	A33536	collagen alpha 2(I	367	196	8.3	1147	1	MWAXIB	myosin heavy chain
295	209	8.8	3137	2	A37797	collagen alpha 3(V	368	195.5	8.3	314	2	T08675	hypothetical prote
296	208.5	8.8	377	2	T08095	oleosin homolog ST	369	195.5	8.3	633	2	B40983	collagen alpha 1(X
297	208	8.8	201	2	T00799	hypothetical prote	370	195.5	8.3	698	2	JH0163	No-on-transient A
298	208	8.8	307	2	T27609	hypothetical prote	371	195.5	8.3	700	2	JH0162	No-on-transient A
299	208	8.8	457	2	H70820	hypothetical glyci	372	195.5	8.3	921	2	S42617	collagen alpha 1(I
300	208	8.8	618	2	S32436	collagen alpha 2(I	373	195.5	8.3	1560	2	T02885	peroxisome prolif
301	207.5	8.8	365	2	A26459	helix-destabilizin	374	195	8.3	358	2	S40776	ribonucleoprotein
302	207	8.8	208	2	T46896	merozoite surface	375	195	8.3	469	2	A24450	collagen alpha 2(V
303	207	8.8	313	2	T04776	hypothetical prote	376	195	8.3	1748	2	S42136	cnfB protein - Tet
304	207	8.8	405	2	T29167	hypothetical prote	377	194.5	8.2	383	2	A53053	dentin sialoprotei
305	207	8.8	645	2	D90782	probable tail fi	378	194.5	8.2	839	2	H90577	lipoprotein vsai l
306	207	8.8	645	2	H85642	probable tail fi	379	194.5	8.2	959	2	S32605	collagen alpha 3(V
307	207	8.8	680	1	CGHUID	collagen alpha 1(X	380	194	8.2	1028	2	T03516	probable outer mem
308	207	8.8	2124	2	A28452	proteoglycan core	381	194	8.2	1406	2	T31555	hypothetical prote
309	206.5	8.7	190	2	A24713	agrecin - silkworm	382	194	8.2	1436	2	B70520	probable PPG prote
310	206.5	8.7	342	2	S10432	heterogeneous ribo	383	193.5	8.2	931	2	S13580	collagen alpha 1(I
311	206.5	8.7	615	2	A05269	collagen alpha 1(I	384	193.5	8.2	1096	2	T08619	probable metallopr
312	206.5	8.7	1025	2	S34839	collagen alpha 1(V	385	192	8.1	526	1	KRBOVI	keratin, 54K type
313	206	8.7	447	2	G84687	probable disease r	386	191.5	8.1	644	1	FGHUA	fibrinogen alpha c
314	206	8.7	1322	2	S07053	ice nucleation pro	387	191.5	8.1	866	2	D44234	fibrinogen alpha c
315	205.5	8.7	506	2	G71404	probable ribonucle	388	191.5	8.1	1315	2	A56101	collagen alpha 1(X
316	205.5	8.7	518	2	A55840	macrophage bacteri	389	191.5	8.1	1774	2	B56101	collagen alpha 1(X
317	205	8.7	502	2	A48679	differentiated ker	390	191	8.1	323	1	T19142	hypothetical prote
318	205	8.7	775	2	A61228	collagen alpha 2(I	391	190.5	8.1	743	1	S23779	collagen alpha 1(V
319	205	8.7	1417	2	A83080	hypothetical prote	392	190.5	8.1	796	2	S57844	lethal(3)malignant
320	205	8.7	1603	2	S23810	collagen alpha 1(X	393	190.5	8.1	2329	2	T28125	hypothetical prote
321	204.5	8.7	382	2	S20375	collagen alpha 3(V	394	190	8.0	344	2	S41707	PopAI protein - Ps

395	190	8.0	963	2	B70524	probable PPG prote	468	178.5	7.6	335	2	T14449	oleosin homolog pc
396	189.5	8.0	289	2	F96770	protein RNA-bindin	469	178	7.5	300	2	T19929	hypothetical prote
397	189	8.0	301	2	B31219	collagen 2 - Caeno	470	178	7.5	393	2	S5499	cellulase egli - s
398	189	8.0	848	2	S02262	glutenin high mole	471	178	7.5	539	2	T50579	probable membrane
399	189	8.0	1176	2	C26427	period clock prote	472	178	7.5	688	2	T48796	probable ATP-depen
400	189	8.0	1218	2	A26588	period clock prote	473	177.5	7.5	314	2	T34269	hypothetical prote
401	189	8.0	1218	2	A26427	period clock prote	474	177.5	7.5	327	2	T34203	hypothetical prote
402	188.5	8.0	203	1	JQ1061	glycine-rich prote	475	177	7.5	176	2	S30147	glycine-rich RNA b
403	188.5	8.0	363	2	T51341	RNA helicase RH9 [476	177	7.5	255	2	AF1857	hypothetical prote
404	188.5	8.0	423	2	A41207	collagen 13, nonfi	477	177	7.5	304	2	T26185	hypothetical prote
405	188.5	8.0	632	2	T02627	hypothetical prote	478	177	7.5	304	2	T26184	hypothetical prote
406	188	8.0	487	2	C70830	probable PPG prote	479	177	7.5	495	2	B71360	hypothetical prote
407	188	8.0	1596	2	A33106	neurogenic locus m	480	177	7.5	908	2	A33280	sarcalumenin precu
408	187.5	7.9	752	2	T34355	hypothetical prote	481	177	7.5	1199	2	A40670	nuclear envelope p
409	187.5	7.9	956	2	T08144	myrosinase-binding	482	177	7.5	3759	2	A35085	trithorax protein
410	187.5	7.9	1076	2	C96620	protein T30E16.23	483	176.5	7.5	137	2	T04930	glycine-rich cell
411	187.5	7.9	1718	2	T14603	hypothetical prote	484	176.5	7.5	367	2	A32068	circumsporozoite p
412	187	7.9	596	2	T26667	hypothetical prote	485	176.5	7.5	638	2	I53169	cytokeratin 2 - hu
413	186.5	7.9	252	2	A55047	collagen alpha 1(V	486	176.5	7.5	798	2	T21369	hypothetical prote
414	186.5	7.9	356	2	S16907	collagen alpha 1(I	487	176.5	7.5	1241	2	S01827	period clock prote
415	186.5	7.9	378	1	OZZQAB	circumsporozoite p	488	176.5	7.5	2554	2	AB3528	extracellular seri
416	186.5	7.9	398	1	OZZQAS	homeotic protein o	489	176	7.4	325	2	T18594	hypothetical prote
417	186	7.9	671	2	A35912	hypothetical prote	490	176	7.4	747	1	EABO	elastin precursor,
418	186	7.9	1763	2	S16366	collagen alpha 2(I	491	175.5	7.4	316	2	S08169	collagen col-12 pr
419	185.5	7.9	346	1	S35500	heterogeneous ribo	492	175.5	7.4	316	2	S08170	collagen col-13 pr
420	185.5	7.9	753	2	JC2099	glutenin, high mol	493	175.5	7.4	403	2	T08471	harpin - Erwinia a
421	185.5	7.9	789	2	A30843	glutenin, high mole	494	175.5	7.4	775	1	EDBE11	immediate-early pr
422	185.5	7.9	791	2	JN0690	glutenin, high-mol	495	175	7.4	201	2	F84596	glycine-rich prote
423	185	7.8	704	2	T34034	hypothetical prote	496	175	7.4	352	2	T24279	hypothetical prote
424	185	7.8	867	2	S57795	probable deoxyribo	497	175	7.4	358	2	T26281	hypothetical prote
425	185	7.8	1004	2	C82672	surface-exposed ou	498	175	7.4	363	2	T16831	hypothetical prote
426	184.5	7.8	330	2	T26004	hypothetical prote	499	175	7.4	464	2	S59513	collagen II Al pro
427	184.5	7.8	388	2	JC6164	circumsporozoite p	500	175	7.4	528	2	D46449	hypothetical prote
428	184.5	7.8	798	2	T33022	hypothetical prote	501	175	7.4	598	2	T38403	probable nucleopor
429	184.5	7.8	1063	2	A40523	acidic nuclear pro	502	174.5	7.4	340	2	T20807	hypothetical prote
430	184	7.8	333	2	T23618	hypothetical prote	503	174.5	7.4	406	2	S38170	SRP40 protein - ye
431	184	7.8	625	2	A34615	profilaggrin - rat	504	174.5	7.4	460	2	T33110	hypothetical prote
432	184	7.8	813	2	S70795	vsaa protein precu	505	174.5	7.4	629	2	A29666	keratin, 65K type
433	184	7.8	1102	2	A32247	virG protein - Shi	506	174.5	7.4	672	2	I40333	tracheal colonizat
434	183.5	7.8	445	2	A27263	50K spicule matrix	507	174	7.4	239	2	S49193	GCR 101 protein -
435	183.5	7.8	541	2	T15299	hypothetical prote	508	174	7.4	314	2	T32247	hypothetical prote
436	182.5	7.7	174	2	S18654	variant surface an	509	174	7.4	330	2	S46657	collagen alpha 1(X
437	182.5	7.7	306	2	S33538	embryogenic cell p	510	174	7.4	344	2	T40167	hypothetical prote
438	182.5	7.7	443	2	C70780	probable PPG prote	511	174	7.4	387	2	E95995	hypothetical calci
439	182.5	7.7	472	2	S28026	nuclear pore compl	512	174	7.4	448	2	T15188	hypothetical prote
440	182.5	7.7	1293	2	B40025	maleless protein,	513	174	7.4	475	2	T03170	hypothetical prote
441	182.5	7.7	2204	2	A70524	probable PPG prote	514	174	7.4	718	1	S33168	gene pointed prote
442	182	7.7	287	2	B39615	merozoite 45K sur	515	174	7.4	782	2	T32155	hypothetical prote
443	182	7.7	305	2	T20906	hypothetical prote	516	173.5	7.3	204	2	T09592	protein corA, cold
444	182	7.7	1033	2	B70987	probable PPG prote	517	173.5	7.3	424	1	Z3BPF1	coat protein A pre
445	181.5	7.7	154	2	E84468	probable glycine-r	518	173.5	7.3	424	1	Z3BPF1	coat protein A pre
446	181.5	7.7	1287	2	I46032	nuclear DNA helica	519	173.5	7.3	424	1	Z3BPF3	coat protein A pre
447	181	7.7	256	2	T11669	protein CPRD22, dr	520	173.5	7.3	542	2	T29707	hypothetical prote
448	181	7.7	356	2	T22827	hypothetical prote	521	173.5	7.3	558	2	E70756	hypothetical glyci
449	181	7.7	416	2	A32947	filaggrin precurs	522	173.5	7.3	779	2	A35006	cell surface glyco
450	181	7.7	569	2	S42886	collagen - silkwor	523	173.5	7.3	1912	2	T29088	vitellogenin I pre
451	181	7.7	614	2	T33149	hypothetical prote	524	173	7.3	258	2	S71561	drought-induced pr
452	181	7.7	1388	2	A53317	collagen alpha 1(X	525	173	7.3	281	2	C90577	lipoprotein vsaa [
453	181	7.7	1533	2	A46221	abdominal segment	526	173	7.3	347	2	B39112	merozoite 45K sur
454	180.5	7.6	196	2	S49194	GCR 17 protein - f	527	173	7.3	656	1	A49358	RNA-binding protei
455	180.5	7.6	605	2	T33913	hypothetical prote	528	173	7.3	1032	2	T34433	hypothetical prote
456	180.5	7.6	744	1	A34246	collagen alpha 1(V	529	173	7.3	1043	2	T13733	FTZ-F1 protein - f
457	180.5	7.6	744	1	S23298	collagen alpha 1(V	530	172.5	7.3	864	2	A48266	protein-tyrosine k
458	180.5	7.6	268	2	B61615	collagen heavy chai	531	172	7.3	446	2	T45525	MSC4 homolog [lmo
459	180	7.6	434	1	Z3BPIK	coat protein A - p	532	172	7.3	1052	2	AF2959	conserved hypochet
460	180	7.6	674	2	T23297	collagen alpha 1(X	533	172	7.3	1341	2	H98323	hypothetical prote
461	180	7.6	792	1	EAHU	elastin precursor,	534	171.5	7.3	655	1	A55726	RNA-binding protei
462	179.5	7.6	784	2	A26601	elastin precursor,	535	171.5	7.3	1127	2	A25018	circadian rhythm p
463	179.5	7.6	838	1	SEWTHW	glutenin, high mol	536	171	7.2	337	2	T23794	hypothetical prote
464	179	7.6	310	2	T29731	hypothetical prote	537	171	7.2	1176	2	T18042	ice nucleation pro
465	179	7.6	314	2	T32985	hypothetical prote	538	170.5	7.2	108	1	S01844	fibronin - silkorm
466	179	7.6	995	2	T22942	hypothetical prote	539	170.5	7.2	367	2	JC4831	adsorption protein
467	178.5	7.6	313	2	T22828	hypothetical prote	540	170.5	7.2	396	2	T29773	hypothetical prote

541	170.5	7.2	1589	2	T42233	submaxillary mucin	614	163	6.9	418	2	T15142	hypothetical prote
542	170.5	7.2	4936	2	AH2515	hypothetical prote	615	163	6.9	490	2	T09084	phosphatidylinosit
543	170	7.2	334	2	S08091	gene III protein -	616	163	6.9	633	2	F84564	probable protein k
544	170	7.2	615	2	T20839	hypothetical prote	617	162.5	6.9	262	1	TLBPM1	tail fiber protein
545	170	7.2	1208	2	S17286	period clock prote	618	162.5	6.9	289	2	T20177	hypothetical prote
546	170	7.2	3498	2	T22330	hypothetical prote	619	162.5	6.9	658	2	T41309	hypothetical threo
547	169.5	7.2	183	2	S57773	early nodulin GRP3	620	162.5	6.9	925	2	JC2033	G protein-coupled
548	169.5	7.2	661	1	S59633	endo-1,4-beta-xyla	621	162.5	6.9	1168	1	MXAXIC	myosin heavy chain
549	169.5	7.2	849	2	A96532	hypothetical prote	622	162	6.9	166	1	KRBO2B	keratin, 68K type
550	169.5	7.2	924	2	F87103	initiation factor	623	162	6.9	198	2	I49558	collagen alpha 1(I
551	169.5	7.2	988	2	T08102	myosinase-binding	624	162	6.9	323	2	T24582	hypothetical prote
552	169.5	7.2	1504	2	T49886	glycine/proline-ri	625	162	6.9	1087	2	S35423	protein kinase egg
553	169	7.2	290	2	T24586	hypothetical prote	626	162	6.9	1888	2	S78476	collagen alpha 1(X
554	169	7.2	304	2	T22482	hypothetical prote	627	161.5	6.8	316	2	T19288	hypothetical prote
555	169	7.2	308	2	T32286	collagen 40 - Caen	628	161.5	6.8	500	2	T20961	hypothetical prote
556	169	7.2	380	2	T28888	cuticle collagen d	629	161.5	6.8	707	2	S52390	D-hordein precurs
557	168.5	7.1	640	2	A54502	S antigen precurs	630	161.5	6.8	800	2	I51653	deRNA-binding prot
558	168	7.1	234	2	G95989	hypothetical glyci	631	161.5	6.8	978	2	D81411	probable lipoprote
559	168	7.1	252	2	T03160	capsid protein - a	632	161.5	6.8	1441	2	B86807	hypothetical prote
560	168	7.1	633	2	A25473	chorion E2 protein	633	161	6.8	284	2	T29528	hypothetical prote
561	168	7.1	673	2	T00328	hypothetical prote	634	161	6.8	290	2	T24590	hypothetical prote
562	168	7.1	684	2	A53019	collagen alpha 1(X	635	161	6.8	591	2	A45135	profilaggrin - hum
563	167.5	7.1	183	2	S57772	early nodulin GRP3	636	161	6.8	650	2	G87572	calcium-binding pr
564	167.5	7.1	276	2	T33925	hypothetical prote	637	161	6.8	805	2	T25795	hypothetical prote
565	167.5	7.1	286	2	B45632	merozoite surface	638	161	6.8	925	2	T19361	hypothetical prote
566	167.5	7.1	629	2	S42629	keratin K3 - rabbi	639	161	6.8	1701	2	T43213	ENBPI protein - ba
567	167.5	7.1	786	2	T16509	hypothetical prote	640	161	6.8	1852	1	VJCH2	vitellogenin II pr
568	167.5	7.1	1075	2	T48805	hypothetical prote	641	160.5	6.8	212	2	E86179	hypothetical prote
569	167.5	7.1	1366	2	T35985	probable large pro	642	160.5	6.8	281	2	C88638	protein P58P6.1 [i
570	167.5	7.1	1747	2	A45974	collagen alpha 1(X	643	160.5	6.8	323	2	T27450	hypothetical prote
571	167.5	7.1	1857	2	S31212	collagen alpha 1(X	644	160.5	6.8	327	2	S25421	hypothetical prote
572	167	7.1	106	2	F84797	hypothetical prote	645	160.5	6.8	1516	2	T01055	ABC-type transport
573	167	7.1	166	2	T10463	glycine-rich prote	646	160.5	6.8	2020	2	C48399	heterogeneous ribo
574	167	7.1	303	2	T19289	hypothetical prote	647	160	6.8	169	2	T10465	heterogeneous ribo
575	167	7.1	325	2	T32248	hypothetical prote	648	160	6.8	282	2	S00275	circumsporozoite p
576	167	7.1	369	2	F96788	protein T4012.22 [649	160	6.8	286	2	T22706	transcription fact
577	167	7.1	407	2	T21956	hypothetical prote	650	160	6.8	299	2	T22705	transcription fact
578	167	7.1	1221	2	T13283	probable transcrip	651	160	6.8	320	1	DDRT	autolysin - Entero
579	167	7.1	1237	2	D71850	probable outer mem	652	160	6.8	330	1	A44485	probable PPG prote
580	166.5	7.0	313	2	T36105	probable large gly	653	160	6.8	320	2	S04617	collar protein iso
581	166.5	7.0	416	2	A28444	filaggrin precurs	654	160	6.8	320	2	S02061	hypothetical prote
582	166.5	7.0	416	2	T32458	hypothetical prote	655	160	6.8	378	1	OZZQAL	hypothetical prote
583	166.5	7.0	522	2	T36501	probable serine/th	656	160	6.8	582	2	S10099	transcription fact
584	166.5	7.0	556	2	AH1981	hypothetical prote	657	160	6.8	671	2	A38109	transcription fact
585	166.5	7.0	634	2	T08145	myosinase-binding	658	160	6.8	987	2	E70808	transcription fact
586	166.5	7.0	738	2	E87627	hypothetical prote	659	160	6.8	1296	2	T13936	transcription fact
587	166.5	7.0	1120	2	H88449	protein P54D8.1 [i	660	160	6.8	1325	2	T13386	transcription fact
588	166	7.0	291	2	T26576	hypothetical prote	661	160	6.8	1649	2	C86822	transcription fact
589	166	7.0	617	2	T49444	lustrin A related	662	159.5	6.7	186	2	S28021	transcription fact
590	166	7.0	1122	2	B26427	period clock prote	663	159.5	6.7	260	2	S00276	transcription fact
591	166	7.0	1519	2	S41525	major ring-forming	664	159.5	6.7	301	2	B84533	transcription fact
592	165.5	7.0	220	2	AD2990	conserved hypotet	665	159.5	6.7	336	2	T20348	transcription fact
593	165.5	7.0	220	2	E98293	hypothetical prote	666	159.5	6.7	654	2	A34734	transcription fact
594	165.5	7.0	389	2	D26395	homeotic protein U	667	159.5	6.7	742	4	C34734	transcription fact
595	165	7.0	291	2	T20083	hypothetical prote	668	159.5	6.7	825	4	B34734	transcription fact
596	165	7.0	319	2	T32250	hypothetical prote	669	159.5	6.7	1534	2	A56734	transcription fact
597	165	7.0	433	2	S20963	homeotic protein H	670	159	6.7	299	2	T19564	transcription fact
598	165	7.0	823	2	S14055	neocosteal-lik	671	159	6.7	302	2	T32872	transcription fact
599	164.5	7.0	200	2	B86181	hypothetical prote	672	159	6.7	494	2	T15502	transcription fact
600	164.5	7.0	600	2	T07638	spore coat protein	673	159	6.7	516	2	C44479	transcription fact
601	164.5	7.0	819	2	T08745	probable RNA helic	674	159	6.7	1711	1	A47392	transcription fact
602	164.5	7.0	1446	1	A45344	immediate-early pr	675	158.5	6.7	307	2	T16842	transcription fact
603	164	6.9	237	2	A88640	protein C34H4.4 [i	676	158.5	6.7	461	2	JN0097	transcription fact
604	164	6.9	368	2	H96990	probable membrane	677	158	6.7	231	2	S17367	transcription fact
605	164	6.9	561	2	T16148	hypothetical prote	678	158	6.7	299	2	T25407	transcription fact
606	163.5	6.9	299	2	T00837	glycine-rich prote	679	158	6.7	306	2	T21938	transcription fact
607	163.5	6.9	414	1	I38977	TAR DNA-binding pr	680	158	6.7	1460	2	S48457	transcription fact
608	163.5	6.9	623	2	A45137	collagen alpha 4(I	681	158	6.7	3124	2	A40020	transcription fact
609	163.5	6.9	666	2	A42296	lysosome 2 (EC 3.2	682	157.5	6.7	317	2	T19143	transcription fact
610	163.5	6.9	668	2	C71868	hypothetical prote	683	157.5	6.7	830	2	S15720	transcription fact
611	163.5	6.9	729	2	S35532	hnRNA-binding prot	684	157	6.6	145	2	T08435	transcription fact
612	163.5	6.9	928	2	C81265	probable lipoprote	685	157	6.6	225	2	S05546	transcription fact
613	163	6.9	254	2	A31488	filaggrin - mouse	686	157	6.6	249	2	B33144	transcription fact

687	157	6.6	299	2	T24833	hypothetical prote	760	151.5	6.4	486	1	KRXL	keratin 3, type 1,
688	157	6.6	363	1	OZZQAK	circumsporozoite p	761	151.5	6.4	797	2	A36811	hypothetical prote
689	157	6.6	366	2	S11449	collagen short cha	762	151.5	6.4	901	2	JC5093	dead ringer nuclea
690	157	6.6	623	2	A45571	surface antigen 2,	763	151.5	6.4	1076	1	A35622	nuclear pore prote
691	157	6.6	624	2	A55576	collagen alpha 2(x	764	151	6.4	161	2	S71453	glycine-rich RNA-b
692	157	6.6	806	2	T13690	hypothetical prote	765	151	6.4	333	2	E48423	homeotic protein e
693	157	6.6	829	2	B81086	iron-regulated pro	766	151	6.4	339	2	T22607	hypothetical prote
694	157	6.6	1910	2	AF0394	probable adhesin h	767	151	6.4	387	2	T34507	cutical collagen 6
695	156.5	6.6	173	2	S53050	RNA binding protei	768	151	6.4	405	2	S13355	hypothetical prote
696	156.5	6.6	273	2	T40618	probable cell wall	769	151	6.4	537	2	B33485	spore coat protein
697	156.5	6.6	387	2	H86445	probable G-Box bin	770	150.5	6.4	387	2	E95933	probable calcium-b
698	156.5	6.6	471	2	A39024	collagen alpha 3(I	771	150.5	6.4	461	2	T51044	related to spore c
699	156.5	6.6	758	2	T48815	mixed-linked gluc	772	150.5	6.4	524	2	A82580	polyvinylalcohol d
700	156.5	6.6	1217	2	T25894	hypothetical prote	773	150	6.3	234	2	T49448	dehydrin 2 - garde
701	156.5	6.6	1777	2	T34369	hypothetical prote	774	150	6.3	255	2	T08811	hypothetical prote
702	156.5	6.6	3295	2	AE0074	probable adhesin Y	775	150	6.3	283	2	T19732	hypothetical prote
703	156	6.6	169	2	S30148	glycine-rich prote	776	150	6.3	327	2	T29031	hypothetical prote
704	156	6.6	259	1	S46286	RNA-binding protei	777	150	6.3	359	2	T22774	hypothetical prote
705	156	6.6	291	2	T34494	hypothetical prote	778	150	6.3	423	2	A55797	collagen precursor
706	156	6.6	330	2	S30192	heterogeneous ribo	779	150	6.3	1072	2	G95851	probable hemolysin
707	156	6.6	431	1	WJH02G	homeotic protein H	780	150	6.3	1390	2	T18883	hypothetical prote
708	156	6.6	571	2	T43456	hypothetical prote	781	149.5	6.3	148	2	T05527	glycine-rich prote
709	156	6.6	1665	2	T29008	hypothetical prote	782	149.5	6.3	287	2	T22637	hypothetical prote
710	155.5	6.6	163	2	T23076	hypothetical prote	783	149.5	6.3	317	2	T29960	hypothetical prote
711	155.5	6.6	169	1	S38331	glycine-rich RNA-b	784	149.5	6.3	325	2	S02170	collagen alpha 1(I
712	155.5	6.6	238	2	T23271	hypothetical prote	785	149.5	6.3	385	2	D41732	heterogeneous nucl
713	155	6.6	419	1	KRXLB2	keratin, 64K type	786	149.5	6.3	419	2	T04886	DAG protein homolo
714	155	6.6	1487	1	EDBEE1	immediate-early pr	787	149.5	6.3	473	2	I50629	collagen - chicken
715	154.5	6.5	270	2	A36034	fibronogen alpha c	788	149.5	6.3	573	2	C86266	F3F19.21 protein -
716	154.5	6.5	304	2	T22602	hypothetical prote	789	149.5	6.3	1028	2	A56038	DNA-binding protei
717	154.5	6.5	343	2	T29547	hypothetical prote	790	149	6.3	264	2	S37137	prion protein - gr
718	154.5	6.5	433	1	Q0BSV2	hypothetical prote	791	149	6.3	318	2	S27977	cuticle collagen d
719	154.5	6.5	705	2	S18733	glutenin high mole	792	149	6.3	329	2	JS0167	collagen col-6 - C
720	154.5	6.5	3436	2	S55659	tegument protein 6	793	149	6.3	345	1	D41732	heterogeneous nucl
721	154	6.5	205	2	T05713	dehydrin - barley	794	149	6.3	371	1	JN0450	conglutinin precur
722	154	6.5	297	2	T30525	hypothetical prote	795	149	6.3	371	2	I45878	conglutinin - bovi
723	154	6.5	2715	2	T13049	eyelid - fruit fly	796	149	6.3	896	2	T51891	hypothetical prote
724	153.5	6.5	115	2	T01322	aluminum-induced p	797	149	6.3	963	2	T48707	related to regulat
725	153.5	6.5	157	2	S18651	variant surface an	798	149	6.3	1112	2	H95964	probable outer mem
726	153.5	6.5	178	2	B88637	protein W09G12.6 [799	148.5	6.3	107	2	B85356	glycine-rich prote
727	153.5	6.5	289	2	T34241	hypothetical prote	800	148.5	6.3	283	2	T29980	hypothetical prote
728	153.5	6.5	304	2	T23801	hypothetical prote	801	148.5	6.3	302	2	T21257	hypothetical prote
729	153.5	6.5	309	2	T19389	hypothetical prote	802	148.5	6.3	364	2	S43574	C05B5.3 protein (c
730	153.5	6.5	311	2	S08110	salivary protein 1	803	148.5	6.3	454	2	T35380	probable membrane
731	153.5	6.5	333	2	T20436	hypothetical prote	804	148.5	6.3	456	2	E86903	hypothetical prote
732	153.5	6.5	401	2	C88571	protein C05B5.3 [I	805	148.5	6.3	660	2	A24266	glutenin high mole
733	153.5	6.5	437	2	S15144	hypothetical prote	806	148	6.3	289	2	T27708	hypothetical prote
734	153.5	6.5	1791	2	T02345	hypothetical prote	807	148	6.3	298	2	E95286	hypothetical prote
735	153.5	6.5	1829	2	S35027	cytotoxin RTX homo	808	148	6.3	299	2	T20605	hypothetical prote
736	153	6.5	112	2	S14977	glycine-rich prote	809	148	6.3	306	2	T21939	hypothetical prote
737	153	6.5	164	2	S11846	rab18B protein - r	810	148	6.3	447	2	T18447	HrpW protein - Erw
738	153	6.5	232	2	S18139	dehydrin DHN3 - ga	811	148	6.3	549	2	B86264	hypothetical prote
739	153	6.5	285	2	T29982	hypothetical prote	812	148	6.3	661	2	A58768	hypothetical prote
740	153	6.5	349	2	A41349	histone-specific t	813	148	6.3	892	2	T27005	Arp-dependent RNA
741	153	6.5	349	2	S77570	transcription fact	814	148	6.3	1305	2	T00670	probable inositol
742	153	6.5	403	1	TVR7KA	protein kinase (EC	815	147.5	6.2	235	2	G01226	leukophysin - huma
743	153	6.5	629	2	T34726	probable dehydroge	816	147.5	6.2	300	2	T24482	hypothetical prote
744	153	6.5	1487	1	EDBEE3	155K transcription	817	147.5	6.2	482	2	B31795	collagen alpha 1(X
745	152.5	6.5	257	2	C84533	hypothetical prote	818	147.5	6.2	589	2	T29299	hypothetical prote
746	152.5	6.5	279	2	T26125	hypothetical prote	819	147.5	6.2	1329	2	T29074	protein-tyrosine k
747	152.5	6.5	299	2	T29956	hypothetical prote	820	147.5	6.2	1584	2	T18276	protein-tyrosine k
748	152.5	6.5	316	2	T19291	hypothetical prote	821	147	6.2	226	2	S27759	maturation-associa
749	152.5	6.5	420	2	D83556	probable coat prot	822	147	6.2	264	2	A54330	major prion protei
750	152.5	6.5	584	2	T07825	hypothetical glyci	823	147	6.2	282	2	JS0168	hypothetical prote
751	152.5	6.5	1198	2	T49726	hypothetical prote	824	147	6.2	283	2	T19731	surfactant protein
752	152	6.4	258	2	A29259	Ubq protein - frui	825	147	6.2	374	1	A42046	RSP2 protein - yea
753	152	6.4	474	2	A26421	shufflon A - Esche	826	147	6.2	578	2	S55102	probable integral
754	152	6.4	735	2	T35778	probable fusidic a	827	147	6.2	684	2	T36771	eye cell developme
755	152	6.4	815	2	B30843	glutenin high mole	828	147	6.2	760	2	A45174	probable integr
756	152	6.4	828	2	C88402	protein H05C05.1 [829	147	6.2	762	2	S08207	siatoglycoprotein
757	151.5	6.4	182	2	A36686	ultra-high-sulfur	830	147	6.2	1317	2	A54831	nuclear pore compl
758	151.5	6.4	294	2	T21668	hypothetical prote	831	147	6.2	1594	2	T43072	hemolysin A - Edwa
759	151.5	6.4	367	2	JC6087	helix-loop-helix t	832	146.5	6.2	166	2	T18691	hypothetical prote

833	146.5	6.2	294	2	T22639	hypotheical prote	906	142	6.0	449	1	S30205	transcription fact
834	146.5	6.2	310	2	T22641	hypotheical prote	907	142	6.0	475	2	C86863	N-acetylmutamoyl-L
835	146.5	6.2	368	2	G84769	hypotheical prote	908	142	6.0	1166	2	T13958	syngap-bl protein
836	146.5	6.2	377	2	A47380	RNG finger-contai	909	142	6.0	1249	2	T14270	Ras-GTPase activat
837	146.5	6.2	393	2	A48459	S antigen, heat st	910	142	6.0	1286	2	T28634	adhesin AIDA-I pre
838	146.5	6.2	704	2	S21911	BCore-NS-23 prote	911	142	6.0	1293	2	T14259	ras GTPase-activat
839	146	6.2	258	2	T13591	tail fiber adhesin	912	142	6.0	1588	2	A86036	probable adhesin 2
840	146	6.2	281	2	T32765	hypotheical prote	913	142	6.0	1588	2	H91188	probable adhesin E
841	146	6.2	283	2	JS0170	collagen col-19 -	914	142	6.0	2535	2	AC0304	probable hemolysin
842	146	6.2	295	2	T22833	hypotheical prote	915	141.5	6.0	255	2	A35026	filaggrin A - mous
843	146	6.2	412	2	A84455	hypotheical prote	916	141.5	6.0	474	2	I38240	transcription fact
844	146	6.2	467	2	I50476	keratin type I - 9	917	141.5	6.0	788	2	JS0747	regulatory protein
845	146	6.2	712	2	A45638	immunodominant mic	918	141.5	6.0	1398	2	T13741	hypotheical prote
846	146	6.2	1215	2	T32734	myosin-1A - Acanth	919	141.5	6.0	3535	2	E83641	probable hemagglut
847	146	6.2	1340	2	A39808	proteoglycan core	920	141.5	6.0	3968	2	A44265	trithorax homolog
848	145.5	6.2	215	2	T17207	hypotheical prote	921	141	6.0	191	2	I46412	keratin KAP5.4 - s
849	145.5	6.2	313	2	T26465	hypotheical prote	922	141	6.0	253	2	A33144	homeotic protein U
850	145.5	6.2	461	2	A43782	keratin, type II -	923	141	6.0	511	2	S10527	endoglucanase B pr
851	145.5	6.2	561	1	CDECP3	cloacin DF13 prote	924	141	6.0	684	2	A56154	Abi substrate ena
852	145.5	6.2	643	2	T03518	hypotheical prote	925	140.5	5.9	148	2	B71419	hypotheical prote
853	145.5	6.2	658	2	AH0110	probable surface p	926	140.5	5.9	309	2	T28708	hypotheical prote
854	145.5	6.2	815	2	JN0689	glutinin, high-mol	927	140.5	5.9	317	2	T39869	probable lysophosp
855	145.5	6.2	1467	2	A75564	conserved hypotet	928	140.5	5.9	431	2	S09824	hypotheical prote
856	145	6.1	150	2	C86224	hypotheical prote	929	140.5	5.9	484	2	S66713	hypotheical prote
857	145	6.1	154	2	S34637	glycine-rich prote	930	140.5	5.9	561	2	T22917	probable ATP-depen
858	145	6.1	170	2	T03018	glycine-rich prote	931	140.5	5.9	579	2	T37248	probable matrix me
859	145	6.1	375	1	A45225	pulmonary surfacta	932	140.5	5.9	1690	2	T35694	ATP dependent DNA
860	145	6.1	380	1	GNVSM8	genome polypeptid	933	140	5.9	111	2	T29295	hypotheical prote
861	145	6.1	451	1	A40168	transcription fact	934	140	5.9	296	2	T21070	hypotheical prote
862	145	6.1	539	2	G95405	hypotheical prote	935	140	5.9	327	2	S38342	fibrillarin - mous
863	145	6.1	556	2	T65502	serine/threonine p	936	140	5.9	360	2	T37285	collagen dpy-2 - C
864	145	6.1	633	2	T02673	heterogeneous nucl	937	140	5.9	425	1	KRXL2A	keratin, 64K type
865	145	6.1	919	2	A39248	androgen receptor	938	140	5.9	669	2	A97443	hypotheical prote
866	145	6.1	3345	2	T13423	hypotheical prote	939	140	5.9	669	2	AC2661	hypotheical prote
867	144.5	6.1	156	2	S52246	transposable retro	940	140	5.9	710	2	S28014	outD protein - Erw
868	144.5	6.1	453	2	A41640	vestigial protein	941	140	5.9	888	2	I58378	tyrosine kinase -
869	144.5	6.1	512	2	S70644	annexin VII - Afri	942	140	5.9	1781	2	T31095	vitellogenin precu
870	144.5	6.1	937	2	A56517	nucleoporin Nup98	943	140	5.9	5627	2	C83339	hypotheical prote
871	144.5	6.1	2761	2	T21064	hypotheical prote	944	139.5	5.9	104	2	JC4190	holotricin 3 precu
872	144	6.1	208	2	T21689	hypotheical prote	945	139.5	5.9	543	2	A32693	steroid receptor p
873	144	6.1	283	2	T29837	hypotheical prote	946	139.5	5.9	576	2	S69214	deformed epidermal
874	144	6.1	294	2	T29839	hypotheical prote	947	139.5	5.9	591	2	AC3528	extracellular seri
875	144	6.1	381	2	T27806	hypotheical prote	948	139.5	5.9	653	2	T34356	hypotheical prote
876	144	6.1	492	2	A87471	hypotheical prote	949	139.5	5.9	746	2	B32693	steroid receptor p
877	144	6.1	1475	2	S42718	nuclear pore compl	950	139.5	5.9	845	2	D96799	hypotheical prote
878	143.5	6.1	168	1	S12312	glycine-rich RNA-b	951	139.5	5.9	900	2	B70694	probable infg - My
879	143.5	6.1	228	2	A44982	collagen UCOL1 - p	952	139.5	5.9	914	2	T08081	probable myrosinas
880	143.5	6.1	341	2	B70700	conserved hypotet	953	139	5.9	282	2	T16036	cuticle collagen c
881	143.5	6.1	527	2	B70700	hypotheical prote	954	139	5.9	294	2	T35892	hypotheical prote
882	143.5	6.1	608	2	T32923	hypotheical prote	955	139	5.9	298	2	T27644	hypotheical prote
883	143.5	6.1	660	1	Q0883	BHLFI protein - hu	956	139	5.9	328	2	G88499	protein K04G7.10 l
884	143.5	6.1	709	2	T28712	hypotheical prote	957	139	5.9	524	2	T27043	hypotheical prote
885	143.5	6.1	720	1	A55160	Tf9 protein - frui	958	139	5.9	860	2	S43846	xylanase B - rumen
886	143.5	6.1	1268	2	B99789	hemagglutinin/hemo	959	139	5.9	1209	2	T13153	brachma associated
887	143.5	6.1	1270	2	B85469	hypotheical prote	960	139	5.9	1279	2	A47363	RNA helicase A - h
888	143.5	6.1	1666	2	T43169	hypotheical prote	961	139	5.9	1839	2	S77626	mannuronan C-5-epi
889	143	6.1	182	2	A02943	keratin, 60K type	962	138.5	5.9	152	2	G96010	hypotheical expor
890	143	6.1	294	2	T29838	hypotheical prote	963	138.5	5.9	299	2	T05494	glycine-rich prote
891	143	6.1	556	2	T42100	serine/threonine p	964	138.5	5.9	469	1	S26097	probable ATP-bindi
892	142.5	6.0	197	2	T46413	keratin KAP5.5 - s	965	138.5	5.9	576	1	S24453	colicin E7 (EC 3.1
893	142.5	6.0	329	2	T32783	hypotheical prote	966	138.5	5.9	735	2	T45059	hypotheical prote
894	142.5	6.0	590	2	A26638	homeotic protein D	967	138.5	5.9	859	2	D96502	hypotheical prote
895	142.5	6.0	648	2	S04932	glutinin high mole	968	138.5	5.9	949	2	D90803	Aida-I adhesin-lik
896	142.5	6.0	693	2	T33251	hypotheical prote	969	138.5	5.9	1005	2	H85611	probable adhesin 2
897	142	6.0	159	2	C49773	ecdysone-dependent	970	138.5	5.9	1111	2	T29070	hypotheical prote
898	142	6.0	164	2	S11847	rab16c protein - f	971	138.5	5.9	1411	2	T48529	hypotheical prote
899	142	6.0	167	2	S71779	glycine-rich RNA-b	972	138.5	5.9	2441	2	D71623	erythrocyte membra
900	142	6.0	266	1	T1BP2X	tail fiber protein	973	138	5.8	283	2	T19141	hypotheical prote
901	142	6.0	269	2	S48444	probable temperatu	974	138	5.8	532	2	T35119	probable aminotran
902	142	6.0	272	2	C75548	hypotheical prote	975	138	5.8	640	2	T08179	LRG5 protein - Chl
903	142	6.0	324	2	T28032	hypotheical prote	976	138	5.8	1087	2	T30844	serine-repeat anti
904	142	6.0	351	1	OZZQRU	circumsporozoite p	977	137.5	5.8	165	2	T03583	glycine-rich RNA-b
905	142	6.0	387	2	S00867	colicin N - Escher	978	137.5	5.8	448	1	A56018	transcription fact

979	137.5	5.8	598	2	T32166	hypothetical prote	1052	134.5	5.7	297	2	T18638	hypothetical prote
980	137.5	5.8	676	2	S41022	hypothetical prote	1053	134.5	5.7	326	2	T29810	hypothetical prote
981	137.5	5.8	1192	2	T18611	probable serine/th	1054	134.5	5.7	326	2	JS0169	collagen col-14 -
982	137.5	5.8	1219	2	T14578	nucleoporin Nup153	1055	134.5	5.7	380	2	T24786	hypothetical prote
983	137.5	5.8	1468	2	A44345	nucleoporin - rat	1056	134.5	5.7	398	2	T34947	hypothetical prote
984	137.5	5.8	1608	2	A28182	hemolysin A - Serr	1057	134.5	5.7	767	2	A35645	major surface prot
985	137.5	5.8	1770	2	A71517	hypothetical prote	1058	134.5	5.7	1199	2	S20969	Na+/Ca2+,K+-exchan
986	137.5	5.8	1805	2	A34736	nestin - rat	1059	134.5	5.7	1938	2	A37361	probable integral
987	137	5.8	179	1	GZRT0	secretory granule	1060	134	5.7	142	2	SL2311	glycine-rich RNA-b
988	137	5.8	197	2	S25088	dehydrin DHN1 - ga	1061	134	5.7	162	2	T10479	glycine-rich RNA-b
989	137	5.8	232	2	S18138	dehydrin DHN2 - ga	1062	134	5.7	210	2	B44984	collagen - nematod
990	137	5.8	383	2	T46707	proteophosphoglyca	1063	134	5.7	235	2	T33380	hypothetical prote
991	137	5.8	691	2	F91251	probable tape meas	1064	134	5.7	278	2	S44796	F09G8.6 protein -
992	137	5.8	858	2	JG0183	myosin Myok - Dict	1065	134	5.7	492	2	D70870	probable PG protei
993	137	5.8	1005	2	T71513	hypothetical prote	1066	134	5.7	627	2	T35608	polyketide hydroxy
994	136.5	5.8	127	2	D84469	probable glycine-r	1067	134	5.7	632	2	T00084	hypothetical prote
995	136.5	5.8	159	2	S18345	environmental stre	1068	134	5.7	803	2	C83561	probable type II s
996	136.5	5.8	222	2	A88102	protein W09G10.1 (1069	134	5.7	1065	2	T13230	hypothetical isoform
997	136.5	5.8	228	2	D86416	probable beta-1,3	1070	134	5.7	1072	2	T13232	dachshund protein
998	136.5	5.8	301	2	T23441	hypothetical prote	1071	134	5.7	1074	2	T13229	dachshund protein
999	136.5	5.8	407	2	T14909	bZIP DNA-binding p	1072	134	5.7	1081	2	T13231	dachshund protein
1000	136.5	5.8	488	2	F86911	conserved hypotet	1073	134	5.7	1174	2	A40853	potassium channel
1001	136.5	5.8	1264	2	S41603	type V adenyl cycl	1074	133.5	5.6	175	2	S54255	probable glycine r
1002	136.5	5.8	1290	2	T00018	period protein hom	1075	133.5	5.6	349	2	T41394	hypothetical serin
1003	136.5	5.8	1365	2	S14871	suppressor two of	1076	133.5	5.6	618	2	T42664	hypothetical prote
1004	136	5.8	440	2	T61183	transcription fact	1077	133.5	5.6	694	2	S71786	wingless receptor
1005	136	5.8	441	2	T49265	hypothetical prote	1078	133.5	5.6	743	2	T34853	probable fusidic a
1006	136	5.8	524	2	T08931	hypothetical prote	1079	133.5	5.6	1367	2	T33819	hypothetical prote
1007	136	5.8	635	2	T00011	ccal protein - rat	1080	133	5.6	127	2	S49195	GCR 20 protein - f
1008	136	5.8	643	1	FOLJLK	gene M-twist prote	1081	133	5.6	133	2	T09608	hypothetical stre
1009	136	5.8	647	2	S06450	steroid hormone re	1082	133	5.6	135	2	C82998	hypothetical prote
1010	136	5.8	924	2	B41359	potassium channel	1083	133	5.6	154	2	T01983	tumor related prot
1011	136	5.8	924	2	S12746	hypothetical prote	1084	133	5.6	154	2	T01983	glycine-rich prote
1012	136	5.8	963	2	T19140	hypothetical prote	1085	133	5.6	199	2	T32123	probable single-st
1013	136	5.8	1823	2	S28974	vitellogenin precu	1086	133	5.6	370	2	T22510	hypothetical prote
1014	135.5	5.7	206	2	J53066	gene M-twist prote	1087	133	5.6	510	2	A32380	nuclear protein fk
1015	135.5	5.7	257	2	T01900	major prion protei	1088	133	5.6	538	2	H86335	T20H2.2 protein -
1016	135.5	5.7	280	2	S53629	major prion protei	1089	133	5.6	611	1	S06047	endo-1,4-beta-xyla
1017	135.5	5.7	298	2	JC1448	collagen col-34 -	1090	133	5.6	622	2	G96762	hypothetical prote
1018	135.5	5.7	342	2	T45886	RNA-binding protei	1091	133	5.6	663	2	S21912	BRCore-Q1-Z1 prote
1019	135.5	5.7	536	2	T37544	hypothetical serin	1092	133	5.6	1077	2	A44067	serine-rich protei
1020	135.5	5.7	610	2	S05807	SAN1 protein - Yea	1093	133	5.6	3828	2	T13857	trichorax protein
1021	135.5	5.7	650	2	T22002	hypothetical prote	1094	132.5	5.6	243	2	S27758	maturation-associa
1022	135.5	5.7	716	2	D69855	conserved hypotet	1095	132.5	5.6	308	2	T19846	hypothetical prote
1023	135.5	5.7	1212	2	T13804	shs protein - frui	1096	132.5	5.6	325	2	T38308	hypothetical prote
1024	135.5	5.7	1290	2	S76853	hypothetical prote	1097	132.5	5.6	333	2	C48423	homeotic protein e
1025	135.5	5.7	1576	2	S65774	homeotic protein H	1098	132.5	5.6	547	2	F71287	probable treponema
1026	135	5.7	98	2	S08137	gene 2C protein -	1099	132.5	5.6	839	2	E84824	hypothetical prote
1027	135	5.7	129	2	T03861	glycine-rich prote	1100	132.5	5.6	1520	1	TVFFA	protein-tyrosine k
1028	135	5.7	139	2	T33868	hypothetical prote	1101	132.5	5.6	1629	2	T06461	DNA-binding protei
1029	135	5.7	162	2	S56703	glycine-rich cell	1102	132.5	5.6	1629	2	F90073	hypothetical prote
1030	135	5.7	174	2	S00273	period clock prote	1103	132	5.6	2271	2	T04346	glycine-rich RNA-b
1031	135	5.7	188	2	S49192	GCR 1 protein - fr	1104	132	5.6	165	2	S59529	RNA-binding glycyl
1032	135	5.7	241	2	T27929	hypothetical prote	1105	132	5.6	165	2	S41773	glycine-rich RNA-b
1033	135	5.7	302	2	A39615	merozoite 45K surf	1106	132	5.6	300	2	A39112	merozoite 45K surf
1034	135	5.7	369	2	S33603	surfactant protein	1107	132	5.6	302	2	A31921	collagen dpy-13 pr
1035	135	5.7	414	2	JN0866	nucleolar protein	1108	132	5.6	305	2	T30165	hypothetical prote
1036	135	5.7	464	2	E82865	conjugal transfer	1109	132	5.6	348	2	A34705	hypothetical prote
1037	135	5.7	467	2	S30839	UTR2 protein - yea	1110	132	5.6	427	2	T20800	collagen - Caenorh
1038	135	5.7	573	2	A33533	cell surface glyco	1111	132	5.6	428	2	T24769	hypothetical prote
1039	135	5.7	595	2	B86212	secreted acid phos	1112	132	5.6	517	2	T10927	3C3.18c protein -
1040	135	5.7	888	2	T46726	iron-regulated pro	1113	132	5.6	647	2	SL8737	gag polyprotein -
1041	135	5.7	1302	2	C81182	nestin - golden ha	1114	132	5.6	700	2	IS1235	DEAD box protein -
1042	135	5.7	1804	2	T34518	tail-host specific	1115	132	5.6	705	2	S32644	nucleolin - Africa
1043	135	5.7	1904	2	T13256	hypothetical prote	1116	132	5.6	782	2	A10062	conserved hypotet
1044	135	5.7	2468	2	A83412	hypothetical prote	1117	132	5.6	1525	2	T14961	hypothetical prote
1045	134.5	5.7	158	2	T08957	glycine-rich prote	1118	131.5	5.6	252	2	T10697	immature seed prot
1046	134.5	5.7	197	2	T03442	glycine-rich prote	1119	131.5	5.6	322	2	G95244	hypothetical prote
1047	134.5	5.7	209	2	A41342	circumsporozoite p	1120	131.5	5.6	355	2	C39725	hypothetical prote
1048	134.5	5.7	278	2	S39310	merozoite surface	1121	131.5	5.6	386	2	A48571	circumsporozoite p
1049	134.5	5.7	289	2	S74632	hypothetical prote	1122	131.5	5.6	461	2	T10265	arabinogalactan-p
1050	134.5	5.7	291	2	T20942	hypothetical prote	1123	131.5	5.6	463	2	T10015	hypothetical prote
1051	134.5	5.7	297	2	T18637	hypothetical prote	1124	131.5	5.6	471	2	SL5035	acetylcholinestera

1125	131.5	5.6	479	2	A38307	metalloproteinase	1198	129	5.5	551	1	NRECE3	colicin E3 (EC 3.1
1126	131.5	5.6	520	2	T375A1	probable glycolipase	1199	129	5.5	581	1	NDECE2	colicin E2 (EC 3.1
1127	131.5	5.6	510	2	A81183	ATP-dependent RNA	1200	129	5.5	626	2	T01485	probable polygalac
1128	131.5	5.6	525	2	A35596	nuclear pore glyco	1201	129	5.5	632	2	T07587	probable polygalac
1129	131.5	5.6	589	2	A22263	hypothetical prote	1202	129	5.5	670	2	F84540	hypothetical prote
1130	131.5	5.6	713	2	UC2534	RVG protein - rat	1203	129	5.5	707	2	A46302	PTB-associated spl
1131	131.5	5.6	940	2	D89723	protein F398B.1b (1204	129	5.5	895	2	AD0541	outer membrane fm
1132	131.5	5.6	945	2	T21998	hypothetical prote	1205	129	5.5	1442	2	T42607	transcription acti
1133	131.5	5.6	962	2	S03818	carboxymethylcellu	1206	129	5.5	1741	2	S74910	hemolysin - Synec
1134	131.5	5.6	1039	2	T35878	hypothetical prote	1207	128.5	5.4	157	1	S14857	glycine-rich prote
1135	131.5	5.6	1130	2	T30251	repetin - mouse	1208	128.5	5.4	271	1	A47156	hexamer-binding pr
1136	131.5	5.6	1704	2	T43141	vitellogenin 1 - m	1209	128.5	5.4	401	2	A48423	engrailed homeodom
1137	131.5	5.6	1732	2	T43026	probable DNA-dirc	1210	128.5	5.4	427	2	A32372	female-specific do
1138	131	5.5	180	2	JC7876	prion protein homo	1211	128.5	5.4	549	2	B32372	male-specific doub
1139	131	5.5	184	1	CGRTS8	collagen alpha 2(I	1212	128.5	5.4	564	1	KRHUEB	keratin 6b, type I
1140	131	5.5	304	2	T16107	hypothetical prote	1213	128.5	5.4	564	2	161771	keratin 6f, type I
1141	131	5.5	307	2	T37287	collagen 36 - Caen	1214	128.5	5.4	634	2	A54495	knob protein precu
1142	131	5.5	355	2	F71435	probable nuclear a	1215	128.5	5.4	710	2	T31502	hypothetical prote
1143	131	5.5	440	2	F71795	transcription fact	1216	128.5	5.4	1275	2	T49362	hypothetical prote
1144	131	5.5	485	2	B40552	bindin fertilizati	1217	128.5	5.4	1367	2	T13703	tamA protein - fru
1145	131	5.5	642	2	S27806	homeotic protein B	1218	128.5	5.4	1621	2	T30200	protein-tyrosine k
1146	131	5.5	653	1	S44749	CO6G4.2 protein -	1219	128	5.4	185	2	JC4085	glycine-rich cutic
1147	131	5.5	724	2	A48569	antigen Em100 - Ei	1220	128	5.4	321	2	A38712	fibrillarlin [valid
1148	131	5.5	728	2	S21931	BRCORE-TNT1-Q1-Z1	1221	128	5.4	339	2	S20880	homeotic protein H
1149	131	5.5	753	2	A27041	tyrosine kinase-re	1222	128	5.4	514	2	S21914	BRCORE-2 protein -
1150	131	5.5	1053	2	T07965	reverse transcript	1223	128	5.4	547	2	H85699	partial probable a
1151	131	5.5	1148	2	A71446	hypothetical prote	1224	128	5.4	547	2	C90842	partial probable a
1152	131	5.5	1332	2	T15670	hypothetical prote	1225	128	5.4	598	2	A84616	hypothetical prote
1153	131	5.5	2703	1	A24420	notch protein - fr	1226	128	5.4	606	2	S13367	Om1D) protein - f
1154	130.5	5.5	163	2	JC6571	cold-inducible RNA	1227	128	5.4	640	2	A41726	homeotic protein B
1155	130.5	5.5	251	2	D96010	hypothetical expor	1228	128	5.4	733	2	S10932	probable protein k
1156	130.5	5.5	286	2	S34665	collagen, cuticula	1229	128	5.4	918	2	A88188	protein C18H9.3 (I
1157	130.5	5.5	369	2	S11980	variable major pro	1230	128	5.4	1870	2	S37671	MHC class III hist
1158	130.5	5.5	381	2	A54415	transcription fact	1231	128	5.4	1970	1	S21054	DNA-directed RNA p
1159	130.5	5.5	473	2	F70031	cell wall-binding	1232	128	5.4	2248	1	D42088	adenylate cyclase
1160	130.5	5.5	643	2	F50539	intermediate filam	1233	127.5	5.4	290	2	B86338	protein F58F6.2 (I
1161	130.5	5.5	748	2	T04011	hypothetical prote	1234	127.5	5.4	321	2	F60110	repetitive protein
1162	130.5	5.5	1036	1	A34755	nitrogen regulator	1235	127.5	5.4	325	2	T16324	hypothetical prote
1163	130.5	5.5	2154	2	F83068	hypothetical prote	1236	127.5	5.4	373	2	S43455	hypothetical prote
1164	130.5	5.5	2440	2	S39162	transcription coac	1237	127.5	5.4	550	1	FGRTA	fibrinogen alpha c
1165	130	5.5	123	2	C39777	hypothetical prote	1238	127.5	5.4	693	2	JC7925	nucleolin - common
1166	130	5.5	182	1	KRB02A	keratin, 68K type	1239	127.5	5.4	817	2	T22442	hypothetical prote
1167	130	5.5	250	2	B35026	filaggrin B - mous	1240	127.5	5.4	827	2	JC4900	transferred entry
1168	130	5.5	253	2	S53618	major prion protei	1241	127.5	5.4	1641	2	T10955	early nodulin bind
1169	130	5.5	253	2	S53619	major prion protei	1242	127.5	5.4	1872	2	S36152	MHC class III hist
1170	130	5.5	331	2	F70820	hypothetical glyci	1243	127.5	5.4	1940	2	F75393	hypothetical prote
1171	130	5.5	334	2	S53490	RNA-binding protei	1244	127	5.4	228	2	T49891	glycine-rich prote
1172	130	5.5	448	2	S05355	hypothetical prote	1245	127	5.4	241	2	S71048	major prion protei
1173	130	5.5	563	2	A36054	mucin homolog - bo	1246	127	5.4	253	1	UJHU	major prion protei
1174	130	5.5	622	2	G86371	hypothetical prote	1247	127	5.4	253	2	S53635	major prion protei
1175	130	5.5	625	2	T41603	alpha-amylase - fi	1248	127	5.4	253	2	S53635	major prion protei
1176	130	5.5	676	2	S61977	transcription fact	1249	127	5.4	253	2	S53614	major prion protei
1177	130	5.5	1618	2	S21424	nestin - human	1250	127	5.4	253	2	S53614	major prion protei
1178	130	5.5	1872	2	T30888	vitellogenin - Ath	1251	127	5.4	253	2	S53614	major prion protei
1179	130	5.5	3705	2	AD0123	probable autotrans	1252	127	5.4	253	2	S53616	major prion protei
1180	129.5	5.5	142	2	C33910	sal homeotic prote	1253	127	5.4	298	2	A40616	34K antigen - Myco
1181	129.5	5.5	287	2	T15779	hypothetical prote	1254	127	5.4	370	2	I57555	c-Maf protein - mo
1182	129.5	5.5	296	2	A31219	collagen 1 - Caeno	1255	127	5.4	378	1	OZZOAV	circumsporozoite p
1183	129.5	5.5	564	1	KRHUEA	keratin 6a, type I	1256	127	5.4	409	2	A70647	probable PPE prote
1184	129.5	5.5	666	2	T05432	hypothetical prote	1257	127	5.4	496	2	A54770	N-acetylglucosamin
1185	129.5	5.5	732	2	T08420	1-phosphatidylinos	1258	127	5.4	579	2	E83144	hypothetical prote
1186	129.5	5.5	900	2	B87957	protein Y10SG6D.7	1259	127	5.4	644	1	I40712	endo-1,4-beta-xyla
1187	129.5	5.5	948	2	T26417	hypothetical prote	1260	127	5.4	718	2	D46675	hypothetical prote
1188	129.5	5.5	1706	1	OYBRC	cyclolysin - Borde	1261	127	5.4	719	2	S61046	ARPI protein - yea
1189	129.5	5.5	4776	2	E95206	cell wall surface	1262	127	5.4	720	2	T51007	hypothetical prote
1190	129	5.5	155	2	S20846	glycine-rich prote	1263	127	5.4	748	2	S19652	cellodextrinase C
1191	129	5.5	156	2	S41771	glycine-rich RNA-b	1264	127	5.4	1145	2	G87284	hypothetical prote
1192	129	5.5	201	2	G01204	twist protein homo	1265	127	5.4	1705	2	S51672	adenylate cyclase
1193	129	5.5	256	2	JU0268	major prion protei	1266	127	5.4	1787	2	AG1360	probable tape-meas
1194	129	5.5	256	2	S37149	prion protein - go	1267	126.5	5.4	301	2	T21314	hypothetical prote
1195	129	5.5	256	2	A54281	major prion protei	1268	126.5	5.4	342	2	S18649	homeotic protein H
1196	129	5.5	323	2	S16318	homeotic protein H	1269	126.5	5.4	420	2	T14911	bZIP DNA-binding p
1197	129	5.5	456	1	KRHU5	keratin 15, type I	1270	126.5	5.4	590	2	A29904	keratin 5, type II

1271	126.5	5.4	742	2	JC7595	scavenger receptor	1344	124.5	5.3	1374	2	AE3259	extracellular seri
1272	126.5	5.4	764	2	H71507	hypothetical prote	1345	124.5	5.3	1613	2	T06678	hypothetical prote
1273	126.5	5.4	910	2	A34721	androgen receptor	1346	124.5	5.3	2860	2	A45259	desmoyokin - human
1274	126.5	5.4	911	2	B34721	androgen receptor	1347	124.5	5.3	3591	1	S21010	filamentous hemagg
1275	126.5	5.4	929	2	C96623	hypothetical prote	1348	124	5.2	254	2	A34759	prion protein - Ch
1276	126.5	5.4	999	2	D99852	fibrinogen-binding	1349	124	5.2	285	2	T31503	hypothetical prote
1277	126.5	5.4	993	2	AE1905	outer membrane sec	1350	124	5.2	437	2	E90996	probable tail fibre
1278	126.5	5.4	2059	2	D82671	surface protein XF	1351	124	5.2	452	2	I49595	cytokeatin 15 - m
1279	126.5	5.4	2142	2	B35098	MHC class III hist	1352	124	5.2	452	2	T30082	hypothetical prote
1280	126	5.3	144	2	S35716	glycine-rich prote	1353	124	5.2	459	2	A59111	hypothetical prote
1281	126	5.3	199	2	S32224	acp-22 protein - y	1354	124	5.2	486	1	A57601	transcription fact
1282	126	5.3	284	2	A35419	neutrophil protein	1355	124	5.2	562	2	T49788	related to merozoi
1283	126	5.3	302	2	T15936	hypothetical prote	1356	124	5.2	580	2	S11890	serine proteinase
1284	126	5.3	305	2	S33690	fibrillarlin - fisa	1357	124	5.2	784	2	AC1091	5'-nucleotidase, p
1285	126	5.3	320	2	T09555	collagen sgt-1 pre	1358	124	5.2	787	2	T00798	hypothetical prote
1286	126	5.3	334	2	A31920	collagen sgt-1 pre	1359	124	5.2	856	2	T13159	E1B-55kDa-associat
1287	126	5.3	340	2	AB3401	hypothetical prote	1360	124	5.2	1325	2	A64905	yedk protein - Esc
1288	126	5.3	417	2	JC7092	Pauli protein - fis	1361	124	5.2	1360	2	T34302	cell polarity prot
1289	126	5.3	518	2	T23745	hypothetical prote	1362	124	5.2	1428	2	T13926	probable protein p
1290	126	5.3	622	2	AP0169	probable exported	1363	124	5.2	4550	2	T18440	hypothetical prote
1291	126	5.3	720	2	T48302	hypothetical prote	1364	124	5.2	7463	2	T36248	CDA peptide synthe
1292	126	5.3	910	2	S68983	auxilin - bovine	1365	123.5	5.2	152	2	T07858	glycine-rich prote
1293	126	5.3	1022	2	T17406	developmental prot	1366	123.5	5.2	198	2	T06813	dehydrin 3 - garde
1294	126	5.3	1070	2	AI0484	probable autotrans	1367	123.5	5.2	260	2	S22373	proline-rich prote
1295	125.5	5.3	165	2	T03392	probable dehydrin	1368	123.5	5.2	280	2	T24454	hypothetical prote
1296	125.5	5.3	199	2	S16063	acp-22 protein - y	1369	123.5	5.2	310	2	T43147	hypothetical prote
1297	125.5	5.3	286	2	A53892	prion-related prot	1370	123.5	5.2	369	1	TVFVAF	transforming prote
1298	125.5	5.3	292	2	T23966	hypothetical prote	1371	123.5	5.2	371	2	T36871	probable pseudouri
1299	125.5	5.3	453	2	S18804	collagen alpha 4(I	1372	123.5	5.2	378	2	H88042	protein F56D12.5 [
1300	125.5	5.3	627	2	T05789	hypothetical prote	1373	123.5	5.2	646	2	H96665	protein F22C12.10
1301	125.5	5.3	634	2	A28412	histidine-rich pro	1374	123.5	5.2	651	2	S18874	nucleolin - Africa
1302	125.5	5.3	933	2	A41539	fibrinogen-binding	1375	123.5	5.2	730	2	T43317	pql-1 protein - Ca
1303	125.5	5.3	936	2	F75622	hypothetical prote	1376	123.5	5.2	761	2	AI0074	probable autotrans
1304	125.5	5.3	960	1	A39651	discs-large tumor	1377	123.5	5.2	770	2	TS1024	related to C2H2 zi
1305	125.5	5.3	1148	2	S72635	exo-poly-alpha-gal	1378	123.5	5.2	771	2	T29177	hypothetical prote
1306	125.5	5.3	1475	2	F86399	protein F17L21.22	1379	123.5	5.2	964	2	AB4693	hypothetical prote
1307	125.5	5.3	1611	2	T06677	hypothetical prote	1380	123.5	5.2	1035	2	AD3203	autotransporter pr
1308	125	5.3	179	2	A85217	hypothetical prote	1381	123.5	5.2	1230	2	E64664	outer membrane pro
1309	125	5.3	254	1	U0HYH	major prion PrP-Sc	1382	123.5	5.2	1237	2	A34598	ecdysone-induced p
1310	125	5.3	254	1	B34759	prion protein - go	1383	123.5	5.2	1394	2	H34598	ecdysone-induced p
1311	125	5.3	296	2	T24827	hypothetical prote	1384	123.5	5.2	1403	2	S77624	mannuronan C-5-epi
1312	125	5.3	323	2	I51417	fibrillarlin - Afri	1385	123	5.2	129	2	T06256	dormancy-associate
1313	125	5.3	338	2	T23006	hypothetical prote	1386	123	5.2	129	2	S14984	glycine-rich prote
1314	125	5.3	343	2	A29319	circumsporozoite p	1387	123	5.2	144	2	S04069	glycine-rich prote
1315	125	5.3	354	2	T06487	probable DNA-bind	1388	123	5.2	257	2	A23545	major prion PrP27-
1316	125	5.3	435	2	T11619	probable nucleopor	1389	123	5.2	318	2	S13550	probable secreted
1317	125	5.3	438	2	D90734	probable tail fibre	1390	123	5.2	321	2	S13550	anther-specific pr
1318	125	5.3	438	2	S62453	hypothetical prote	1391	123	5.2	385	2	H89046	protein C10G8.8 [i
1319	125	5.3	440	2	S37303	sox-4 protein - mo	1392	123	5.2	407	2	G90907	probable tail fibre
1320	125	5.3	466	2	T35164	probable secreted	1393	123	5.2	483	2	A55033	keratin 12 - mouse
1321	125	5.3	509	2	T09572	cdc2-like protein	1394	123	5.2	511	2	S24345	Balbani ring 1 pr
1322	125	5.3	534	2	T39903	serine-rich protei	1395	123	5.2	522	2	S41819	nucleoporin p82 -
1323	125	5.3	570	2	S56132	cellulase (EC 3.2.	1396	123	5.2	559	2	G82326	MSHA biogenesis pr
1324	125	5.3	635	2	F75477	hypothetical prote	1397	123	5.2	624	2	T02289	probable polygalac
1325	125	5.3	642	1	S34416	transcription fact	1398	123	5.2	656	1	S59631	endo-1,4-beta-xyla
1326	125	5.3	712	2	B47021	pectic enzyme secr	1399	123	5.2	841	2	C87331	ISCc2, transposase
1327	125	5.3	943	2	JC4081	sucrase/fructanase	1400	123	5.2	902	2	T26775	hypothetical prote
1328	125	5.3	955	2	G64866	probable membrane	1401	123	5.2	1070	2	S75712	cellulase (EC 3.2.
1329	125	5.3	1315	2	T05300	hypothetical prote	1402	123	5.2	1334	2	T50568	probable multi-dom
1330	124.5	5.3	341	2	S37749	collagen alpha 2(X	1403	123	5.2	1560	2	T30282	calcium-binding pr
1331	124.5	5.3	355	2	A33821	hypothetical prote	1404	122.5	5.2	160	2	T26289	hypothetical prote
1332	124.5	5.3	360	2	G85014	chromosomal protei	1405	122.5	5.2	296	2	B39581	GRESAG protein 9u
1333	124.5	5.3	360	2	G85014	GBF2, G-box bindin	1406	122.5	5.2	391	2	A49645	transcription fact
1334	124.5	5.3	458	2	T31631	hypothetical prote	1407	122.5	5.2	437	2	A55682	keratin l3, type I
1335	124.5	5.3	481	2	A26483	bindin precursor -	1408	122.5	5.2	532	2	B35621	spore germination
1336	124.5	5.3	516	2	AC1540	ATP-dependent RNA	1409	122.5	5.2	626	2	F85295	hypothetical prote
1337	124.5	5.3	682	2	JC7670	cathepsin-B mRNA 3	1410	122.5	5.2	685	2	JC6331	rho-type guanine e
1338	124.5	5.3	687	2	F83671	hypothetical prote	1411	122.5	5.2	748	2	TS1738	rRNA helicase RH3 l
1339	124.5	5.3	690	2	A31841	daughterless (da)	1412	122.5	5.2	867	2	T27136	hypothetical prote
1340	124.5	5.3	812	1	MMECOF	outer membrane ush	1413	122.5	5.2	871	2	T27135	hypothetical prote
1341	124.5	5.3	995	2	T32466	hypothetical prote	1414	122.5	5.2	930	2	D86546	polymorphic outer
1342	124.5	5.3	997	2	B71617	SERA antigen/papai	1415	122.5	5.2	930	2	D72078	polymorphic outer
1343	124.5	5.3	1262	2	T30524	protein phosphatas	1416	122.5	5.2	930	2	A81591	polymorphic membra

Db 725 GGNSETGSGDGGAGNGGAAGTGTGCGDGLTGTG 759

RESULT 2

A70934

hypothetical glycine-rich protein Rv0578c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: A70934

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; PMID:98295987; PMID:9634230

A;Accession: A70934

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1306 <COL>

A;Cross-references: UNIPROT:O53775; GB:AL021942; GB:AL123456; NID:g3242298; PIDN:CAA1744

A;Experimental source: strain H37RV

C:Genetics:

C;Superfamily: collagen alpha 1(IV) chain

Query Match 18.6%; Score 439.5; DB 2; Length 1306;

Best Local Similarity 30.9%; Pred. No. 8e-16;

Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

QY 17 GSCEAGPLQSGESTGTN--IGALGHGLGDALSEGVGKAIGK-----EAGGAAGSKV 67

Db 567 GHGAAGAL-----GVNGGVGAGHG--GD---PGVGGAGGGGSGSTPGANGAENTP 615

QY 68 SEA--LQQGTREAVGTGVRQVPGFGAADALGNRVGE-AAHALGNTGHE----IGROAEDV 120

Db 616 TSGGNGNGRGADATGFGQTGASGGRGDGLVNGGAGGAGSGSKGLPGLRLGNP- 674

QY 121 IRHGADAVRGSWGVPHSGAWTSGHGLFGSQGLGGQ-----CGNPG 166

Db 675 ---GLDGGTGGNGGAGGSGGAMAGNGGTGAGGTGGVGTGGSGSDGVANGSSAGADGHFG 731

QY 167 GLCTPWHVHGPNGSAGSFGMNPQG-----APWGOGNGGPPNPGTN-----TOG 210

Db 732 GTGGVGTGKGDDGGDGGGAAPNVAGSQCPGAGSDGGTGGVGGNGRGIDGADATAG 791

QY 211 AVAQPGYGVSRASNQNEGCTNPP-----PGSG-----CGGSSNSQGGSGSQSGSGSNGD 262

Db 792 ARQDGGAGGAGGKGRGGTGGPGGAGPAGTTGSGAGGNGGSGGTGGDPDGGNGANGS 851

QY 263 --NNNGSSGSSGSSGSSGSSGSSG-----GSS-----GSSGNSG----- 298

Db 852 VFTNNGITGGNGGNGAGPSAGGSGAGSTFTGATGSSSIHVNGGNGGNGGNGDHALSG 911

QY 299 -GSRGDSGSSWSSTGS--SSNGHGGSG-----GNGHKPGCKPGNEARGSGESGI 349

Db 912 NGAAGNGGNGGNSLRGSGGAGHGNGGNGNARGMGDGTGTGAGAGNAGQITGNGAGGN 971

QY 350 QGFRGQGVSSNMREISKEGNR-----LIGGSGDNRYRQGGSSWGSWGGDVGGV---NTVNS 402

Db 972 GDDGTGSDGNPCAITGSGGRGGDGGVGGQGGSVAGDGDGGRGAGGTGGTGLRGTGTA 1031

QY 403 ETSFGMFPN 410

Db 1032 TGATGTFD 1039

RESULT 3

T49109

glycine-rich protein - Arabidopsis thaliana

N;Alternate names: protein AT4g22020

C:Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C;Accession: T49109

R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Me submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25016

A;Accession: T49109

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-396 <REV>

A;Cross-references: UNIPROT:O65450; EMBL:AL022140; GSPDB:GN00062; ATSP:AT4g22020

A;Experimental source: cultivar Columbia; BAC clone FIN20

C:Genetics:

A;Gene: ATSP:AT4g22020

A;Map position: 4

C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match 17.9%; Score 423; DB 2; Length 396;

Best Local Similarity 33.2%; Pred. No. 2e-15;

Matches 133; Conservative 22; Mismatches 169; Indels 76; Gaps 14;

QY 17 GSCEAGPLQSGESTGTNIGALGHGLGDALSEGVGKAIGKEAGGAAGSKVSEALGQGT 76

Db 63 GGG 122

QY 77 EAVGTGV-RQVPFGAADALGNRVGEAAHALGNTGHEIGROAEDVIRHGADAVRGSWQGV 135

Db 123 SCAGAGVGGTTGTVGG 164

QY 136 PCHSGAWTSGHGLFGSQGLGGQGNPGGLGTPWHVHGPNGSAGSFGMNPQGPAGWQ 195

Db 165 GAGAGVGGSSGAG--GG 214

QY 196 CGNGGPPNPGTWTQGAQPGYGVSRASNQNEGCTNPPPSGGSGGSSNGGSGSGSGS 255

Db 215 GGGGG--GG 258

QY 256 GGGSN---GDNNGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSS 312

Db 259 GSGGSKVGGYGHGSGFGGSGFGNGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 314

QY 313 STGSSSGNHGSGGNGHKGPKCEKPGNEARGSGES-GIOGFRGQGVSSNMREISKEGNRL 371

Db 315 CMGKSGSGGG 356

QY 372 LGSGDNYRQGGSSWGS--GGDAVGG-----VNTVNSETSP 406

Db 357 NCGGGVGFPMGIGFGLGIGGGSGGTGTTLTGDKNSP 396

RESULT 4

E70806

hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: E70806

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; PMID:98295987; PMID:9634230

A;Accession: E70806

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1381 <COL>

A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17744.1; PID:g2924444

A;Experimental source: strain H37RV

C:Genetics:

A;Gene: Rv3507

C;Superfamily: collagen alpha 1(IV) chain

Query Match 17.6%; Score 415.5; DB 2; Length 1381;

Best Local Similarity 29.9%; Pred. No. 1.5e-14;

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OM protein - protein search, using sw model

Run on: April 7, 2005, 00:04:15 ; Search time 179 Seconds
(without alignments)
1258.742 Million cell updates/sec

Title: US-10-063-561-52
Perfect score: 2363
Sequence: 1 MKFQGPLACLLALCLGSGE.....KLGFINWDAINKDQRSSRIP 440

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2363	100.0	440	2	Q6UXC7
2	1996	84.5	476	2	Q6E0U4
3	1043	44.1	517	2	Q6E0U6
4	1038.5	43.9	508	2	Q6P253
5	1030	43.6	493	2	Q6S2J9
6	546.5	23.1	407	2	Q6C4L6
7	486	20.6	1553	2	Q6FPR0
8	471	19.9	1274	2	Q6CHN8
9	460.5	19.5	1938	2	Q7TW50
10	450.5	19.1	1079	2	Q6MW7
11	439.5	18.6	1306	2	Q7D9L6
12	439.5	18.6	1306	2	Q6MX28
13	439.5	18.6	1306	2	Q7U1Q7
14	433	18.3	725	2	Q7SEB7
15	430	18.2	1391	2	Q6C6W0
16	428	18.1	528	2	Q63WJ8
17	426.5	18.0	1815	2	Q6CF66
18	426	18.0	512	2	Q62HK1
19	423	17.9	396	2	Q65450
20	420.5	17.8	1384	2	Q8V1Z1
21	415.5	17.6	1381	2	Q6MW9
22	412.5	17.5	484	2	Q6MWY1
23	412.5	17.5	1360	2	Q7TW4
24	406	17.2	1901	1	PG54 MYCTU
25	404.5	17.1	532	2	Q7D7F8
26	403	17.1	1224	2	Q6CN84
27	403	17.1	1489	2	Q6MW6
28	400.5	16.9	992	2	Q7TW8
29	400.5	16.9	1538	2	Q6MW70
30	399.5	16.9	853	2	Q79F55
31	399	16.9	786	2	O18740 canis famil

32	398	16.8	850	2	Q7U0P1
33	397.5	16.8	743	2	Q6RHW0
34	397.5	16.8	763	2	Q7U0R0
35	397.5	16.8	1217	2	Q8VIY9
36	397.5	16.8	1460	2	Q7TWC3
37	397.5	16.8	1507	2	Q8VJ23
38	397	16.8	897	2	Q6Q294
39	396.5	16.8	1715	2	Q8VIZ0
40	395	16.7	714	2	Q6MMW8
41	395	16.7	749	2	Q7TWK6
42	395	16.7	1660	2	Q79FD4
43	395	16.7	1685	2	Q7D721
44	393	16.6	626	2	Q7TWM2
45	392.5	16.6	923	2	Q79FU3
46	392.5	16.6	923	2	Q7U0X8
47	392	16.6	731	2	Q6MWX5
48	392	16.6	775	2	Q8VJ15
49	392	16.6	1329	2	Q79FP2
50	392	16.6	1408	2	Q8VK17
51	392	16.6	5263	1	FBOH_BOMMO
52	391	16.5	2249	2	Q9NHW4
53	390.5	16.5	635	2	Q8VK71
54	389.5	16.5	1408	2	Q7U022
55	388	16.4	1150	2	Q7TYG8
56	387.5	16.4	619	2	Q91PQ9
57	386	16.3	778	1	PG46 MYCTU
58	385.5	16.3	518	2	Q67WR0
59	383.5	16.2	767	2	Q79FT0
60	383	16.2	641	1	EBN1_EBV
61	383	16.2	641	2	Q777E1
62	381.5	16.1	738	2	Q8VK15
63	381.5	16.1	741	2	Q79FP1
64	381.5	16.1	774	2	Q7U0P7
65	381	16.1	390	2	Q9M3Y2
66	380.5	16.1	749	2	Q7D974
67	380.5	16.1	837	2	Q79FY9
68	380.5	16.1	2401	2	Q7RF52
69	379.5	16.1	628	2	Q8VJ19
70	379.5	16.1	1618	2	Q6FQ10
71	379	16.0	465	1	GRP2_PHAVU
72	378.5	16.0	490	2	Q7V5E6
73	378	16.0	588	2	Q6MWX7
74	378	16.0	617	2	Q46172
75	376.5	15.9	749	2	Q79FV7
76	375	15.9	914	1	WA22 MYCTU
77	374	15.8	831	2	Q7U2D6
78	373.5	15.8	584	2	Q7D580
79	373.5	15.8	584	2	Q7TW48
80	373.5	15.8	667	2	Q7D8W7
81	373.5	15.8	667	2	Q79FT3
82	373.5	15.8	1382	2	Q6BN56
83	373	15.8	871	2	O44358
84	372	15.7	694	2	Q7D724
85	372	15.7	909	2	Q7U1D3
86	371.5	15.7	671	2	Q7U0R1
87	371	15.7	400	2	Q8GTL0
88	371	15.7	615	2	Q6MX26
89	371	15.7	615	2	Q7TXQ0
90	371	15.7	644	2	Q8WSW4
91	371	15.7	747	1	SPD1_NEPCL
92	370.5	15.7	491	2	Q79FP3
93	369.5	15.6	491	2	Q7U027
94	369.5	15.6	795	2	Q7U020
95	369.5	15.6	1428	2	O44341
96	369	15.6	557	2	Q6BVD0
97	369	15.6	622	2	Q8VKN3
98	367.5	15.6	606	2	Q7U2C0
99	367.5	15.6	608	2	Q7U125
100	366.5	15.5	877	2	Q7U2D7
101	366	15.5	408	2	Q43688
102	366	15.5	610	2	Q9V5V8
103	366	15.5	691	2	Q9B1U3
104	365.5	15.5	496	2	Q79G09

Q7u0p1	mycobacteri
Q6rhw0	mus musculu
Q7u0r0	mycobacteri
Q8viy9	mycobacteri
Q7tWC3	mycobacteri
Q8vj23	mycobacteri
Q6q294	agelenopais
Q8vizo	mycobacteri
Q6mmw8	mycobacteri
Q7twk6	mycobacteri
Q79fd4	mycobacteri
Q7d721	mycobacteri
Q7tWM2	mycobacteri
Q79fu3	mycobacteri
Q7u0x8	mycobacteri
Q6mwX5	mycobacteri
Q8vj15	mycobacteri
Q79fp2	mycobacteri
Q8vk17	mycobacteri
P5790	bombyx mori
Q8nhw4	nephila cla
Q8vk71	mycobacteri
Q7u022	mycobacteri
Q7y98	mycobacteri
Q91pq9	cynomolgus
P71933	mycobacteri
Q67wr0	oryza sativ
Q79ft0	mycobacteri
P03211	epstein-bar
Q777e1	human herpe
Q8vk15	mycobacteri
Q79fp1	mycobacteri
Q7u0p7	mycobacteri
Q9m3y2	tritium ae
Q7d974	mycobacteri
Q79fy9	mycobacteri
Q7rf52	plasmodium
Q8vj19	mycobacteri
Q6fq10	candida gla
P10496	phaseolus v
Q7vep6	mycobacteri
Q6mwX7	mycobacteri
Q46172	nephila cla
Q79fv7	mycobacteri
Q66794	mycobacteri
Q7u2d6	mycobacteri
Q7d580	mycobacteri
Q7tw48	mycobacteri
Q7d8w7	mycobacteri
Q79ft3	mycobacteri
Q6bn56	debaromyce
O44358	nephila cla
Q7d724	mycobacteri
Q7u1d3	mycobacteri
Q8gtl0	oryza sativ
Q6mx26	mycobacteri
Q7txq0	mycobacteri
Q8wsW4	nephila cla
P19837	nephila cla
Q79fp3	mycobacteri
Q7u027	mycobacteri
Q7u020	mycobacteri
O44341	halotis ru
Q6bvd0	debaromyce
Q8vkn3	mycobacteri
Q7u2c0	mycobacteri
Q7u125	mycobacteri
Q7u2d7	mycobacteri
Q43688	vigna ungui
Q9v5v8	drosophila
Q9b1u3	dolomedea t
Q79g09	mycobacteri

105	365.5	15.5	496	2	Q7U2U5	Q7u2u5 mycobacteri	178	342	14.5	515	1	PG34 MYCTU	Q50594 mycobacteri
106	365.5	15.5	533	2	Q8VKR5	Q8vkr5 mycobacteri	179	341.5	14.5	1468	2	Q9GUB5	Q9gub5 gallaria me
107	365	15.4	576	2	P71664	P71664 mycobacteri	180	341	14.4	674	2	Q681A9	Q681a9 arabidopsis
108	365	15.4	591	2	Q6MX50	Q6mx50 mycobacteri	181	340.5	14.4	452	2	Q7U049	Q7u049 mycobacteri
109	365	15.4	663	2	Q8VJC0	Q8vjc0 mycobacteri	182	339.5	14.4	487	2	Q79G08	Q79g08 mycobacteri
110	364.5	15.4	524	2	Q8I7U1	Q8i7u1 araneus ven	183	339	14.3	614	2	Q9LH97	Q9lh97 arabidopsis
111	364.5	15.4	801	1	PG10 MYCTU	O53810 mycobacteri	184	339	14.3	937	1	HYR1 CANAL	P46591 candida alb
112	364.5	15.4	907	2	O44359	O44359 nephila cla	185	338	14.3	429	2	Q8I7T9	Q8i7t9 araneus ven
113	364	15.4	421	2	Q9DEY1	Q9dey1 cyprinus ca	186	337	14.3	270	2	Q7U0C3	Q7u0c3 arabidopsis
114	364	15.4	606	2	Q79FV3	Q79fv3 mycobacteri	187	337	14.3	290	2	Q7Y218	Q7y218 arabidopsis
115	364	15.4	609	2	Q8VKC5	Q8vkc5 mycobacteri	188	337	14.3	840	2	Q95YF6	Q95yf6 patinopecte
116	364	15.4	626	2	Q9NHW1	Q9nhw1 nephila ina	189	337	14.3	1002	2	Q9BIU8	Q9biu8 argiope tri
117	363.5	15.4	349	1	GRP ARATH	Q9nhw1 nephila ina	190	336.5	14.2	338	2	Q8VJ24	Q8vj24 mycobacteri
118	363	15.4	639	2	Q79FU9	P27483 arabidopsis	191	335	14.2	581	2	Q7U1U2	Q7u1u2 mycobacteri
119	363	15.4	650	2	Q8VJW1	Q79fj9 mycobacteri	192	334.5	14.2	531	2	Q6BZJ0	Q6bzj0 debaryomyce
120	363	15.4	1114	2	Q6CCAL	Q8vfw1 mycobacteri	193	334	14.1	255	2	Q95IH2	Q95ih2 arabidopsis
121	362.5	15.3	561	2	Q8VKR1	Q8vkr1 mycobacteri	194	334	14.1	284	2	Q73E49	Q73e49 bacillus ce
122	362.5	15.3	2850	1	HORN HUMAN	Q86vz3 homo sapien	195	334	14.1	498	1	PG33 MYCTU	Q50615 mycobacteri
123	362	15.3	486	1	LORI_MOUSE	Q86vz3 mus musculu	196	333.5	14.1	501	2	Q66RZ1	Q66rz1 mycobacteri
124	361.5	15.3	422	2	Q6Z142	Q6z142 oryza sativ	197	333	14.1	466	2	Q7TZG4	Q7tzg4 mycobacteri
125	361	15.3	540	2	Q7TZI3	Q7tziz mycobacteri	198	332.5	14.1	342	2	Q9VKR8	Q9vkr8 drosophila
126	360.5	15.3	342	2	Q6HNZ6	Q6hnz6 bacillus th	199	332.5	14.1	356	2	Q6NNY8	Q6nn8 drosophila
127	360	15.2	562	2	Q79FQ7	Q79fq7 mycobacteri	200	332.5	14.1	491	1	PG36 MYCTU	Q10707 mycobacteri
128	360	15.2	562	2	Q7U0B1	Q7u0b1 mycobacteri	201	332.5	14.1	501	2	Q7TZH0	Q7tzh0 mycobacteri
129	360	15.2	586	2	Q7U0B1	Q7d8j2 mycobacteri	202	332.5	14.1	563	2	Q6J6N0	Q6j6n0 araneus ven
130	359.5	15.2	340	2	Q63G11	Q63g11 bacillus ce	203	331.5	14.0	622	2	Q8VKJ6	Q8vkj6 mycobacteri
131	359.5	15.2	773	2	Q7U160	Q7u160 mycobacteri	204	330	14.0	447	2	Q9BIV1	Q9biv1 argiope aur
132	359.5	15.2	1011	2	Q7U167	Q7u167 mycobacteri	205	330	14.0	513	2	Q61O67	Q61o67 plasmodium
133	359.5	15.2	1011	2	Q79FJ8	Q79fj8 mycobacteri	206	329.5	13.9	504	2	Q7TXZ9	Q7txz9 mycobacteri
134	359.5	15.2	1018	2	Q7TZU3	Q7tzu3 mycobacteri	207	329.5	13.9	2174	2	Q6CD35	Q6cd35 yarrowia li
135	359	15.2	463	1	PG20 MYCTU	O53416 mycobacteri	208	329	13.9	549	2	Q19318	Q19318 caenorhabdi
136	359	15.2	854	2	Q9BIU4	Q9biu4 dolomedes t	209	325.5	13.8	439	2	Q6MWV6	Q6mwv6 mycobacteri
137	358.5	15.2	486	2	Q9AR23	Q9ar23 oryza sativ	210	325.5	13.8	452	2	Q9LW52	Q9lw52 arabidopsis
138	358.5	15.2	988	2	O17434	O17434 nephila cla	211	324.5	13.7	1458	2	Q910B9	Q910b9 oncorhynch
139	358	15.2	359	2	O6Z498	O6z498 oryza sativ	212	323.5	13.7	436	2	Q8VIX6	Q8vix6 mycobacteri
140	358	15.2	774	2	Q6B8B4	Q6b8b4 caenorhabdi	213	323.5	13.7	1729	2	Q9U617	Q9u617 drosophila
141	357	15.1	760	2	Q6PV84	Q6pv84 kukulcania	214	323	13.7	268	2	Q9FIQ2	Q9fiq2 arabidopsis
142	357	15.1	766	2	Q6CV63	Q6cv63 kluyveromyc	215	322.5	13.6	355	2	Q7VEL2	Q7vel2 mycobacteri
143	357	15.1	1884	2	Q9NHW2	Q9nhw2 nephila ina	216	322	13.6	1169	2	Q21535	Q21535 caenorhabdi
144	356	15.1	281	2	Q22843	Q22843 caenorhabdi	217	321.5	13.6	431	2	Q692G4	Q692g4 nephila cla
145	356	15.1	603	2	Q7U079	Q7u079 mycobacteri	218	320.5	13.6	756	2	Q8J1W4	Q8j1w4 claviceps p
146	355.5	15.0	922	2	Q6BTJ4	Q6btj4 debaryomyce	219	320.5	13.6	1071	2	Q7YU48	Q7yu48 drosophila
147	355	15.0	291	2	Q39337	Q39337 brassica na	220	320.5	13.6	1713	2	Q6VTR6	Q6vtr6 drosophila
148	355	15.0	831	2	Q7U159	Q7u159 mycobacteri	221	320	13.5	594	2	Q6MX30	Q6mx30 mycobacteri
149	355	15.0	868	2	Q7U2D8	Q7u2d8 mycobacteri	222	320	13.5	620	2	Q9V7U0	Q9v7u0 drosophila
150	354.5	15.0	340	2	O81I38	Q81i38 bacillus ce	223	320	13.5	1953	2	Q9BI77	Q9bi77 nephila ina
151	353	14.9	588	2	Q9IPQ8	Q9ipq8 cynomolgus	224	318	13.5	1464	2	Q6P912	Q6p912 xenopus lae
152	353	14.9	624	2	Q7TZL0	Q7tzl0 mycobacteri	225	317	13.4	2655	2	Q964F4	Q964f4 antheraea y
153	352.5	14.9	384	1	GRP1_PETHY	P09789 petunia hyb	226	316	13.4	546	2	Q7TY98	Q7ty98 mycobacteri
154	352	14.9	603	1	PG24 MYCTU	Q10637 mycobacteri	227	316	13.4	1036	2	Q6FX21	Q6fx21 candida gla
155	351.5	14.9	895	2	Q6FPM8	Q6fpm8 candida gla	228	315	13.3	302	2	Q9SL09	Q9sl09 arabidopsis
156	351	14.9	316	2	Q6FHY3	Q6fhy3 homo sapien	229	315	13.3	462	2	Q9NHW3	Q9nhw3 nephila cla
157	351	14.9	957	1	PG03 MYCTU	P56877 mycobacteri	230	314.5	13.3	543	1	PG44 MYCTU	Q50630 mycobacteri
158	350.5	14.8	461	2	Q79FC3	Q79fc3 mycobacteri	231	314	13.3	304	2	Q7XJ17	Q7xj17 lycopersico
159	350.5	14.8	476	2	Q7D5W4	Q7d5w4 mycobacteri	232	314	13.3	367	2	Q6PXP6	Q6pxp6 anopheles g
160	350.5	14.8	879	2	Q8VKD2	Q8vkd2 mycobacteri	233	314	13.3	387	2	Q692G3	Q692g3 nephila cla
161	350	14.8	316	1	LORI HUMAN	P23490 homo sapien	234	314	13.3	521	2	Q6V5C3	Q6v5c3 arabidopsis
162	349	14.8	618	2	Q79FK9	Q79fk9 mycobacteri	235	313.5	13.3	3659	2	Q98LN6	Q98lne rhizobium l
163	349	14.8	882	2	Q79FV6	Q79fv6 mycobacteri	236	313	13.2	1449	2	Q910C0	Q910c0 oncorhynch
164	347.5	14.7	464	2	Q7TYB3	Q7tyb3 mycobacteri	237	312.5	13.2	252	1	GRP1 PHAVU	P10495 phaseolus v
165	347.5	14.7	544	2	Q46171	Q46171 nephila cla	238	310.5	13.1	775	2	Q6BGF1	Q6b6p1 debaryomyce
166	346	14.6	648	2	Q9BIU7	Q9biu7 argiope tri	239	310	13.1	321	2	Q69XV3	Q69xv3 oryza sativ
167	346	14.6	974	1	GLH2_CABEL	Q96619 caenorhabdi	240	309.5	13.1	265	2	Q69K59	Q69k59 oryza sativ
168	345	14.6	672	1	PHX5_MOUSE	P08399 mus musculu	241	309.5	13.1	509	2	Q7TYG7	Q7tyg7 mycobacteri
169	345	14.6	966	1	FIB1_PETMA	P02674 petromyzon	242	309	13.1	454	2	Q8VUD7	Q8vud7 mycobacteri
170	344.5	14.6	797	2	Q7UID4	Q7uid4 mycobacteri	243	308.5	13.1	251	2	Q9UVE7	Q9uve7 yarrowia li
171	344	14.6	525	2	Q79FB3	Q79fb3 mycobacteri	244	308.5	13.1	2639	2	Q76786	Q76786 antheraea p
172	344	14.6	651	2	Q9BIU9	Q9biu9 argiope tri	245	308	13.0	271	2	Q08529	Q08529 nicotiana t
173	344	14.6	783	2	Q7D9C6	Q7d9c6 mycobacteri	246	308	13.0	246	1	HORN_MOUSE	Q8vh8 mus musculu
174	344	14.6	783	2	Q79FW8	Q79fw8 mycobacteri	247	307	13.0	526	2	Q6WEQ9	Q6weq9 arabidopsis
175	343	14.5	538	2	Q7U2T0	Q7u2t0 mycobacteri	248	306.5	13.0	419	1	CSP_PLACM	Q8676 mycobacteri
176	342.5	14.5	575	2	Q86P83	Q86p83 drosophila	249	306.5	13.0	904	2	Q76271	Q76271 mytilus edu
177	342.5	14.5	636	2	Q16987	Q16987 araneus dia	250	306	12.9	284	2	Q21073	Q21073 caenorhabdi

251	306	12.9	1034	2	Q6FX23	Q6fx23 candida gla	324	286	12.1	563	2	Q9BIT5	Q9bit5 nephila ina
252	305.5	12.9	267	2	Q6I417	Q6i417 bacillus an	325	286	12.1	1112	2	Q9VEL9	Q9vel9 drosophila
253	305.5	12.9	343	2	Q9FJ63	Q9fj63 aradidopsis	326	285.5	12.1	1370	2	Q6C3B8	Q6c3b8 yarrowia li
254	305.5	12.9	511	2	Q9I332	Q9i332 cercopithe	327	285	12.1	227	2	Q6Z8R3	Q6z8r3 oryza sativ
255	305.5	12.9	902	2	Q16161	Q16161 mytilus edu	328	285	12.1	250	2	Q92P84	Q92p84 rhizobium m
256	305.5	12.9	905	2	Q8MW55	Q8mw55 mytilus gal	329	284	12.0	233	2	Q9DEX9	Q9dex9 cyprinus ca
257	305.5	12.9	922	2	Q8MW53	Q8mw53 mytilus gal	330	284	12.0	296	2	Q6Z495	Q6z495 oryza sativ
258	305	12.9	404	2	Q6C7Y4	Q6c7y4 yarrowia li	331	284	12.0	543	2	Q94FQ0	Q94fq0 aradidopsis
259	303.5	12.8	1884	2	Q7S737	Q7s737 neuropepsa	332	283.5	12.0	379	2	Q692G2	Q692g2 nephila cla
260	302.5	12.8	678	2	Q93486	Q93486 oncorhynch	333	283	12.0	464	2	Q7XDI5	Q7xd5 oryza sativ
261	302	12.8	426	2	Q8Y293	Q8y293 xalstonia s	334	283	12.0	464	2	Q9FWK8	Q9fwk8 oryza sativ
262	302	12.8	592	2	Q9PF60	Q9pf60 xylella fas	335	283	12.0	689	2	Q8BSK0	Q8bsk0 mus musculu
263	301.5	12.8	285	2	Q9STW7	Q9stw7 oryza sativ	336	283	12.0	1051	2	Q26055	Q26055 paracentrot
264	301	12.7	388	2	Q7SXQ3	Q7sxq3 brachydanio	337	283	12.0	1160	2	Q8R564	Q8r564 mus musculu
265	301	12.7	393	1	CSP_PLABR	P14593 plasmodium	338	283	12.0	1160	2	Q9WUN1	Q9wun1 mus musculu
266	301	12.7	1666	2	Q7PTQ3	Q7ptq3 anopheles g	339	283	12.0	1198	2	Q924G8	Q924g8 mus musculu
267	300.5	12.7	622	1	K1CI_HUMAN	P35527 homo sapien	340	283	12.0	1198	2	Q99PM6	Q99pm6 mus musculu
268	300	12.7	738	2	Q024Q2	Q02402 pinctada fu	341	283	12.0	1260	2	Q7TSJ9	Q7tsj9 mus musculu
269	300	12.7	1346	2	Q8U0J3	Q8uuj3 oncorhynch	342	283	12.0	1346	2	Q80IM5	Q80im5 xenopus lae
270	299.5	12.7	490	2	Q6V5D8	Q6v5d8 olimarabido	343	283	12.0	1736	2	Q80TJ5	Q80tj5 mus musculu
271	299.5	12.7	618	2	Q8CI59	Q8ci59 rattus norv	344	283	12.0	1987	2	Q99PB3	Q99pb3 mus musculu
272	299.5	12.7	3198	2	Q26639	Q26639 strongyloce	345	283	12.0	2087	2	Q6DIC6	Q6dic6 mus musculu
273	299	12.7	280	2	Q7XDU0	Q7xd0 oryza sativ	346	282.5	12.0	1447	2	Q9IB91	Q9ib91 xenopus lae
274	299	12.7	373	2	Q9BIT9	Q9bit9 latrodectus	347	282	11.9	338	2	Q6O354	Q6o354 homo sapien
275	298.5	12.6	210	2	Q41187	Q41187 aradidopsis	348	282	11.9	394	2	Q7SHJ4	Q7shj4 neuropepsa
276	298.5	12.6	262	2	Q8MYJ1	Q8myj1 dictyosteli	349	282	11.9	400	1	RTOA_DICDI	P54681 dictyosteli
277	298.5	12.6	284	2	Q94CI8	Q94ci8 lycopersico	350	282	11.9	543	2	Q9LY09	Q9ly09 aradidopsis
278	298.5	12.6	922	2	Q44367	Q44367 mytilus edu	351	281.5	11.9	185	2	Q7XDV1	Q7xdv1 oryza sativ
279	298.5	12.6	2174	2	Q92U08	Q92u08 rhizobium m	352	281.5	11.9	1147	2	Q733C1	Q733c1 bacillus ce
280	298	12.6	214	2	Q6P82	Q6py82 kukulcania	353	281	11.9	827	2	Q7P288	Q7p288 anopheles g
281	298	12.6	2359	2	Q8I519	Q8i519 plasmodium	354	281	11.9	1439	1	APMU_PIG	P12021 sus scrofa
282	297.5	12.6	270	2	Q7XDP4	Q7xd4 oryza sativ	355	281	11.9	476	2	Q974Q6	Q974q6 halictis di
283	296.5	12.5	429	2	Q872Y8	Q872y8 neuropepsa	356	280.5	11.9	1449	2	Q6N890	Q6n890 herpesvirus
284	296.5	12.5	480	2	Q8T215	Q8t215 dictyosteli	357	280.5	11.9	1449	2	Q6N215	Q6n215 brachydanio
285	296.5	12.5	1047	2	Q7UN71	Q7un71 rhodopirell	358	280	11.8	444	2	Q9BIU6	Q9biu6 argiope tri
286	296	12.5	486	2	Q9SPN6	Q9spa6 hordeum vul	359	280	11.8	1380	1	DXK3_MOUSE	P02461 homo sapien
287	296	12.5	627	1	SPD2_NEPCL	P46804 nephila cla	360	280	11.8	1466	1	CAL3_HUMAN	P04082 xenopus tro
288	296	12.5	1124	2	Q6C7C1	Q6c7c1 yarrowia li	361	279.5	11.8	1449	2	Q640B2	Q640b2 xenopus tro
289	296	12.5	1450	2	Q9YIB4	Q9yib4 cynops pyr	362	278.5	11.8	526	1	FUS_HUMAN	P35637 homo sapien
290	295.5	12.5	894	2	Q8MW54	Q8mw54 mytilus gal	363	278.5	11.8	526	2	Q8TER3	Q8tbr3 homo sapien
291	295	12.5	1352	2	Q8UJ34	Q8uj34 oncorhynch	364	278.5	11.8	929	2	Q9NBL3	Q9nb3 drosophila
292	294.5	12.5	614	2	Q87AH4	Q87ah4 xylella fas	365	278.5	11.8	929	2	Q9NBL3	Q9nbw0 drosophila
293	294	12.4	273	2	Q7Y215	Q7y215 aradidopsis	366	278.5	11.8	939	2	Q9NBL3	Q9nhq0 drosophila
294	294	12.4	1356	1	CA21_ONCMY	Q93484 oncorhynch	367	278.5	11.8	939	2	Q9NBL3	Q9nhq0 drosophila
295	293.5	12.4	222	2	Q7XDV2	Q7xdv2 oryza sativ	368	278.5	11.8	978	2	Q6BLF5	Q6blf5 debaryomyce
296	293.5	12.4	586	2	Q9VGH5	Q9vgh5 drosophila	369	278.5	11.8	2280	2	Q9V8E6	Q9v8e6 drosophila
297	293.5	12.4	794	2	Q93560	P33560 sagittaria	370	278.5	11.8	2302	2	Q9N693	Q9n693 drosophila
298	293	12.4	256	2	Q79FH2	Q79fh2 mycobacteri	371	278	11.8	220	2	Q93367	Q93367 brassica ol
299	293	12.4	257	2	Q81275	Q81275 bacillus an	372	278	11.8	270	2	Q61764	Q61764 mus musculu
300	292.5	12.4	707	2	Q61869	Q61869 mus musculu	373	278	11.8	1447	2	Q6P4U1	Q6p4u1 brachydanio
301	292	12.4	912	2	Q9BIT2	Q9bit2 plectreureys	374	277.5	11.7	230	2	Q7XDU2	Q7xd2 oryza sativ
302	291.5	12.3	367	2	Q86KL5	Q86kl5 dictyosteli	375	277.5	11.7	621	2	Q8VJK6	Q8vjk6 mycobacteri
303	291.5	12.3	502	2	Q9ZTR5	Q9ztr5 hordeum vul	376	277.5	11.7	1398	2	Q7PKP4	Q7pkp4 anopheles g
304	291	12.3	821	2	Q8VPM9	Q8vpm9 micrococcus	377	277.5	11.7	1378	2	Q974Q5	Q974q5 halictis di
305	290.5	12.3	406	2	Q82524	Q82524 streptomyce	378	277.5	11.7	1449	2	Q6PEI9	Q6pei9 brachydanio
306	290.5	12.3	1387	1	TROP_HUMAN	Q12816 homo sapien	379	277.5	11.7	1449	2	Q802B5	Q802b5 xenopus lae
307	290	12.3	543	2	Q433Q2	Q433q2 aradidopsis	380	277	11.7	256	2	Q24568	Q24568 zea mays (m
308	290	12.3	751	2	Q7M3U9	Q7m3u9 riftia pach	381	277	11.7	335	2	Q6I899	Q6i899 drosophila
309	289.5	12.3	543	2	Q94FQ4	Q94fq4 aradidopsis	382	277	11.7	1355	1	CA21_RANCA	Q42350 rana catesb
310	289	12.2	1414	2	Q26634	Q26634 strongyloce	383	277	11.7	1447	2	Q6UJ35	Q6ulj5 brachydanio
311	288.5	12.2	499	2	Q6C268	Q6c268 yarrowia li	384	276.5	11.7	682	2	Q22537	Q22537 caenorhabdi
312	288.5	12.2	528	2	Q13344	Q13344 homo sapien	385	276.5	11.7	748	2	Q636W5	Q636w5 bacillus ce
313	288.5	12.2	543	2	Q94FRO	Q94fr0 aradidopsis	386	276.5	11.7	1372	1	CA21_RAT	P02466 rattus norv
314	288	12.2	535	2	Q942Q2	Q942q2 oryza sativ	387	276.5	11.7	2332	2	Q6ALH4	Q6alh4 desulfotale
315	288	12.2	1031	2	Q6MJ51	Q6mj51 bdellovibri	388	276	11.7	1366	2	Q15177	Q15177 homo sapien
316	288	12.2	1962	2	Q873K2	Q873k2 emeritella	389	276	11.7	1366	2	Q15177	Q15177 homo sapien
317	287.5	12.2	185	2	Q6PY83	Q6py83 kukulcania	390	275	11.6	193	2	Q7YWK8	Q7ywk8 caenorhabdi
318	287.5	12.2	2363	2	Q6ALH2	Q6alh2 desulfotale	391	275	11.6	950	2	Q9VK59	Q9vk59 drosophila
319	287	12.1	2795	2	Q70BL5	Q70bl5 paracentrot	392	275	11.6	1156	1	GLH4_CAEEL	Q76743 caenorhabdi
320	287	12.1	13288	2	Q18758	Q18758 sus scrofa	393	274.5	11.6	929	2	Q9NGW5	Q9ngw5 drosophila
321	286.5	12.1	857	2	Q6RH33	Q6rh33 dinocampus	394	274.5	11.6	1376	2	Q7SSH8	Q7ssh8 neuropepsa
322	286	12.1	399	2	Q7ZX33	Q7zx33 xenopus lae	395	274	11.6	460	2	Q6C0R1	Q6c0r1 yarrowia li
323	286	12.1	543	2	Q94FP9	Q94fp9 aradidopsis	396	274	11.6	593	1	K1CJ_HUMAN	P13645 homo sapien

397	274	11.6	730	2	Q9ZU23	O9zu23 arabisopsis	470	263.5	11.2	2147	2	Q98MG8	Q98mg8 rhizobium l
398	274	11.6	889	2	Q7Q5L2	Q7q5l2 anophelies g	471	263	11.1	435	2	Q7Z152	Q7z152 caenorhabdi
399	274	11.6	3016	2	Q7Q5L2	P73590 synchocyst	472	263	11.1	907	2	Q26312	Q26312 strongyloce
400	273	11.6	970	2	Q7Q5V4	Q7q6v4 anophelies g	473	283	11.1	1097	2	Q6C029	Q6c029 yarrowia li
401	273	11.6	1168	2	Q6HF99	O6hf99 bacillus th	474	263	11.1	1752	2	Q07265	Q07265 strongyloce
402	273	11.6	1491	2	Q91718	O91718 xenopus lae	475	262.5	11.1	410	2	Q72UE3	Q72ue3 brachydania
403	273	11.6	1491	2	Q7ZTM4	Q7ztm4 xenopus lae	476	262.5	11.1	645	2	Q79FW4	Q79fw4 mycobacteri
404	272.5	11.5	604	2	Q91252	Q91252 streptomyc	477	262.5	11.1	645	2	Q7ULC5	Q7ulc5 mycobacteri
405	272.5	11.5	1372	1	CA21_MOUSE	Q01149 mus musculu	478	262.5	11.1	646	2	Q7D9B9	Q7d9b9 mycobacteri
406	272.5	11.5	1445	2	Q93251	Q93251 rana catesb	479	262.5	11.1	685	2	Q61G02	Q61g02 rattus norv
407	272.5	11.5	2104	2	Q81KG1	O81kg1 plasmodium	480	262.5	11.1	1049	1	CA13_BOVIN	P04358 bos taurus
408	272.5	11.5	2310	2	Q9AG9	O9ag9a drosophila	481	262.5	11.1	2038	1	FSH_DROME	P13709 drosophila
409	272	11.5	375	1	SANT_PLAFV	P09593 plasmodium	482	262	11.1	245	2	Q6BYG2	Q6byg2 debaryomyce
410	271.5	11.5	370	2	Q79FF0	Q79ff0 mycobacteri	483	262	11.1	1549	2	Q60444	Q60444 cricetus
411	271.5	11.5	370	2	Q7U007	Q7u007 mycobacteri	484	261.5	11.1	815	2	Q632W4	Q632w4 bacillus ce
412	271.5	11.5	375	2	Q7D8E3	Q7d8e3 mycobacteri	485	261.5	11.1	1110	2	Q81RN6	Q81rn6 drosophila
413	271	11.5	681	2	Q8YTC9	O8ytc9 anabaena sp	486	261.5	11.1	2038	2	Q9W3L3	Q9w3l3 drosophila
414	271	11.5	1364	1	CA21_BOVIN	P02465 bos taurus	487	261	11.0	1226	2	Q7UL12	Q7ul12 rhodopirell
415	270.5	11.4	1027	1	Q7TVF1	Q7typ1 mycobacteri	488	260.5	11.0	1321	2	Q72202	Q72202 bacillus ce
416	270.5	11.4	1027	1	CAFF_RIFPA	P30754 rifia pach	489	260	11.0	359	2	Q81G99	Q81g99 drosophila
417	270.5	11.4	1226	2	Q7Q3B9	Q7q3b9 anophelies g	490	260	11.0	722	2	Q76B22	Q76b22 bombyx mori
418	270.5	11.4	1366	1	CA21_HUMAN	P08123 homo sapien	491	260	11.0	730	2	Q26052	Q26052 paracentroc
419	270	11.4	779	2	Q76B23	Q76b23 bombyx mori	492	260	11.0	1366	1	CA21_CANFA	Q46392 canis famli
420	270	11.4	854	2	Q09238	O09238 pseudocorti	493	260	11.0	1486	2	Q91717	Q91717 xenopus lae
421	270	11.4	1035	2	Q76C74	Q76c74 saccharomyc	494	260	11.0	1486	2	Q7ZTI6	Q7zt16 xenopus lae
422	270	11.4	1366	2	Q6N964	O6n964 rhodopsuendo	495	259.5	11.0	261	2	Q92WM2	Q92wm2 cucumis sat
423	270	11.4	1713	2	Q8TGE1	Q8tge1 saccharomyc	496	259.5	11.0	399	2	Q9BIT8	Q9bit8 latrodectus
424	270	11.4	1844	2	Q7SGQ1	Q7sgq1 neurospora	497	259.5	11.0	1186	2	Q76B21	Q76b21 bombyx mori
425	269.5	11.4	360	2	Q9BIU0	O9biu0 latrodectus	498	259.5	11.0	1222	2	CA13_L73	Q8k173 mus musculu
426	269.5	11.4	443	2	Q9GUB4	O9gub4 galleria me	499	259.5	11.0	1464	1	CA13_MOUSE	P08121 mus musculu
427	269	11.4	361	2	Q79FE6	Q79fe6 mycobacteri	500	259.5	11.0	1464	2	Q7TT32	Q7tt32 mus musculu
428	269	11.4	382	2	Q7D777	Q7d777 mycobacteri	501	259.5	11.0	1464	2	Q8BKY2	Q8bky2 mus musculu
429	269	11.4	410	2	Q16988	Q16988 araneus dia	502	259.5	11.0	1464	2	Q8BLW4	Q8blw4 mus musculu
430	269	11.4	422	2	Q803K3	O803k3 brachydania	503	259	11.0	263	2	Q6ZLW9	Q6zlw9 oryza sativ
431	269	11.4	1025	2	Q7WIW0	Q7wiw0 bordetella	504	259	11.0	441	2	Q26062	Q26062 plasmodium
432	268.5	11.4	259	2	Q02049	O02049 caenorhabdi	505	259	11.0	517	2	Q8CFQ9	Q8cfq9 mus musculu
433	268.5	11.4	323	2	Q6BC34	O6bc34 patinopecte	506	259	11.0	684	2	P90679	P90679 arenicola m
434	268.5	11.4	557	2	Q8BQ46	O8bq46 mus musculu	507	259	11.0	886	2	Q9VKR7	Q9vkr7 drosophila
435	268.5	11.4	584	2	Q6C4S0	Q6c4s0 yarrowia li	508	259	11.0	3145	2	Q98MG7	Q98mg7 rhizobium l
436	268	11.3	183	1	GRP2_ORYSA	P29834 oryza sativ	509	258.5	10.9	1309	2	Q812N4	Q812n4 bacillus ce
437	268	11.3	241	2	Q6H1W5	O6hiw5 drosophila	510	258	10.9	138	2	Q964C4	Q964c4 enccephalito
438	268	11.3	647	2	Q6H519	O6hs19 bacillus an	511	258	10.9	208	2	Q92RV2	Q92rv2 cicer ariet
439	268	11.3	870	2	Q6FPN0	O6fpn0 candida gla	512	258	10.9	394	1	THVD_CLAFS	Q9uv14 claviceps f
440	268	11.3	1055	2	Q6HCP4	O6hcf4 bacillus th	513	258	10.9	604	2	Q6BQ06	Q6bq06 debaryomyce
441	267.5	11.3	429	2	Q76966	O76966 podocoryne	514	257.5	10.9	386	1	RB87_DROME	P48810 drosophila
442	267.5	11.3	1207	2	Q9PVF5	O9pvf5 brachydania	515	257.5	10.9	503	2	Q734G5	Q734g5 bacillus ce
443	266.5	11.3	561	2	Q7TPC1	Q7tpc1 mus musculu	516	257.5	10.9	518	1	FUS_MOUSE	P56959 mus musculu
444	266.5	11.3	987	2	Q89CB5	O89cb5 bradyrhizob	517	257.5	10.9	584	2	Q8N175	Q8n175 homo sapien
445	266	11.3	243	2	Q98DS7	O98ds7 rhizobium l	518	257.5	10.9	735	2	Q7Z009	Q7z009 anagasta ku
446	266	11.3	342	2	Q8SX59	O8sx59 drosophila	519	257	10.9	385	2	Q9VFT2	Q9vft2 drosophila
447	266	11.3	586	2	Q8EXJ2	Q8exj2 leptospira	520	257	10.9	433	2	O61152	O61152 plasmodium
448	266	11.3	683	2	Q9PDW2	O9pdw2 xylella fas	521	257	10.9	632	2	Q7TX52	Q7tx52 mycobacteri
449	266	11.3	1088	2	Q69UP6	O69up6 oryza sativ	522	257	10.9	686	2	O8VJ65	O8vj65 mycobacteri
450	265.5	11.2	175	2	Q9LSN6	O9lsn6 arabisopsis	523	257	10.9	998	2	Q8CFM4	Q8cfm4 mus musculu
451	265.5	11.2	265	2	Q69PC6	O69pc6 oryza sativ	524	257	10.9	1160	2	Q14046	Q14046 homo sapien
452	265.5	11.2	461	2	Q6V5F7	O6v5f7 capsella ru	525	257	10.9	1352	2	Q90XJ0	Q90xj0 brachydania
453	265.5	11.2	568	2	Q9NL38	Q9nl38 pinctada ma	526	256.5	10.9	508	2	Q7KHL0	Q7khl0 drosophila
454	265.5	11.2	614	2	Q7TYR8	Q7tyr8 mycobacteri	527	256.5	10.9	809	2	O93485	O93485 oncornynchuo
455	265.5	11.2	615	2	Q7D7A1	Q7d7a1 mycobacteri	528	256.5	10.9	1352	2	O61QX2	O61qx2 brachydania
456	265	11.2	331	2	Q692G6	O692g6 nephila cla	529	256	10.8	429	2	O93119	O93119 antheraea p
457	265	11.2	717	2	Q75FL0	Q75fl0 leptospira	530	256	10.8	429	2	O61150	O61150 plasmodium
458	265	11.2	1119	2	Q75DC8	Q75dc8 ashbya gos	531	256	10.8	436	2	Q967T8	Q967t8 antheraea p
459	264.5	11.2	297	2	Q7XDU7	Q7xdw7 oryza sativ	532	256	10.8	743	2	Q6S6B2	Q6s6b2 vibriophaga
460	264.5	11.2	536	1	FAEB_PIREQ	O9y871 piromyces e	533	256	10.8	1487	2	Q77753	Q77753 canis famli
461	264.5	11.2	1820	2	Q91907	O91907 pagrus maj	534	255.5	10.8	501	2	Q86X94	Q86x94 homo sapien
462	264	11.2	227	2	Q84W21	O84w21 arabisopsis	535	255.5	10.8	592	1	RB56_HUMAN	Q92804 homo sapien
463	264	11.2	741	2	Q6RCF4	O6rcf4 vibriophaga	536	255.5	10.8	1369	2	Q6V5D4	Q6v5d4 olinarabido
464	264	11.2	818	2	Q812Y5	Q812y5 bacillus ce	537	255	10.8	357	2	Q6V5F6	Q6v5f6 capsella ru
465	264	11.2	1163	2	Q8N6U4	Q8n6u4 homo sapien	538	255	10.8	632	2	O9N2N7	O9n2n7 hemiceotrot
466	263.5	11.2	561	2	Q7W7Z1	Q7w7z1 bordetella	539	255	10.8	1052	2	Q7Z284	Q7z284 plasmodium
467	263.5	11.2	763	1	GLH1_CABEL	P34689 caenorhabdi	540	254.5	10.8	413	2	Q8IME3	Q8ime3 drosophila
468	263.5	11.2	1412	2	Q8MUF5	O8muf5 hydra atten	541	254.5	10.8	496	2	Q7KRL6	Q7krl6 drosophila
469	263.5	11.2	1418	2	Q9W7R9	O9w7r9 cynops pyrr	542	254.5	10.8	502	2	Q7KRL7	Q7krl7 drosophila

543	254.5	10.8	700	2	Q8C1P9	Q8cit9 mus musculus	616	247.5	10.5	1419	2	Q80X38	Q80X38 mus musculus
544	254	10.7	1419	2	Q63123	Q63123 rattus norv	617	247.5	10.5	1487	2	Q641K3	Q641K3 mus musculus
545	254	10.7	1487	2	Q14047	Q14047 homo sapien	618	247.5	10.5	1739	2	Q9JLI2	Q9JLI2 mus musculus
546	254	10.7	1745	1	CA35_HUMAN	CA35_HUMAN	619	247.5	10.5	3275	2	Q8VKM3	Q8VKM3 mycobacteri
547	254	10.7	1747	2	Q26640	Q26640 strongyloce	620	247.5	10.5	3300	2	Q6MX44	Q6MX44 mycobacteri
548	253.5	10.7	396	2	Q03136	Q03136 plasmodium	621	247.5	10.5	3507	2	Q7U270	Q7U270 mycobacteri
549	253.5	10.7	401	1	CSP_PLACG	CSP_PLACG	622	247	10.4	425	2	Q61146	Q61146 plasmodium
550	253.5	10.7	509	2	Q875B1	Q875B1 podospora a	623	246.5	10.4	1225	2	Q6PCL3	Q6PCL3 mus musculus
551	253.5	10.7	539	2	Q8MQ99	Q8mq99 caenorhabdi	624	246.5	10.4	1453	1	CA11_MOUSE	CA11_MOUSE
552	253.5	10.7	660	2	Q86D04	Q86D04 caenorhabdi	625	246.5	10.4	1453	1	Q81079	Q81079 mus musculus
553	253.5	10.7	1492	2	Q6P422	Q6P422 xenopus tro	626	246.5	10.4	1453	1	Q89E17	Q89E17 canis fami
554	253	10.7	818	2	Q9N1P0	Q9N1P0 bos taurus	627	246.5	10.4	1460	1	CA11_CANFA	CA11_CANFA
555	253	10.7	1217	2	Q17240	Q17240 bombyx mori	628	246	10.4	1958	2	Q69340	Q69340 suid herpes
556	253	10.7	1418	1	CA12_HUMAN	CA12_HUMAN	629	246	10.4	182	2	Q9CR91	Q9CR91 m mus muscu
557	252.5	10.7	386	2	Q24486	Q24486 homo sapien	630	246	10.4	250	2	Q9V7B7	Q9V7B7 drosophila
558	252.5	10.7	496	2	Q7KA80	Q7KA80 drosophila	631	246	10.4	886	2	Q8CE77	Q8CE77 mus musculus
559	252	10.7	582	2	Q7D5C5	Q7D5C5 mycobacteri	632	245.5	10.4	1262	1	CA13_CHICK	CA13_CHICK
560	252	10.7	582	2	Q7TW98	Q7TW98 mycobacteri	633	245.5	10.4	185	2	Q7XDT5	Q7XDT5 oryza sativ
561	252	10.7	1497	2	Q61431	Q61431 mus musculus	634	245.5	10.4	354	2	Q79FP3	Q79FP3 mycobacteri
562	252	10.7	1583	2	Q6C398	Q6C398 yarrowia li	635	245.5	10.4	636	1	CA13_RAT	CA13_RAT
563	251.5	10.6	343	2	Q01914	Q01914 phytophthor	636	245	10.4	373	2	Q23062	Q23062 caenorhabdi
564	251.5	10.6	490	2	Q9SUW9	Q9SUW9 arabidopsis	637	245	10.4	894	1	ILF3_HUMAN	ILF3_HUMAN
565	251.5	10.6	810	2	Q9ES29	Q9ES29 mus musculus	638	245	10.4	1349	2	Q8AW17	Q8AW17 brachydanio
566	251.5	10.6	860	1	ELS_MOUSE	ELS_MOUSE	639	245	10.4	1694	2	Q80815	Q80815 arabidopsis
567	251.5	10.6	860	2	Q8C9J8	Q8C9J8 mus musculus	640	245	10.4	1759	1	CA14_CAEEL	CA14_CAEEL
568	251.5	10.6	1723	2	Q9GQ81	Q9GQ81 hydra atten	641	244.5	10.3	1804	1	CA1B_MOUSE	CA1B_MOUSE
569	251	10.6	125	2	Q964C1	Q964C1 encephalito	642	244.5	10.3	1453	1	CA11_CHICK	CA11_CHICK
570	251	10.6	232	2	Q7S4R3	Q7S4R3 neurospora	643	244.5	10.3	1461	2	Q76045	Q76045 homo sapien
571	251	10.6	315	2	Q8IGP8	Q8IGP8 drosophila	644	244.5	10.3	1464	1	CA11_HUMAN	CA11_HUMAN
572	251	10.6	425	2	Q61151	Q61151 plasmodium	645	244.5	10.3	1454	2	Q8N473	Q8N473 homo sapien
573	251	10.6	429	1	CSP_PLAMA	CSP_PLAMA	646	243.5	10.3	1737	2	Q9J104	Q9J104 rattus norv
574	251	10.6	429	2	Q61144	Q61144 plasmodium	647	243.5	10.3	413	2	Q89UQ1	Q89UQ1 bradyrhizob
575	251	10.6	429	2	Q61148	Q61148 plasmodium	648	243.5	10.3	418	2	Q7PGN6	Q7PGN6 anopheles g
576	251	10.6	429	2	Q62597	Q62597 plasmodium	649	243.5	10.3	615	2	Q8MS22	Q8MS22 drosophila
577	251	10.6	671	1	CA11_RAT	CA11_RAT	650	243	10.3	1046	1	IF2_STRAW	IF2_STRAW
578	251	10.6	1420	2	Q6FW44	Q6FW44 candida gla	651	243	10.3	237	2	Q7TW10	Q7TW10 mycobacteri
579	251	10.6	1453	2	Q63079	Q63079 rattus norv	652	243	10.3	424	2	Q42626	Q42626 brassica na
580	250.5	10.6	360	2	Q16985	Q16985 araneus dia	653	243	10.3	555	2	Q8SX80	Q8SX80 drosophila
581	250.5	10.6	540	2	Q7N121	Q7N121 gloebacter	654	243	10.3	712	2	Q6HL98	Q6HL98 bacillus th
582	250.5	10.6	585	2	Q8NN98	Q8NN98 corynebacte	655	243	10.3	1069	2	Q6LAN8	Q6LAN8 homo sapien
583	250	10.6	315	2	Q7KRL5	Q7KRL5 drosophila	656	243	10.3	1092	2	Q964R2	Q964R2 theileria t
584	250	10.6	326	2	Q854M0	Q854M0 mycobacteri	657	243	10.3	1160	2	Q7YXC8	Q7YXC8 caenorhabdi
585	250	10.6	603	2	Q8VJ66	Q8VJ66 mycobacteri	658	242.5	10.3	1357	2	Q9W4M4	Q9W4M4 drosophila
586	250	10.6	813	2	Q636W4	Q636W4 bacillus ce	659	242.5	10.3	205	2	Q22432	Q22432 pinus taeda
587	250	10.6	1497	2	Q7TMS0	Q7TMS0 mus musculus	660	242.5	10.3	207	2	Q03797	Q03797 schistosoma
588	250	10.6	1570	2	Q6INP8	Q6INP8 xenopus lae	661	242.5	10.3	243	2	Q67WQ9	Q67WQ9 oryza sativ
589	249.5	10.6	395	2	Q7M3X0	Q7M3X0 plasmodium	662	242.5	10.3	423	2	Q9FW47	Q9FW47 arabidopsis
590	249.5	10.6	589	2	Q7TX53	Q7TX53 mycobacteri	663	242.5	10.3	803	2	Q7XJ36	Q7XJ36 chlamydomon
591	249.5	10.6	940	2	Q00405	Q00405 homo sapien	664	242.5	10.3	940	2	Q96QC0	Q96QC0 homo sapien
592	249.5	10.6	1033	1	IF2_STRCO	IF2_STRCO	665	242.5	10.3	1496	1	CA25_HUMAN	CA25_HUMAN
593	249	10.5	516	2	Q9XEJ0	Q9XEJ0 streptomyce	666	242.5	10.3	1562	2	Q6GQS7	Q6GQS7 mus musculus
594	249	10.5	590	2	Q6MX04	Q6MX04 mycobacteri	667	242.5	10.3	1775	1	CA14_DROME	CA14_DROME
595	249	10.5	773	2	Q95TR3	Q95TR3 drosophila	668	242	10.2	1779	2	Q9VMV4	Q9VMV4 drosophila
596	249	10.5	1215	2	Q9W2K4	Q9W2K4 drosophila	669	242	10.2	193	2	Q7XDR9	Q7XDR9 oryza sativ
597	248.5	10.5	2465	2	Q6CB66	Q6CB66 yarrowia li	670	242	10.2	347	2	Q9GZC7	Q9GZC7 trypanosoma
598	248.5	10.5	507	2	Q8ICB3	Q8ICB3 antheraea m	671	242	10.2	385	2	Q93424	Q93424 caenorhabdi
599	248.5	10.5	710	2	Q8VMD1	Q8VMD1 streptomyce	672	242	10.2	421	2	Q61145	Q61145 plasmodium
600	248.5	10.5	1011	2	Q7VXS7	Q7VXS7 bordetella	673	242	10.2	779	1	CA11_BOVIN	CA11_BOVIN
601	248.5	10.5	1016	2	Q9XTX5	Q9XTX5 caenorhabdi	674	241.5	10.2	1804	2	Q80WR4	Q80WR4 bos taurus
602	248.5	10.5	1442	2	Q62031	Q62031 mus musculus	675	241.5	10.2	185	2	Q7XDT7	Q7XDT7 oryza sativ
603	248.5	10.5	1442	2	Q62033	Q62033 mus musculus	676	241.5	10.2	608	2	Q9SUX1	Q9SUX1 arabidopsis
604	248.5	10.5	1459	1	CA12_MOUSE	CA12_MOUSE	677	241.5	10.2	685	2	Q6CE66	Q6CE66 yarrowia li
605	248.5	10.5	1459	2	Q62032	Q62032 mus musculus	678	241.5	10.2	1258	2	Q8AW11	Q8AW11 brachydanio
606	248	10.5	117	2	Q964C2	Q964C2 encephalito	679	241	10.2	1347	2	Q96QB3	Q96QB3 homo sapien
607	248	10.5	343	2	Q81761	Q81761 arabidopsis	680	241	10.2	342	2	Q9BIU1	Q9BIU1 gasteracant
608	248	10.5	385	1	RO32_XENLA	RO32_XENLA	681	241	10.2	380	2	Q07138	Q07138 microciona
609	248	10.5	425	2	Q61147	Q61147 plasmodium	682	241	10.2	678	2	Q7TXZ3	Q7TXZ3 mycobacteri
610	247.5	10.5	279	2	Q57148	Q57148 human herpe	683	241	10.2	730	2	Q7Q3C5	Q7Q3C5 anopheles g
611	247.5	10.5	347	2	Q01916	Q01916 phytophthor	684	240	10.2	1928	2	Q8T9H1	Q8T9H1 drosophila
612	247.5	10.5	399	1	CAZ_DROME	CAZ_DROME	685	240	10.2	170	2	Q43539	Q43539 lilium long
613	247.5	10.5	481	2	Q97641	Q97641 equus cabal	686	240	10.2	421	2	Q61149	Q61149 plasmodium
614	247.5	10.5	1418	2	Q28396	Q28396 equus cabal	687	240	10.2	512	1	FUS_BOVIN	Q28009 bos taurus
615	247.5	10.5	1419	2	Q80VY3	Q80VY3 mus musculus	688	240	10.2	678	1	FP21_MYCTU	Q10778 mycobacteri
										1015	2	Q7XZU9	Q7XZU9 hordeum vul

689	240	10.2	1348	2	07PXX1	Q7pyx1 anopheles g	762	234	9.9	237	2	Q6DXX9	Q6dxx9 plasmodium
690	239.5	10.1	469	2	Q81KL9	Q81k19 bacillus an	763	234	9.9	301	2	Q01927	Q01927 phytoptchor
691	239.5	10.1	538	2	Q8NOR6	Q8n0r6 turbo marmo	764	234	9.9	309	2	Q8V6M8	Q8v6m8 halovirus h
692	239.5	10.1	663	2	Q8N1Y6	Q8n1y6 streptomyc	765	234	9.9	339	2	Q841H8	Q841h8 solanum tub
693	239.5	10.1	706	2	Q41972	Q41972 murid herpe	766	234	9.9	1626	2	Q8NFW1	Q8ntw1 homo sapien
694	239.5	10.1	727	2	Q41973	Q41973 murid herpe	767	234	9.9	1655	2	Q24754	Q24754 drosophila
695	239.5	10.1	774	2	Q41971	Q41971 murid herpe	768	233.5	9.9	165	1	GRP1_ORYSA	P25074 oryza sativ
696	239.5	10.1	812	2	Q06452	Q06452 ephydatia m	769	233.5	9.9	171	2	Q04139	P04039 aradidopsis
697	239.5	10.1	1669	1	CA14_MOUSE	P02463 mus musculu	770	233.5	9.9	180	2	P91207	P91207 caenorhabdi
698	239	10.1	584	2	Q62EE4	Q62ee4 burkholderi	771	233.5	9.9	811	2	Q9AD50	Q9ad50 streptomyc
699	239	10.1	826	2	Q8KN06	Q8kn06 mus musculu	772	233.5	9.9	966	2	Q01385	Q01385 neurospora
700	239	10.1	1041	2	Q66S51	Q66s51 oikopleura	773	233.5	9.9	1617	2	Q6MGB2	Q6mgb2 rattus norv
701	239	10.1	2165	2	Q8NPD5	Q8nfd5 homo sapien	774	233.5	9.9	2936	2	Q7YRK8	Q7yrk8 canis famil
702	238.5	10.1	121	2	Q964C5	Q964c5 encephalito	775	233	9.9	237	2	Q6DXZ7	Q6dxz7 plasmodium
703	238.5	10.1	212	1	EGG1_SCHJA	P19470 schistosoma	776	233	9.9	296	2	Q8RUS0	Q8rus0 aradidopsis
704	238.5	10.1	267	2	Q9B088	P94088 mycobacteri	777	233	9.9	373	1	R031_XENLA	P51968 xenopus lae
705	238.5	10.1	387	2	Q7M3W8	Q7m3w8 plasmodium	778	233	9.9	536	2	Q6DKB4	Q6dkb4 xenopus lae
706	238.5	10.1	387	2	Q7M3W9	Q7m3w9 plasmodium	779	233	9.9	658	2	Q6FRG1	Q6frg1 candida gla
707	238.5	10.1	450	1	SWP1_ENCCU	Q9xv1 encephalito	780	233	9.9	783	2	Q9XAI1	Q9xai1 streptomyc
708	238.5	10.1	615	2	Q9VYL7	Q9vy17 drosophila	781	233	9.9	864	1	ELS_RAT	Q93172 rattus norv
709	238.5	10.1	689	2	Q75EH4	Q75eh4 ashbya goss	782	232.5	9.8	253	2	Q7ADR2	Q7xdr2 oryza sativ
710	238.5	10.1	1420	2	Q90W37	Q90w37 gallus gall	783	232.5	9.8	290	2	Q21294	Q21294 caenorhabdi
711	238	10.1	963	2	Q9UVL2	Q9uvl2 neurospora	784	232.5	9.8	342	1	CUS36_MANSE	Q6frg1 candida gla
712	238	10.1	1011	2	Q6CF27	Q6cf27 yarrowia li	785	232.5	9.8	388	2	Q9VR77	Q9vrf7 drosophila
713	238	10.1	1736	1	CA2B_HUMAN	P13942 homo sapien	786	232.5	9.8	652	2	Q86NR7	Q86nr7 drosophila
714	238	10.1	1806	1	CA1B_HUMAN	P12107 homo sapien	787	232.5	9.8	2109	2	P79787	P79787 gallus gall
715	238	10.1	1991	2	Q7RTD0	Q7rtd0 plasmodium	788	232	9.8	329	2	Q9BEY0	Q9bey0 cyprinus ca
716	238	10.1	2037	2	Q9PVZ2	Q9pvz2 xenopus lae	789	232	9.8	460	1	CYS7_DICDI	Q94504 dictyostell
717	237.5	10.1	185	2	Q7XDT6	Q7xdt6 oryza sativ	790	232	9.8	793	2	Q97640	Q97640 felis silve
718	237.5	10.1	247	2	Q6DX38	Q6dx38 plasmodium	791	232	9.8	467	2	Q9GV13	Q9gv13 hydra magni
719	237.5	10.1	349	2	Q9BIV0	Q9biv0 argiope aur	792	232	9.8	913	2	Q6C979	Q6c979 yarrowia li
720	237.5	10.1	495	2	Q718P0	Q718p0 ovine herpe	793	231.5	9.8	239	2	Q9BMN2	Q9bmn2 plasmodium
721	237.5	10.1	940	2	Q7YR38	Q7yr38 pan troglod	794	231.5	9.8	244	2	Q9LTF08	Q9lyt08 aradidopsis
722	237.5	10.1	1362	1	CA21_CHICK	P02467 gallus gall	795	231.5	9.8	487	2	Q9ZB39	Q9zb39 ureaplasma
723	237.5	10.1	1831	2	Q7Q1Y4	Q7q1y4 anopheles g	796	231.5	9.8	544	2	Q6BU19	Q6bul19 debaryomyce
724	237.5	10.1	2944	2	Q6RNR1	Q6rnr1 mus musculu	797	231.5	9.8	925	2	Q767K9	Q767k9 sus scrofa
725	237	10.0	309	2	Q8FNR1	Q8fnr1 aradidopsis	798	231.5	9.8	1475	2	Q9XEP3	Q9xep3 sorghum bic
726	237	10.0	365	2	Q61P29	Q6ip29 xenopus lae	799	231	9.8	185	2	Q948R3	Q948r3 oryza sativ
727	237	10.0	490	2	Q9V948	Q9v948 drosophila	800	231	9.8	221	2	Q6S514	Q6s514 aradidopsis
728	237	10.0	535	2	Q7WLD1	Q7wld1 bordetella	801	231	9.8	237	2	Q6DXZ8	Q6dxz8 plasmodium
729	237	10.0	642	2	Q6G364	Q6g364 bartonella	802	231	9.8	237	2	Q6DXZ9	Q6dxz9 plasmodium
730	237	10.0	854	2	Q8IVT9	Q8ivt9 homo sapien	803	231	9.8	237	2	Q6DY01	Q6dy01 plasmodium
731	237	10.0	1024	2	Q6FLA5	Q6fla5 candida gla	804	231	9.8	237	2	Q7XLA1	Q7xla1 oryza sativ
732	237	10.0	3409	2	Q6SSE6	Q6sse6 chlamydomon	805	231	9.8	350	2	Q8C2H8	Q8c2h8 mus musculu
733	236.5	10.0	247	2	Q6DX44	Q6dy44 plasmodium	806	231	9.8	373	2	Q9P639	Q9p639 neurospora
734	236.5	10.0	717	2	Q6MI66	Q6mi66 bdellovibri	807	231	9.8	413	2	Q7D7A7	Q7d7a7 mycobacteri
735	236.5	10.0	747	1	CA12_BOVIN	P02459 bos taurus	808	231	9.8	413	2	Q77YS4	Q7ty94 mycobacteri
736	236.5	10.0	961	2	Q7RW88	Q7rw88 neurospora	809	231	9.8	422	2	Q94KD0	Q94kd0 aradidopsis
737	236.5	10.0	977	2	Q8X005	Q8x005 neurospora	810	231	9.8	501	2	Q6GLD1	Q6glld1 xenopus tro
738	236.5	10.0	1733	1	VNUA_PRVKA	P33485 pseudotrabie	811	231	9.8	536	2	Q7ZXQ2	Q7zxq2 xenopus lae
739	236.5	10.0	1736	1	CA2B_MOUSE	Q64739 mus musculu	812	231	9.8	898	2	Q8K588	Q8k588 mus musculu
740	236	10.0	504	2	Q6FL65	Q6fl65 candida gla	813	231	9.8	911	2	Q812A1	Q812a1 mus musculu
741	236	10.0	518	2	Q8MQ08	Q8mq08 caenorhabdi	814	231	9.8	1758	1	CA24_CABEL	P17140 caenorhabdi
742	236	10.0	524	2	Q02123	Q02123 caenorhabdi	815	230.5	9.8	284	2	Q6BEEZ3	Q6eez3 euprosthen
743	236	10.0	888	2	Q90796	Q90796 gallus gall	816	230.5	9.8	485	2	Q9UV68	Q9uv68 neocallimas
744	236	10.0	1827	2	Q8U0M5	Q8uums oryzae lac	817	230.5	9.8	643	2	Q87E00	Q87e00 xylella fas
745	235.5	10.0	228	2	Q6DY00	Q6dy00 plasmodium	818	230.5	9.8	859	2	Q8IRV3	Q8irv3 drosophila
746	235.5	10.0	643	1	K2C1_HUMAN	P04264 homo sapien	819	230.5	9.8	887	2	Q944V1	Q944v1 alcelaphine
747	235.5	10.0	682	2	Q9VRM2	Q9vrm2 drosophila	820	230.5	9.8	1300	2	Q36421	Q36421 alcelaphine
748	235.5	10.0	1714	2	Q7Z515	Q7z515 homo sapien	821	230.5	9.8	2096	2	Q7TWN7	Q7twn7 mycobacteri
749	235	9.9	448	2	Q18265	Q18265 caenorhabdi	822	230.5	9.8	3157	2	Q6MXX9	Q6mxx9 mycobacteri
750	235	9.9	568	2	Q6E1Z0	Q6eiz0 canis famil	823	230	9.7	115	1	SEB1_GALME	Q96614 gallieria me
751	235	9.9	839	2	Q9RX57	Q9rx57 deinococcus	824	230	9.7	1023	2	Q7Q3C0	Q7q3c0 anopheles g
752	235	9.9	891	2	Q8OVX8	Q8ovx8 mus musculu	825	230	9.7	1778	1	N189_SCHPO	Q9uk4 schizosacch
753	235	9.9	1269	2	Q7T227	Q7t227 gallus gall	826	229.5	9.7	160	2	Q94669	Q94669 plasmodium
754	234.5	9.9	207	1	EGG2_SCHJA	P19469 schistosoma	827	229.5	9.7	167	2	Q7QIN7	Q7qin7 anopheles g
755	234.5	9.9	419	2	Q42638	Q42638 brassica ol	828	229.5	9.7	175	2	Q7XDT1	Q7xdt1 oryza sativ
756	234.5	9.9	438	2	Q7M3U7	Q7m3u7 parvalinell	829	229.5	9.7	294	2	Q16986	Q16986 araneus dia
757	234.5	9.9	455	2	Q28495	Q28495 macaca mula	830	229.5	9.7	398	2	Q7QIA7	Q7qia7 anopheles g
758	234.5	9.9	2109	1	PGCA_CHICK	P07898 gallus gall	831	229.5	9.7	539	2	Q7TWN9	Q7twn9 mycobacteri
759	234.5	9.9	2585	2	Q23587	Q23587 caenorhabdi	832	229.5	9.7	569	1	K1CJ_MOUSE	P02535 mus musculu
760	234.5	9.9	2944	1	CA17_HUMAN	Q02388 homo sapien	833	229.5	9.7	585	2	Q7QB99	Q7qby9 anopheles g
761	234	9.9	237	2	Q26166	Q26166 plasmodium	834	229.5	9.7	708	2	Q7ZWN8	Q7zwn8 xenopus lae

835	229.5	9.7	740	2	Q73J82	Q73j82 treponema d	908	225	9.5	767	2	Q7PM40	Q7pm40 anopheles g
836	229.5	9.7	824	2	Q81B45	Q81b45 bacillus ce	909	225	9.5	1796	1	ICEV_PSESX	Q33479 pseudomonas
837	229.5	9.7	853	2	Q8VQZ0	Q8vqz0 myxococcus	910	225	9.5	1746	2	Q7PVR9	Q7pvr9 anopheles g
838	229.5	9.7	857	2	Q85783	Q85783 myxococcus	911	224.5	9.5	174	2	Q9LTP5	Q9ltp5 arabidopsis
839	229	9.7	162	2	Q9M0B4	Q9m0b4 arabidopsis	912	224.5	9.5	235	2	Q9LI22	Q9liz2 oryza sativ
840	229	9.7	192	2	Q7XDT3	Q7xdt3 oryza sativ	913	224.5	9.5	442	2	Q7PUR2	Q7puk2 anopheles g
841	229	9.7	391	2	Q85216	Q85216 triticum ae	914	224.5	9.5	561	2	Q8BVU3	Q8bv3 mus musculus
842	229	9.7	570	2	Q8RSI6	Q8rsi6 uncultured	915	224.5	9.5	775	2	Q8BVU3	Q8f342 streptomyce
843	228.5	9.7	197	2	Q8ATP3	Q8atp3 pennisetum	916	224.5	9.5	801	2	Q8T5G4	Q8t5g4 anopheles g
844	228.5	9.7	228	2	Q6DXY0	Q6dxy0 plasmodium	917	224.5	9.5	830	2	Q7PVR8	Q7pvr8 anopheles g
845	228.5	9.7	429	1	D848_YEAST	P18899 saccharomyc	918	224.5	9.5	910	1	ILF3_RAT	Q9jil3 rattus norv
846	228.5	9.7	560	2	Q50275	Q50275 mycoplasma	919	224	9.5	167	2	Q63115	Q63115 rattus norv
847	228.5	9.7	561	2	Q44664	Q44664 homo sapien	920	224	9.5	387	2	Q6S7B1	Q6s7b1 arabidopsis
848	228.5	9.7	800	2	Q6NU13	Q6nu13 xenopus lae	921	224	9.5	404	2	O22791	O22791 arabidopsis
849	228.5	9.7	2523	2	Q8TJS8	Q8tjs8 methanosarc	922	224	9.5	447	2	O9YTJ3	O9ytj3 ateline her
850	228.5	9.7	5146	2	Q9VXR3	Q9vrx3 drosophila	923	224	9.5	544	2	O8I6C4	O8i6c4 drosophila
851	228	9.6	189	2	Q7XDS0	Q7xdso oryza sativ	924	224	9.5	625	2	O6IMEF3	O6imf3 rattus norv
852	228	9.6	196	2	O22638	O22638 zea mays (m	925	224	9.5	681	2	Q6AZQ8	Q6azq8 xenopus lae
853	228	9.6	238	2	Q7TQ07	Q7tq07 plasmodium	926	224	9.5	1115	2	O6PFB1	O6pfb1 mus musculus
854	228	9.6	690	2	Q73T97	Q73t97 mycobacteri	927	224	9.5	1497	1	CA1G_HUMAN	Q9umd9 homo sapien
855	228	9.6	738	2	Q82YD4	Q82yd4 streptomyce	928	224	9.5	1691	2	Q9ESQ1	Q9esq1 mus musculus
856	228	9.6	738	2	Q90779	Q90779 gallus gall	929	224	9.5	2310	2	Q9W2U7	Q9w2u7 drosophila
857	228	9.6	1684	2	Q8JNB6	Q8jnb6 white spot	930	223.5	9.5	339	2	O6CA18	Q6cal8 yarrowia li
858	228	9.6	1684	2	Q8VAAL	Q8vaal white spot	931	223.5	9.5	572	2	F71187	F71187 enterobacte
859	228	9.6	1684	2	Q9ILK9	Q9ilk9 white spot	932	223.5	9.5	572	2	Q936Y6	Q936y6 pseudomonas
860	227.5	9.6	116	2	Q9NI04	Q9ni04 plasmodium	933	223.5	9.5	572	2	O6UP53	O6up53 alcaligenes
861	227.5	9.6	228	2	Q6TQ08	Q6tq08 plasmodium	934	223.5	9.5	572	2	O76M30	O76m30 comamonas a
862	227.5	9.6	237	2	O6DY02	O6dy02 plasmodium	935	223.5	9.5	572	2	Q7X3E2	O7x3e2 uncultured
863	227.5	9.6	277	2	Q7PMP8	Q7pmp8 anopheles g	936	223.5	9.5	631	2	Q9N1P1	Q9nlp1 bos taurus
864	227.5	9.6	372	2	Q7Z008	Q7z008 anagata ku	937	223.5	9.5	659	2	Q8MT98	Q8mt98 drosophila
865	227.5	9.6	431	2	Q7QCQ9	Q7qcq9 anopheles g	938	223.5	9.5	824	2	Q69YU0	Q69yt0 homo sapien
866	227.5	9.6	726	2	Q81ZX1	Q81zx1 streptomyce	939	223.5	9.5	974	2	O9YVL3	O9yvl3 neurospora
867	227.5	9.6	1130	2	Q6CIH1	Q6cih1 kluyveromyc	940	223.5	9.5	978	2	P91777	P91777 pacifastacu
868	227.5	9.6	1297	2	O6VBI9	O6vbi9 candida gla	941	223.5	9.5	1075	2	O86X41	O86x41 homo sapien
869	227.5	9.6	1997	2	Q7RXD0	Q7rxd0 neurospora	942	223.5	9.5	1427	2	O8GIZ2	O8giz2 mycoplasma
870	227	9.6	236	2	Q44FQ5	Q44fq5 arabidopsis	943	223.5	9.5	1855	2	Q80ZF0	Q80zf0 rattus norv
871	227	9.6	371	2	O45114	O45114 caenorhabdi	944	223	9.4	192	2	Q92WM7	Q92wm7 zea mays (m
872	227	9.6	536	2	Q8I6B9	Q8i6b9 drosophila	945	223	9.4	441	2	O6G4M7	O6g4m7 bartonella
873	227	9.6	544	2	Q8I6C5	Q8i6c5 drosophila	946	223	9.4	544	2	O8I6C3	O8i6c3 drosophila
874	227	9.6	645	2	Q63P58	Q63p58 burkholderi	947	223	9.4	911	1	ILF3_MOUSE	Q9z1x4 mus musculus
875	227	9.6	703	1	CA28_HUMAN	P35067 homo sapien	948	223	9.4	1001	2	Q05164	Q05164 saccharomyc
876	227	9.6	1148	1	ICEK_PSESX	Q30611 pseudomonas	949	223	9.4	1200	1	ICEN_PSESX	P06620 pseudomonas
877	227	9.6	1210	1	ICEN_PSEBFL	P09815 pseudomonas	950	222.5	9.4	228	2	Q6TOR2	Q6tor2 plasmodium
878	227	9.6	1622	2	Q7GF99	Q7gf99 vibrio para	951	222.5	9.4	655	2	O8IRV2	O8irv2 drosophila
879	226.5	9.6	228	2	Q6DY45	Q6dy45 plasmodium	952	222.5	9.4	739	-2	O70575	O70575 mus musculus
880	226.5	9.6	252	2	Q7VEJ9	Q7vej9 prochloroco	953	222.5	9.4	1063	2	O9CH86	O9ch86 lactococcus
881	226.5	9.6	469	1	CS66_WHEAT	P46526 triticum ae	954	222.5	9.4	1280	2	Q9UGY9	Q9ugy9 homo sapien
882	226.5	9.6	637	2	Q9D2R8	Q9d2k8 mus musculus	955	222.5	9.4	1761	2	O18407	O18407 drosophila
883	226.5	9.6	641	2	Q17740	Q17740 caenorhabdi	956	222.5	9.4	2523	2	O6MWY2	O6mw2 mycobacteri
884	226.5	9.6	1022	1	CA26_CHICK	P15988 gallus gall	957	222	9.4	363	2	O9FGH5	O9fgh5 arabidopsis
885	226.5	9.6	1709	2	Q86L43	Q86l43 dictyosteli	958	222	9.4	365	1	ROAL_XENLA	P17130 xenopus lae
886	226	9.6	189	2	Q7XDS8	Q7xd8 oryza sativ	959	222	9.4	504	2	O7QDT6	O7qdt6 anopheles g
887	226	9.6	199	2	Q94476	Q94476 dictyosteli	960	222	9.4	544	2	Q8I081	Q8i081 drosophila
888	226	9.6	251	2	Q85386	Q85386 mycobacteri	961	222	9.4	552	2	Q6MMW0	Q6mmw0 mycobacteri
889	226	9.6	544	2	Q8I072	Q8i072 drosophila	962	222	9.4	552	2	Q7TW76	Q7tw76 mycobacteri
890	226	9.6	544	2	Q8I6C7	Q8i6c7 drosophila	963	222	9.4	623	2	Q8VIY0	Q8viy0 mycobacteri
891	226	9.6	834	2	Q8W056	Q8w056 oryza sativ	964	222	9.4	676	2	O6DE50	O6de50 xenopus lae
892	226	9.6	1600	2	Q9UEH6	Q9ueh6 homo sapien	965	222	9.4	946	2	O857Y4	O857y4 mycobacteri
893	226	9.6	1621	2	Q9H4R9	Q9h4r9 homo sapien	966	222	9.4	1519	2	O7Z3C4	O7z3c4 homo sapien
894	226	9.6	1669	1	CA14_HUMAN	P02462 homo sapien	967	221.5	9.4	100	2	O964C3	O964c3 encephalito
895	226	9.6	1691	1	CA64_HUMAN	Q14031 homo sapien	968	221.5	9.4	173	2	Q41191	Q41191 arabidopsis
896	226	9.6	2189	2	Q9BI05	Q9bi05 eimeria ten	969	221.5	9.4	193	2	Q9VNM4	Q9vnm4 drosophila
897	225.5	9.5	265	2	Q6DDA7	Q6dda7 xenopus tro	970	221.5	9.4	228	2	O6T0R0	O6t0r0 plasmodium
898	225.5	9.5	751	2	Q9RLN9	Q9rln9 mus musculus	971	221.5	9.4	228	2	O6T0R5	O6t0r5 plasmodium
899	225.5	9.5	770	2	Q6BIY3	Q6biy3 debaryomyce	972	221.5	9.4	349	2	O6C605	O6c605 yarrowia li
900	225.5	9.5	809	2	O76869	O76869 drosophila	973	221.5	9.4	503	2	Q9HEH4	Q9neh4 neurospora
901	225.5	9.5	1113	1	N116_YEAST	Q02630 saccharomyc	974	221	9.4	273	2	O65X75	O65x75 oryza sativ
902	225.5	9.5	1338	2	Q7TWFO	Q7twp0 mycobacteri	975	221	9.4	310	2	Q90612	Q90612 gallus gall
903	225.5	9.5	1474	2	O86G87	O86g87 pseudoplusi	976	221	9.4	544	2	O8I6C0	O8i6c0 drosophila
904	225	9.5	325	2	Q8I6C1	Q8i6c1 drosophila	977	221	9.4	544	2	O8I6C1	O8i6c1 drosophila
905	225	9.5	544	2	Q8I6C8	Q8i6c8 drosophila	978	221	9.4	544	2	O8I6C6	O8i6c6 drosophila
906	225	9.5	572	2	Q63IU2	Q63iu2 burkholderi	979	221	9.4	561	2	O9CXH6	O9cxh6 mus musculus
907	225	9.5	624	2	Q8N1V1	Q8n1v1 neurospora	980	221	9.4	575	2	Q9SB17	Q9sb17 hordeum vul

981	221	9.4	594	2	Q67Q95	Q67g95 symbiobacte	1054	217	9.2	718	2	Q91TR1	Q91tr1 tupalid her
982	221	9.4	758	2	Q6TSC0	Q6tec0 crasostrea	1055	217	9.2	1045	2	Q801S8	Q801s8 xenopus lae
983	220.5	9.3	141	2	Q9BJP8	Q9bjp8 plasmodium	1056	216.5	9.2	212	2	Q949P9	Q949p9 oryza sativ
984	220.5	9.3	316	2	Q19111	Q19111 caenorhabdi	1057	216.5	9.2	244	2	Q6V5C2	Q6v5c2 aradidopsis
985	220.5	9.3	618	2	Q79F80	Q79f80 mycobacteri	1058	216.5	9.2	290	2	Q26054	Q26054 paracentrot
986	220.5	9.3	618	2	Q7U0K5	Q7u0k5 mycobacteri	1059	216.5	9.2	419	2	Q6FT22	Q6ft22 candida gla
987	220.5	9.3	636	2	Q8VK65	Q8vk65 mycobacteri	1060	216.5	9.2	674	1	CA1A BOVIN	P23206 bos taurus
988	220.5	9.3	645	1	K22E HUMAN	P35908 homo sapien	1061	216.5	9.2	837	2	Q81B46	Q81b46 bacillus ce
989	220	9.3	192	2	Q7XDS2	Q7xds2 oryza sativ	1062	216.5	9.2	1019	1	CA26 HUMAN	P12110 homo sapien
990	220	9.3	302	2	Q8MML4	Q8mml4 dictyosteli	1063	216.5	9.2	1019	2	Q6PUQ1	Q6puq1 homo sapien
991	220	9.3	332	2	Q6C127	Q6c127 yarrowia li	1064	216.5	9.2	2090	1	N214 HUMAN	P35658 homo sapien
992	220	9.3	413	2	Q9HEJ0	Q9hej0 neurospora	1065	216.5	9.2	2091	2	Q75R47	Q75r47 homo sapien
993	220	9.3	568	2	Q8CD80	Q8cd80 mus musculu	1066	216	9.1	191	2	Q7XDR5	Q7xdr5 oryza sativ
994	220	9.3	572	2	Q9AUG8	Q9aug8 comamonas t	1067	216	9.1	405	2	Q6WMT4	Q6wmt4 bdellovibri
995	220	9.3	595	2	Q7XJ24	Q7xj24 oryza sativ	1068	216	9.1	409	2	Q19414	Q19414 caenorhabdi
996	220	9.3	954	2	Q8WXV8	Q8wxv8 homo sapien	1069	216	9.1	569	2	Q6CH78	Q6ch78 yarrowia li
997	220	9.3	954	2	Q96P44	Q96p44 homo sapien	1070	216	9.1	1838	1	CA15 HUMAN	P20308 homo sapien
998	220	9.3	957	2	Q9H0V3	Q9h0v3 homo sapien	1071	216	9.1	1838	2	Q88207	Q88207 mus musculu
999	220	9.3	1206	2	Q869X8	Q869x8 dictyosteli	1072	216	9.1	2090	2	Q9W2T1	Q9w2t1 drosophila
1000	220	9.3	1333	2	Q8PD38	Q8pd38 xanthomonas	1073	216	9.1	2093	2	Q15010	Q15010 homo sapien
1001	220	9.3	1740	2	Q9HCU0	Q9hcj0 homo sapien	1074	215.5	9.1	102	2	Q964C0	Q964c0 enccephalito
1002	219.5	9.3	207	2	Q43522	Q43522 lycopersico	1075	215.5	9.1	424	2	Q6H9M8	Q6h9m8 erwinia pyr
1003	219.5	9.3	214	2	Q6H3Y0	Q6h3y0 oryza sativ	1076	215.5	9.1	520	1	MRCO HUMAN	Q9uew3 homo sapien
1004	219.5	9.3	262	2	Q6CBL5	Q6cbl5 yarrowia li	1077	215.5	9.1	1034	2	Q8K229	Q8k229 mus musculu
1005	219.5	9.3	311	2	Q8V6M2	Q8vem2 halovirus h	1078	215.5	9.1	2132	1	PGCA MOUSE	Q61282 mus musculu
1006	219.5	9.3	539	2	Q81097	Q8i097 drosophila	1079	215	9.1	200	1	GRP HORVU	P17816 hordeum vul
1007	219.5	9.3	684	1	CA39 HUMAN	Q14050 homo sapien	1080	215	9.1	232	2	Q94FR1	Q94fr1 aradidopsis
1008	219.5	9.3	1191	2	Q6PCK7	Q6pck7 xenopus lae	1081	215	9.1	250	2	Q9VX64	Q9vx64 drosophila
1009	219	9.3	191	2	Q7XDR3	Q7xdr3 oryza sativ	1082	215	9.1	340	2	Q6WEQ0	Q6weq0 boechea dr
1010	219	9.3	193	2	Q70592	Q70592 rattus norv	1083	215	9.1	448	2	Q7XDS3	Q7xds3 oryza sativ
1011	219	9.3	294	2	Q6MGT3	Q6mgt3 bdellovibri	1084	215	9.1	479	2	O06292	Q06292 mycobacteri
1012	219	9.3	342	2	Q9LH90	Q9lh90 aradidopsis	1085	215	9.1	479	2	Q7U280	Q7u280 mycobacteri
1013	219	9.3	345	2	Q7TDH1	Q7tdh1 halovirus h	1086	215	9.1	541	2	Q9NA97	Q9na97 aradidopsis
1014	219	9.3	368	2	Q8MPJ9	Q8mpj9 plasmodium	1087	215	9.1	566	2	Q91VL4	Q91vl4 mus musculu
1015	219	9.3	379	1	ROA3 MOUSE	Q8bg05 mus musculu	1088	215	9.1	575	2	Q9SPA7	Q9spa7 hordeum vul
1016	219	9.3	379	1	ROA3 RAT	Q6urk4 rattus norv	1089	215	9.1	594	2	Q7WKH2	Q7wkh2 bordetella
1017	219	9.3	413	2	Q64939	Q64939 lophopyrum	1090	215	9.1	635	2	Q6UD62	Q6ud62 uncultured
1018	219	9.3	473	2	Q84WQ1	Q84wq1 aradidopsis	1091	215	9.1	669	2	Q7UE67	Q7ue67 rhodopirell
1019	219	9.3	544	2	Q816B7	Q816b7 drosophila	1092	215	9.1	1029	1	CA26 MOUSE	Q02788 mus musculu
1020	219	9.3	544	2	Q816B8	Q816b8 drosophila	1093	215	9.1	1319	1	MNI HUMAN	Q10571 homo sapien
1021	219	9.3	544	2	Q816C2	Q816c2 drosophila	1094	215	9.1	1405	2	Q8KMK1	Q8kmk1 mycoplasma
1022	219	9.3	716	2	Q825D6	Q825d6 streptomyc	1095	215	9.1	1567	1	ICEN XANCT	P18127 xanthomonas
1023	219	9.3	734	2	Q61VJ4	Q61vj4 clona intes	1096	215	9.1	1690	1	CA44 HUMAN	P53420 homo sapien
1024	219	9.3	775	2	Q82CQ3	Q82cq3 streptomyc	1097	215	9.1	1838	2	Q15094	Q15094 homo sapien
1025	219	9.3	1053	2	Q920S4	Q920s4 mus musculu	1098	215	9.1	3848	2	P94772	P94772 erwinia chr
1026	219	9.3	1212	2	Q80U93	Q80u93 mus musculu	1099	214.5	9.1	191	2	Q7XDR8	Q7xdr8 oryza sativ
1027	219	9.3	2303	2	Q7QCA2	Q7qca2 anopheles g	1100	214.5	9.1	241	2	Q6V5D7	Q6v5d7 ollimarabido
1028	218.5	9.2	297	2	Q8HEH5	Q8heh5 dictyosteli	1101	214.5	9.1	373	2	Q9U2I7	Q9u2i7 caenorhabdi
1029	218.5	9.2	370	2	Q95TX4	Q95tx4 drosophila	1102	214.5	9.1	465	2	Q9RXC3	Q9rcx3 deinococcus
1030	218.5	9.2	378	1	ROA3 HUMAN	P51291 homo sapien	1103	214.5	9.1	558	2	Q6BI51	Q6bi51 debaryomyc
1031	218.5	9.2	497	2	Q7KS36	Q7ks36 drosophila	1104	214.5	9.1	589	2	Q91LJ6	Q91lj6 mus musculu
1032	218.5	9.2	589	2	Q66043	Q66043 cercopithe	1105	214.5	9.1	678	2	Q6P467	Q6p467 homo sapien
1033	218.5	9.2	612	2	Q7X678	Q7x678 chlamydomon	1106	214.5	9.1	778	2	Q86BH1	Q86bh1 drosophila
1034	218.5	9.2	705	2	Q04310	Q04310 aradidopsis	1107	214.5	9.1	792	2	Q8MT89	Q8mt89 drosophila
1035	218.5	9.2	1218	2	Q6VBJ4	Q6vbj4 candida gla	1108	214.5	9.1	970	2	Q8VBY1	Q8vby1 rattus norv
1036	218.5	9.2	1416	2	Q6VBD3	Q6vbj3 candida gla	1109	214.5	9.1	1018	2	Q9WU6	Q9wu6 pseudomonas
1037	218.5	9.2	1535	2	Q62D27	Q62d27 burkholderi	1110	214	9.1	301	2	Q8WSZ3	Q8wsz3 nephila cla
1038	218.5	9.2	1580	2	Q8BLX7	Q8blx7 mus musculu	1111	214	9.1	399	2	Q9W927	Q9w927 rhizobium l
1039	218.5	9.2	1940	2	Q9VMV5	Q9vmv5 drosophila	1112	214	9.1	594	2	Q9W927	P04104 mus musculu
1040	218	9.2	284	2	Q9BLS8	Q9bls8 tetragantha	1113	214	9.1	627	1	K2C1 MOUSE	Q641c4 mus musculu
1041	218	9.2	481	2	Q8VKM5	Q8vkm5 mycobacteri	1114	214	9.1	699	2	Q6PLC4	Q28083 bos taurus
1042	218	9.2	763	2	Q7Q1W5	Q7qlw5 anopheles g	1115	214	9.1	911	1	CA18 BOVIN	Q28602 caenorhabdi
1043	218	9.2	2119	2	Q86XD3	Q86xd3 homo sapien	1116	214	9.1	1275	2	Q76602	Q76602 drosophila
1044	217.5	9.2	218	2	Q8SX22	Q8sy22 drosophila	1117	214	9.1	1332	2	Q8SZ27	Q8sz27 drosophila
1045	217.5	9.2	355	2	Q9L8W2	Q9l8w2 mycoplasma	1118	214	9.1	1332	2	Q86S06	Q86s06 drosophila
1046	217.5	9.2	384	2	Q9L8V9	Q9l8v9 mycoplasma	1119	214	9.1	1375	2	Q86S05	Q86s05 drosophila
1047	217.5	9.2	1521	2	Q8CHS9	Q8chs9 mus musculu	1120	214	9.1	1461	2	Q8MKQ2	Q8mkq2 drosophila
1048	217.5	9.2	1666	2	Q8LPE8	Q8lp8 chlamydomon	1121	214	9.1	1472	2	Q9V358	Q9v358 drosophila
1049	217.5	9.2	1752	2	Q7QBX5	Q7qbx5 anopheles g	1122	214	9.1	1756	2	Q7PWG9	Q7pwg9 anopheles g
1050	217.5	9.2	1880	2	O18465	O18465 hirudo medi	1123	214	9.1	1840	2	Q6Q467	Q6q467 cricetus
1051	217	9.2	391	2	Q8GX10	Q8gx10 aradidopsis	1124	214	9.1	2447	2	Q6SF13	Q6sf13 uncultured
1052	217	9.2	575	2	Q40042	Q40042 hordeum vul	1125	213.5	9.0	195	2	Q6MWV0	Q6mwv0 mycobacteri
1053	217	9.2	632	2	Q6C5E6	Q6c5e6 yarrowia li	1126	213.5	9.0	575	2	Q8CIF9	Q8cif9 mus musculu

1127	213.5	9.0	687	1	DSPP_RAT	Q62598 rattus norv	1200	209.5	8.9	2333	1	PGCA_CANFA	Q28343 canis fami1
1128	213.5	9.0	695	2	Q9XU00	Q9xuq0 caenorhabd1	1201	209.5	8.9	3080	2	Q9V602	Q9v602 drosophila
1129	213.5	9.0	959	1	N100_YEARST	Q02629 saccharomyc	1202	209.5	8.9	3109	2	Q9BMQ0	Q9bmq0 drosophila
1130	213.5	9.0	1653	2	Q63M66	Q63m66 burkholderi	1203	209.5	8.9	3276	2	Q9W321	Q9w321 drosophila
1131	213.5	9.0	1670	1	CA34_HUMAN	Q01955 homo sapien	1204	209	8.8	288	2	Q6L8H1	Q6l8h1 homo sapien
1132	213.5	9.0	1840	2	Q9J103	Q9j103 rattus norv	1205	209	8.8	457	2	Q7U0X5	Q7u0x5 mycobacteri
1133	213.5	9.0	2415	1	FGCA_HUMAN	P16112 homo sapien	1206	209	8.8	554	2	Q8S7B5	Q8s7b5 oryza sativ
1134	213	9.0	193	2	Q7XD70	Q7xdt0 oryza sativ	1207	209	8.8	554	2	Q7XFL8	Q7xfl8 oryza sativ
1135	213	9.0	218	2	Q6K574	Q6k5t4 oryza sativ	1208	209	8.8	610	2	Q6FU80	Q6fu80 candida gla
1136	213	9.0	368	2	Q8MPK1	Q8mpk1 plasmodium	1209	209	8.8	799	2	Q8BNS7	Q8bns7 mus musculu
1137	213	9.0	457	2	Q9VC90	Q9vc90 drosophila	1210	209	8.8	847	2	Q69T67	Q69t67 oryza sativ
1138	213	9.0	529	2	Q43509	Q43509 homo sapien	1211	209	8.8	934	2	Q9GMD3	Q9gmd3 bos taurus
1139	213	9.0	529	2	Q8IZU4	Q8izu4 homo sapien	1212	209	8.8	1707	1	CA24_MOUSE	P08122 mus musculu
1140	212.5	9.0	189	2	Q66K53	Q66k53 homo sapien	1213	209	8.8	2573	2	Q7SAE9	Q7sae9 neurospora
1141	212.5	9.0	220	1	SER2_GALME	Q96615 galliera me	1214	209	8.8	3137	1	CA36_CHICK	P15989 gallus gall
1142	212.5	9.0	829	2	Q94C88	Q94c88 arabidopsis	1215	208.5	8.8	194	2	Q96853	Q96853 schistosoma
1143	212.5	9.0	857	2	Q69Z83	Q69z83 mus musculu	1216	208.5	8.8	353	2	Q7QPF4	Q7qpf4 anopheles g
1144	212.5	9.0	882	2	Q80VW9	Q80vw9 mus musculu	1217	208.5	8.8	377	2	Q42627	Q42627 brassica na
1145	212.5	9.0	950	2	Q86SC8	Q86sc8 ciona intes	1218	208.5	8.8	442	1	CYS4_DICTDI	P54639 dictyostelli
1146	212.5	9.0	1035	2	Q6FU56	Q6fu56 candida gla	1219	208.5	8.8	491	2	Q6EI03	P90534 dictyosteli
1147	212.5	9.0	1804	2	Q9ZVV0	Q9zvv0 arabidopsis	1220	208.5	8.8	809	2	P90534	Q48848 arabidopsis
1148	212.5	9.0	1835	2	Q9IAU4	Q9iau4 gallus gall	1221	208	8.8	201	2	Q48848	Q48848 arabidopsis
1149	212.5	9.0	1845	2	Q80UA8	Q80ua8 mus musculu	1222	208	8.8	370	2	Q9BPK6	Q9bpk6 plasmodium
1150	212.5	9.0	2285	2	Q9HBV5	Q9hbv5 homo sapien	1223	208	8.8	370	2	Q9BPK8	Q9bpk8 plasmodium
1151	212.5	9.0	2551	2	Q8CY18	Q8cy18 streptococc	1224	208	8.8	377	2	Q26116	Q26116 plasmodium
1152	212.5	9.0	2572	2	Q7PRV6	Q7prv6 anopheles g	1225	208	8.8	394	2	Q6FX84	Q6fx84 candida gla
1153	212	9.0	347	2	Q9XT25	Q9xt25 bos taurus	1226	208	8.8	436	2	Q7QDL5	Q7qdl5 anopheles g
1154	212	9.0	390	1	CS12_WHEAT	P46525 triticum ae-	1227	208	8.8	457	2	Q79FU0	Q79fu0 mycobacteri
1155	212	9.0	568	2	Q6NUV1	Q6nuv1 brachydanio	1228	208	8.8	529	2	Q7YR44	Q7yr44 pan troglod
1156	212	9.0	619	2	Q7PQ47	Q7pq47 anopheles g	1229	208	8.8	588	2	Q9QEK6	Q9qek6 cynomolgus
1157	212	9.0	633	2	Q6EIX21	Q6eix21 canis fami1	1230	208	8.8	680	1	CA1A_MOUSE	Q05306 mus musculu
1158	212	9.0	645	2	Q9KXB9	Q9kxb9 escherichia	1231	208	8.8	689	1	CA29_HUMAN	Q14055 homo sapien
1159	212	9.0	907	2	Q26675	Q26675 theileria a	1232	208	8.8	1691	2	Q9ESQ2	Q9esq2 mus musculu
1160	212	9.0	975	2	Q6FUM3	Q6fum3 candida gla	1233	208	8.8	1691	2	Q63ZW6	Q63zw6 mus musculu
1161	212	9.0	1023	2	Q7RT42	Q7rt42 plasmodium	1234	207.5	8.8	186	2	Q9DEX8	Q9dex8 cyprinus ca
1162	212	9.0	1046	2	Q8K388	Q8k388 mus musculu	1235	207.5	8.8	236	2	Q6VSH3	Q6vsh3 arabidopsis
1163	212	9.0	3056	2	Q7USO0	Q7usq0 rhodospirell	1236	207.5	8.8	332	2	Q692G1	Q692g1 nephila cla
1164	211.5	9.0	193	2	Q9D6J0	Q9d6j0 mus musculu	1237	207.5	8.8	334	2	Q9JKB4	Q9jkb4 mus musculu
1165	211.5	9.0	226	2	Q7QCJ2	Q7qcj2 anopheles g	1238	207.5	8.8	365	1	ROAL_DROME	P07909 drosophila
1166	211.5	9.0	248	2	Q8VIW6	Q8viw6 mycobacteri	1239	207.5	8.8	389	1	SERI_BOWMO	P07856 bombyx mori
1167	211.5	9.0	286	2	Q9UIG9	Q9ulg9 drosophila	1240	207.5	8.8	428	2	Q8H9M9	Q8h9m9 erwinia sp.
1168	211.5	9.0	394	2	Q9VVC3	Q9vvc3 drosophila	1241	207.5	8.8	476	2	Q8VKAS	Q8vks5 mycobacteri
1169	211.5	9.0	431	2	Q7N1B7	Q7n1b7 photorhabdu	1242	207.5	8.8	522	2	Q9P9G7	Q9p9g7 methanococc
1170	211.5	9.0	457	2	Q7TYR9	Q7tyr9 mycobacteri	1243	207.5	8.8	603	2	Q6FLA7	Q6fla7 candida gla
1171	211.5	9.0	480	2	Q8IGI0	Q8igi0 drosophila	1244	207.5	8.8	632	2	Q8CJT6	Q8cjt6 streptomyc
1172	211.5	9.0	957	2	Q641F3	Q641f3 xenopus lae	1245	207.5	8.8	662	2	Q8VHY3	Q8vhy3 mus musculu
1173	211	8.9	253	2	Q9BLT4	Q9blt4 nephila sen	1246	207.5	8.8	981	2	Q8MQ11	Q8mq11 drosophila
1174	211	8.9	286	2	Q9VB86	Q9vb86 drosophila	1247	207	8.8	208	2	Q25949	Q25949 plasmodium
1175	211	8.9	367	2	Q7QEF9	Q7qef9 anopheles g	1248	207	8.8	303	2	Q82BN1	Q82bn1 streptomyc
1176	211	8.9	371	1	ROAL_HUMAN	P09651 homo sapien	1249	207	8.8	313	2	Q9SYZ5	Q9syz5 arabidopsis
1177	211	8.9	643	2	Q68ED0	Q68ed0 mus musculu	1250	207	8.8	314	2	Q9FCY2	Q9fcy2 arabidopsis
1178	211	8.9	890	2	Q77087	Q77087 alvinella p	1251	207	8.8	405	2	Q23057	Q23057 caenorhabdi
1179	211	8.9	967	2	Q08294	Q08294 saccharomyc	1252	207	8.8	448	2	Q715P3	Q716p3 mycobacteri
1180	210.5	8.9	255	2	Q692G5	Q692g5 nephila cla	1253	207	8.8	529	2	Q63TRS	Q63tr5 burkholderi
1181	210.5	8.9	428	2	Q6XDB9	Q6xdb9 erwinia pyr	1254	207	8.8	645	2	Q776P1	Q776p1 bacterioph
1182	210.5	8.9	471	2	Q9UAY0	Q9uay0 caenorhabdi	1255	207	8.8	645	2	Q7V2W1	Q7v2w1 stx2 conver
1183	210.5	8.9	509	2	Q7Z010	Q7z010 plodia inte	1256	207	8.8	645	2	Q7Y3C2	Q7y3c2 stx1 conver
1184	210.5	8.9	623	2	Q7SZR6	Q7szr6 brachydanio	1257	207	8.8	645	2	Q9XJK8	Q9xjk8 bacterioph
1185	210.5	8.9	624	2	Q6NUX1	Q6nux1 brachydanio	1258	207	8.8	645	2	Q8YAX7	Q8yax7 escherichia
1186	210.5	8.9	941	2	Q85Y78	Q85y78 mycobacteri	1259	207	8.8	680	1	CA1A_HUMAN	Q03652 homo sapien
1187	210.5	8.9	1488	2	Q8NPK0	Q8npk0 corynebacte	1260	207	8.8	824	2	Q7QJH6	Q7qjh6 anopheles g
1188	210.5	8.9	3190	2	Q01368	Q01368 drosophila	1261	207	8.8	1306	2	Q93N36	Q93n36 pantoea ana
1189	210	8.9	192	2	Q7XDR7	Q7xd7 oryza sativ	1262	207	8.8	1336	2	Q6RZ41	Q6rz41 homo sapien
1190	210	8.9	430	2	Q95RR2	Q95rr2 drosophila	1263	207	8.8	1516	2	Q6RZ39	Q6rz39 homo sapien
1191	210	8.9	459	2	Q6FB76	Q6fb76 acinetobact	1264	207	8.8	1751	2	Q6RZ40	Q6rz40 homo sapien
1192	210	8.9	1315	2	Q8QHLU9	Q8qhl9 xenopus lae	1265	207	8.8	2124	1	FGCA_RAT	P07857 rattus norv
1193	209.5	8.9	302	2	Q84Q60	Q84q60 arabidopsis	1266	206.5	8.7	322	2	Q8G4E5	Q8g4e5 bifidobacte
1194	209.5	8.9	319	2	Q6C4B0	Q6c4b0 yarrowia li	1267	206.5	8.7	342	1	ROAL_SCHAM	R21522 schistocerc
1195	209.5	8.9	595	2	Q82K69	Q82k69 streptomyc	1268	206.5	8.7	434	2	Q7N1B8	Q7n1b8 photorhabdu
1196	209.5	8.9	597	2	Q640K4	Q640k4 xenopus lae	1269	206.5	8.7	456	2	Q6CAZ4	Q6caz4 yarrowia li
1197	209.5	8.9	688	1	CA29_MOUSE	Q07643 mus musculu	1270	206.5	8.7	504	2	Q6J4Y8	Q6j4y8 gallus gall
1198	209.5	8.9	688	2	Q8K2W0	Q8k2w0 mus musculu	1271	206.5	8.7	528	2	Q81ZU5	Q81zu5 homo sapien
1199	209.5	8.9	920	2	Q78EC6	Q78ec6 mus sp. typ	1272	206.5	8.7	528	2	Q81ZU6	Q81zu6 homo sapien

1273	206.5	8.7	528	2	Q8NSP3	Q8n5p3 homo sapien	1346	203.5	8.6	456	2	Q638E4	Q638e4 bacillus ce
1274	206.5	8.7	573	2	Q8K7M7	Q8k7m7 streptococ	1347	203.5	8.6	476	2	Q9VA86	Q9va86 drosophila
1275	206.5	8.7	597	2	Q7P8S59	Q7p8s59 anopheles g	1348	203.5	8.6	486	1	CDSN_HUMAN	Q1517 homo sapien
1276	206.5	8.7	647	2	Q9PT10	Q9pt10 oncorhynchus	1349	203.5	8.6	500	2	Q9NP52	Q9np52 homo sapien
1277	206.5	8.7	691	2	Q66L59	Q66l59 brachydanio	1350	203.5	8.6	513	2	Q85IF9	Q85if9 mus musculu
1278	206.5	8.7	1025	1	CA16_MOUSE	Q44857 mus musculu	1351	203.5	8.6	943	2	Q8BK12	Q8bki2 mus musculu
1279	206	8.7	202	2	Q25952	Q25952 plasmodium	1352	203.5	8.6	1124	2	Q63UH1	Q63uh1 burkholderi
1280	206	8.7	370	2	Q8MPK2	Q8mpk2 plasmodium	1353	203.5	8.6	1335	2	Q6NVE4	Q6nve4 mus musculu
1281	206	8.7	374	2	Q75JC9	Q75jc9 dictyosteli	1354	203.5	8.6	1533	2	Q98HJ2	Q98hj2 rhizobium 1
1282	206	8.7	447	2	Q9SIA8	Q9sia8 arabidopsis	1355	203	8.6	196	2	Q8EFZ2	Q8efz2 methanosarc
1283	206	8.7	713	2	Q9GV24	Q9gv24 sarcophaga	1356	203	8.6	223	2	Q9C6Y9	Q9c6y9 arabidopsis
1284	206	8.7	770	2	Q7WHU6	Q7whu6 bordetella	1357	203	8.6	260	2	Q8ISA8	Q8isa8 plasmodium
1285	206	8.7	1257	2	O14654	O14654 homo sapien	1358	203	8.6	277	2	Q9GQP0	Q9gqp0 plasmodium
1286	206	8.7	1322	1	ICEN_PANAN	P20469 pantoea ana	1359	203	8.6	439	2	Q8S7B4	Q8s7b4 oryza sativ
1287	205.5	8.7	406	2	Q23288	Q23288 arabidopsis	1360	203	8.6	439	2	Q7XFL9	Q7xfl9 oryza sativ
1288	205.5	8.7	411	2	Q8W034	Q8w034 arabidopsis	1361	203	8.6	499	2	Q9NRH4	Q9nrh4 homo sapien
1289	205.5	8.7	424	2	Q6H9M6	Q6h9m6 erwinia pyr	1362	203	8.6	526	2	Q6IFW6	Q6ifw6 rattus norv
1290	205.5	8.7	428	2	Q82FT8	Q82ft8 streptomyc	1363	203	8.6	637	2	Q7Q5C7	Q7q5c7 anopheles g
1291	205.5	8.7	518	1	MTCO_MOUSE	Q60754 mus musculu	1364	203	8.6	680	2	P93658	P93658 brassica na
1292	205.5	8.7	561	2	Q961F4	Q961f4 homo sapien	1365	203	8.6	690	2	Q6K2M1	Q6k2m1 oryza sativ
1293	205.5	8.7	592	2	Q90W75	Q90w75 oncorhynchus	1366	203	8.6	813	2	Q8GFF3	Q8gff3 streptomyc
1294	205.5	8.7	680	2	Q8BSX1	Q8bsx1 mus musculu	1367	203	8.6	825	1	SES_RAT	Q63003 rattus norv
1295	205.5	8.7	1028	2	Q7Z645	Q7z645 homo sapien	1368	203	8.6	1034	1	ICEN_PANAN	Q47879 pantoea ana
1296	205.5	8.7	1112	2	Q7R9N0	Q7r9n0 plasmodium	1369	203	8.6	1253	1	DSPH_HUMAN	Q9nz44 homo sapien
1297	205	8.7	164	2	Q7XDT8	Q7xdt8 oryza sativ	1370	203	8.6	2149	2	Q6XL68	Q6xl68 bos taurus
1298	205	8.7	177	2	Q26577	Q26577 schistosoma	1371	203	8.6	2364	1	PGCA_BOVIN	P13608 bos taurus
1299	205	8.7	187	2	Q8L3S8	Q8l3s8 zea mays (m	1372	203	8.6	2365	2	Q6XL67	Q6xl67 bos taurus
1300	205	8.7	207	2	Q25701	Q25701 plasmodium	1373	202.5	8.6	425	2	Q8WSL2	Q8wsl2 plasmodium
1301	205	8.7	224	2	Q94FP7	Q94fp7 arabidopsis	1374	202.5	8.6	431	2	Q8GLD8	Q8glld8 bacillus th
1302	205	8.7	224	2	Q94FP7	Q94fp7 arabidopsis	1375	202.5	8.6	456	2	Q7UJ76	Q7uj76 rhodospirill
1303	205	8.7	368	2	Q8MPK0	Q8mpk0 plasmodium	1376	202.5	8.6	667	2	Q8XR8	Q8xrm8 ralatonia s
1304	205	8.7	393	2	Q8MPK3	Q8mpk3 plasmodium	1377	202.5	8.6	677	1	CA29_CHICK	P12108 gallus gall
1305	205	8.7	640	2	Q6KQAQ4	Q6kqa4 mus musculu	1378	202.5	8.6	771	2	Q63LV4	Q63lv4 burkholderi
1306	205	8.7	775	2	Q7M2X5	Q7m2x5 oryctolagus	1379	202.5	8.6	831	2	Q62BI8	Q62bi8 burkholderi
1307	205	8.7	1012	2	Q62KN5	Q62kn5 burkholderi	1380	202.5	8.6	1028	1	CA16_HUMAN	P12109 homo sapien
1308	205	8.7	1036	2	Q6CWM9	Q6cwm9 kluyveromyc	1381	202.5	8.6	1456	2	Q6C4S5	Q6c4s5 yarrowia li
1309	205	8.7	1084	2	O01212	O01212 homo sapien	1382	202.5	8.6	3176	1	CA36_HUMAN	P12111 homo sapien
1310	205	8.7	1131	2	Q75DJ5	Q75dj5 ashbya goss	1383	202	8.5	324	2	Q7SD81	Q7sdb1 neurospora
1311	205	8.7	1301	2	Q6P3M9	Q6p3m9 xenopus tro	1384	202	8.5	348	2	Q75CJ3	Q75cj3 ashbya goss
1312	205	8.7	1417	2	Q9HVN6	Q9hvn6 pseudomonas	1385	202	8.5	430	1	NU42 YEAST	P49686 saccharomyc
1313	205	8.7	1516	1	CA1H_HUMAN	P39060 homo sapien	1386	202	8.5	468	2	Q8WSL4	Q8wsl4 plasmodium
1314	205	8.7	1603	1	CA1F_HUMAN	Q7092 homo sapien	1387	202	8.5	484	2	Q6RBZ1	Q6rbz1 chlamydomon
1315	205	8.7	1610	2	Q92KQ8	Q92kq8 rhizobium m	1388	202	8.5	571	2	Q6H086	Q6h086 fremyella d
1316	205	8.7	2189	2	Q8IKV6	Q8ikv6 plasmodium	1389	202	8.5	692	2	Q8XT20	Q8xt20 ralatonia s
1317	205	8.7	2351	2	Q8PCQ5	Q8pcq5 xanthomonas	1390	202	8.5	700	2	Q9VXH1	Q9vxh1 drosophila
1318	204.5	8.7	279	2	Q6C3L2	Q6c3l2 yarrowia li	1391	202	8.5	733	2	Q9ADN4	Q9adn4 streptomyc
1319	204.5	8.7	280	2	Q91VQ2	Q91vq2 mus musculu	1392	202	8.5	742	2	Q8IR16	Q8ir16 drosophila
1320	204.5	8.7	443	1	Q28243	Q28243 canis famil	1393	202	8.5	749	2	Q82FQ7	Q82fq7 streptomyc
1321	204.5	8.7	483	1	MRCO_MESAU	Q9wub9 mesocricetu	1394	202	8.5	1432	2	Q9FPR8	Q9fpr8 chlamydomon
1322	204.5	8.7	611	2	Q6Z4M4	Q6z4m4 oryza sativ	1395	201.5	8.5	231	2	Q7SQN8	Q7sqn8 triticum ae
1323	204.5	8.7	654	2	Q9BX50	Q9bx50 homo sapien	1396	201.5	8.5	233	2	Q9BIT6	Q9bit6 nephila ina
1324	204.5	8.7	1019	1	CA16_CHICK	P20785 gallus gall	1397	201.5	8.5	393	2	Q18880	Q18880 caenorhabdi
1325	204.5	8.7	1310	2	Q6DFR4	Q6dfr4 xenopus tro	1398	201.5	8.5	425	2	Q6WMT5	Q6wmt5 bdellovibri
1326	204	8.6	177	1	EGG2_SCHMA	P12796 schistosoma	1399	201.5	8.5	433	2	Q9VEF5	Q9vef5 drosophila
1327	204	8.6	177	1	EGG3_SCHMA	P13396 schistosoma	1400	201.5	8.5	531	2	Q97468	Q97468 drosophila
1328	204	8.6	177	1	Q7XDR4	Q7xdr4 oryza sativ	1401	201.5	8.5	531	2	Q8SXP8	Q8sxp8 drosophila
1329	204	8.6	131	2	Q43308	Q43308 arabidopsis	1402	201.5	8.5	555	2	Q6ZQR0	Q6zqr0 homo sapien
1330	204	8.6	228	2	Q95254	Q95254 plasmodium	1403	201.5	8.5	623	2	Q8K2U8	Q8k2u8 mus musculu
1331	204	8.6	247	2	Q95254	Q95254 plasmodium	1404	201.5	8.5	888	2	Q8QW00	Q8qwu0 mus musculu
1332	204	8.6	364	2	Q7QGC0	Q7qgc0 anopheles g	1405	201.5	8.5	1344	2	Q93419	Q93419 gallus gall
1333	204	8.6	476	2	O18453	O18453 heterodera	1406	201.5	8.5	1671	2	Q7SE26	Q7se26 neurospora
1334	204	8.6	547	1	CAF1_EPHMU	P18856 ephydacia m	1407	201.5	8.5	1711	1	N214_DROME	Q9w1x4 drosophila
1335	204	8.6	717	2	Q9L0I2	Q9l0i2 streptomyc	1408	201	8.5	233	2	Q6WEQ8	Q6weq8 arabidopsis
1336	204	8.6	798	2	Q9H4U3	Q9h4u3 homo sapien	1409	201	8.5	302	2	Q9GQL8	Q9gql8 plasmodium
1337	204	8.6	832	2	Q96JF7	Q96jf7 homo sapien	1410	201	8.5	302	2	Q9GQL9	Q9gql9 plasmodium
1338	204	8.6	866	2	Q6FPD8	Q6fpd8 candida gla	1411	201	8.5	317	2	Q9BH54	Q9bh54 plasmodium
1339	204	8.6	953	2	Q67QD7	Q67qd7 symbiobacte	1412	201	8.5	381	2	Q76450	Q76450 strongyloce
1340	204	8.6	1146	1	CA1G_CHICK	Q90584 gallus gall	1413	201	8.5	422	2	Q6H9N0	Q6h9n0 erwinia sp.
1341	204	8.6	1802	2	Q17163	Q17163 brugia mala	1414	201	8.5	433	2	Q69TP6	Q69tp6 oryza sativ
1342	204	8.6	1860	2	Q81ZC6	Q81zc6 homo sapien	1415	201	8.5	445	2	Q9VEB9	Q9veb9 drosophila
1343	203.5	8.6	262	2	Q767M8	Q767m8 sus scrofa	1416	201	8.5	690	2	Q8JGL8	Q8jgl8 brachydanio
1344	203.5	8.6	280	1	C36A_MANSE	Q8t634 manduca sex	1417	201	8.5	798	2	Q8SX18	Q8sx18 drosophila
1345	203.5	8.6	341	2	Q91ZR9	Q91zr9 mus musculu	1418	201	8.5	798	2	Q9VHP0	Q9vhp0 drosophila
			353	2	Q8CJ71	Q8cj71 mus musculu							

1419	201	8.5	836	2	Q8S3T3	Q8e3t3 aegilops ta
1420	201	8.5	990	2	Q15206	Q15206 homo sapien
1421	201	8.5	1012	2	Q8XUM6	Q8xum6 ralestonia s
1422	201	8.5	1619	2	Q05331	Q05331 homo sapien
1423	201	8.5	1268	2	Q9QZS0	Q9qzs0 mus musculus
1424	201	8.5	1712	1	CA24_HUMAN	CA24_HUMAN
200.5	201	8.5	239	2	Q69T79	Q69t79 mus sapien
1426	200.5	8.5	312	2	Q18097	Q18097 oryza sativ
1427	200.5	8.5	341	2	Q18097	Q18097 caenorhabdi
1428	200.5	8.5	341	1	ROA2_MOUSE	ROA2_MOUSE
1429	200.5	8.5	353	1	ROA2_HUMAN	ROA2_HUMAN
1430	200.5	8.5	538	2	Q8BPX3	Q8bpX3 mus sapien
1431	200.5	8.5	623	1	PNT1_DROME	PNT1_DROME
1432	200.5	8.5	663	2	Q7SEL6	Q7sel6 neurospora
1433	200.5	8.5	675	2	Q90800	Q90800 gallus gall
1434	200.5	8.5	678	2	Q8SCA4	Q8sca4 stx2 conyer
1435	200.5	8.5	911	2	Q7PUV5	Q7puv5 anopheles g
1436	200.5	8.5	1271	2	Q7PC53	Q7pc53 microbubif
1437	200.5	8.5	1605	1	RRB1_MOUSE	RRB1_MOUSE
1438	200.5	8.5	2232	2	Q8IFX6	Q8ifx6 mus musculus
1439	200	8.5	125	2	Q69RC8	Q69rc8 caenorhabdi
1440	200	8.5	313	2	Q692G0	Q692g0 oryza sativ
1441	200	8.5	345	2	Q7ZWV4	Q7zwv4 nephila cla
1442	200	8.5	523	2	Q7PYW0	Q7pyw0 xenopus lae
1443	200	8.5	759	2	Q82IJ7	Q82ij7 anopheles g
1444	200	8.5	1096	2	Q8Y8Y3	Q8y8y3 streptomyc
1445	200	8.5	1258	1	ICEN_ERWHE	ICEN_ERWHE
1446	200	8.5	1743	2	Q7PVF6	Q7pvf6 erwinia her
1447	200	8.5	3716	2	Q6MYX8	Q6myx8 anopheles g
1448	199.5	8.4	212	2	Q9SFV8	Q9sfv8 mycobacteri
1449	199.5	8.4	214	1	GRP2_NICSY	GRP2_NICSY
1450	199.5	8.4	269	2	Q6C1I7	Q6c1i7 arabidopsis
1451	199.5	8.4	341	2	Q9F2Q1	Q9f2q1 nicotiana s
1452	199.5	8.4	393	2	Q261I0	Q261i0 streptomyc
1453	199.5	8.4	480	2	Q89EV2	Q89ev2 plasmodium
1454	199.5	8.4	482	2	Q6DCR4	Q6dcr4 bradyrhizob
1455	199.5	8.4	493	2	Q7SDQ7	Q7sdq7 xenopus lae
1456	199.5	8.4	519	2	Q8NCA5	Q8ncas oryza sativ
1457	199.5	8.4	670	2	Q7SDQ7	Q7sdq7 neurospora
1458	199.5	8.4	673	2	Q14052	Q14052 homo sapien
1459	199.5	8.4	737	2	Q8RUT8	Q8rut8 chlamydomon
1460	199.5	8.4	790	2	Q22872	Q22872 caenorhabdi
1461	199.5	8.4	886	2	Q9NUB7	Q9nub7 homo sapien
1462	199.5	8.4	1022	2	Q22308	Q22308 caenorhabdi
1463	199.5	8.4	1599	2	Q854N0	Q854n0 mycobacteri
1464	199.5	8.4	1685	1	CA54_HUMAN	CA54_HUMAN
1465	199.5	8.4	1961	2	Q86G33	Q86g33 drosophila
1466	199.5	8.4	1962	2	Q8NDV7	Q8ndv7 homo sapien
1467	199.5	8.4	7116	2	Q7UWZ8	Q7uwz8 rhodospirill
1468	199	8.4	173	1	EGG1_SCHMA	EGG1_SCHMA
1469	199	8.4	183	2	Q9VRT3	Q9vrt3 schistosoma
1470	199	8.4	571	1	Q6CVL4	Q6cvl4 kluyveromyc
1471	199	8.4	585	1	PGA_DROME	PGA_DROME
1472	199	8.4	675	1	CA39_CHICK	CA39_CHICK
1473	199	8.4	825	1	ICP0_HRV2H	ICP0_HRV2H
1474	199	8.4	826	2	P89473	P89473 human herpe
1475	199	8.4	1307	2	Q8JPF7	Q8jpf7 xenopus lae
1476	198.5	8.4	157	2	Q9FCT4	Q9fct4 mycoplasma
1477	198.5	8.4	191	2	Q42448	Q42448 medicago sa
1478	198.5	8.4	264	2	Q9VYL8	Q9vyl8 drosophila
1479	198.5	8.4	380	2	Q42637	Q42637 brassica ol
1480	198.5	8.4	388	2	Q95RA1	Q95ra1 drosophila
1481	198.5	8.4	465	2	Q16001	Q16001 hydra atten
1482	198.5	8.4	747	2	Q6NW57	Q6nw57 brachydanio
1483	198.5	8.4	921	1	CA19_MOUSE	CA19_MOUSE
1484	198.5	8.4	923	2	Q7YIG5	Q7yig5 oryza sativ
1485	198.5	8.4	979	2	Q919K3	Q919k3 gallus gall
1486	198.5	8.4	1329	2	Q7RZK3	Q7rzx3 neurospora
1487	198.5	8.4	1470	1	CA1G_MOUSE	CA1G_MOUSE
1488	198	8.4	346	1	RO21_XENLA	RO21_XENLA
1489	198	8.4	386	2	Q8NL07	Q8nl07 xenomonas
1490	198	8.4	393	2	Q26124	Q26124 plasmodium
1491	198	8.4	437	2	Q9VRB0	Q9vrB0 drosophila

Q9ngf7 drosophila
P48837 saccharomyc
Q73b40 bacillus ce
Q8stp5 encephalito
Q8n178 sus scrofa
Q9nd52 homo sapien
Q8t8l9 drosophila
Q9w4f0 drosophila
Q8ex56 drosophila

1492 198 8.4 453 2 Q9NGF7
1493 198 8.4 541 1 NU57 YEAST
1494 198 8.4 585 2 Q73B40
1495 198 8.4 597 2 Q8STP5
1496 198 8.4 675 2 Q9N178
1497 198 8.4 717 2 Q9ND52
1498 198 8.4 1222 2 Q8T8L9
1499 198 8.4 1222 2 Q9W4F0
1500 198 8.4 1351 2 Q8EX56

ALIGNMENTS

Q6UXC7 PRELIMINARY; PRT; 440 AA.
AC Q6UXC7; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KFGQ729.
GN ORENAMES-UNQ729;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358412; AAQ8778.1; -;
SQ SEQUENCE 440 AA; 42208 MW; B4COAFD0CAAE18B0 CRC64;

Query Match 100.0%; Score 2363; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFQGPLACLLALCLGSGEAGPLQGEESTGTNIGALGHGLDLSGVGKRAIGKAG 60
Db 1 MKFQGPLACLLALCLGSGEAGPLQGEESTGTNIGALGHGLDLSGVGKRAIGKAG 60
Qy 61 GAAGSKVSEALGGTREAQVGTQVPGFGAADALGNRVGEAAHALGNTGHEIGRAEDV 120
Db 61 GAAGSKVSEALGGTREAQVGTQVPGFGAADALGNRVGEAAHALGNTGHEIGRAEDV 120
Qy 121 IIRGADAVRGSWGQVPGHSGAWETSGGHGIFGSGGGLGGQGNPGGLGTTPWHVGPNS 180
Db 121 IIRGADAVRGSWGQVPGHSGAWETSGGHGIFGSGGGLGGQGNPGGLGTTPWHVGPNS 180
Qy 181 AGSFGHNPQCAPGQCGNGGPPNFGTNTQGAQVAPQYGSVRASNQNEGCTNPPPSGGGG 240
Db 181 AGSFGHNPQCAPGQCGNGGPPNFGTNTQGAQVAPQYGSVRASNQNEGCTNPPPSGGGG 240
Qy 241 SSNSGGSGSQSGSSGSGNGDNNSSCGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSS 300
Db 241 SSNSGGSGSQSGSSGSGNGDNNSSCGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSS 300
Qy 301 RGDSSGSSGSSGSSGSSGSGNGHGGSGGNGHKPCCKPCKPCKPCKPCKPCKPCKPCKPCK 360
Db 301 RGDSSGSSGSSGSSGSSGSGNGHGGSGGNGHKPCCKPCKPCKPCKPCKPCKPCKPCKPCK 360

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QY 361 MREISKEGNRLGGSGDNYRGQSSWGS GGGDAVGGVNTVNTSETSPGMFNFTFWKNFKS 420
DB 361 MREISKEGNRLGGSGDNYRGQSSWGS GGGDAVGGVNTVNTSETSPGMFNFTFWKNFKS 420
QY 421 KLGFINWDAINKQDQSRIP 440
DB 421 KLGFINWDAINKQDQSRIP 440

RESULT 2
Q6E0U4 PRELIMINARY; PRT; 476 AA.
AC Q6E0U4;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Dermokine-beta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Imai T., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RT complex on human chromosome 19q13.1.";
RL Genomics 84:384-397(2004).
DR ENBL; AY622965; AAT68269.1; -.
SQ SEQUENCE 476 AA; 47010 MW; E2206CCB64AC4992 CRC64;

Query Match 84.5%; Score 1996; DB 2; Length 476;
Best Local Similarity 87.1%; Pred. No. 2.8e-86;
Matches 378; Conservative 2; Mismatches 0; Indels 54; Gaps 2;

QY 1 MKFOGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLDGLDSEGVGAIGKEAG 60
DB 1 MKFOGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLDGLDSEGVGAIGKEAG 60
QY 61 GAAGSKVSEALGQGTREAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGROAEDV 120
DB 61 GAAGSKVSEALGQGTREAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGROAEDV 120
QY 121 IRHGADAVRGSWQVPGHSGAWETSGGHGIFGSGGLGGQGGNPGGLGTPWVHGYPGNS 180
DB 121 IRHGADAVRGSWQVPGHSGAWETSGGHGIFGSGGLGGQGGNPGGLGTPWVHGYPGNS 180
QY 181 AGSGFMNPQAPWGQGGNGGPPNFGTNTQGAVAQPGYGVSRASQNEGGCTNPPPSGGG 240
DB 181 AGSGFMNPQAPWGQGGNGGPPNFGTNTQGAVAQPGYGVSRASQNEGGCTNPPPSGGG 240
QY 241 SSNSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 300
DB 241 SSNSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 296
QY 301 RGDGSGESSWGSSTGSSSGHGGSGGGNGHKPKGCEKPGNEARGSGESGIGQFRRGQGYSSN 360
DB 297 RGDGSGESSWGSSTGSSSGHGGSGGGNGHKPKGCEKPGNEARGSGESGIGQFRRGQGYSSN 346
QY 361 MREISKEGNRLGGSGDNYRGQSSWGS GGGDAVGGVNTVNTSETSPGMFNFTFWKNFKS 420
DB 347 -----NSETSPGMFNFTFWKNFKS 366
QY 421 KLGFINWDAINKQ 434
DB 367 KLGFINWDAINKQ 380

RESULT 3
Q6E0U6 PRELIMINARY; PRT; 517 AA.
AC Q6E0U6;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Dermokine-beta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Imai T., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RT complex on human chromosome 19q13.1.";
RL Genomics 84:384-397(2004).
DR ENBL; AY622963; AAT68267.1; -.
SQ SEQUENCE 517 AA; 51660 MW; 61E2974EEB36650B CRC64;

Query Match 44.1%; Score 1043; DB 2; Length 517;
Best Local Similarity 48.9%; Pred. No. 1.3e-41;
Matches 231; Conservative 41; Mismatches 102; Indels 98; Gaps 13;

QY 1 MKPQGPPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLDGLDSEGVGAIGKEAG 60
DB 1 MKLQGSILACLLALCLGGAANPLHSGEGTGA-----SAAHGAGDAISHGIGAVGQAK 56
QY 61 GAAGSKVSEALGQGTREAVGTGVRQVPGFCAADALGNRVGEAAHALGNTGHEIGROAEDV 120
DB 57 EAASSGIQNALGQGHGEGGTLGMSRG-----DVFEHRLGEAAARSIGNAGNEIGROAEDI 112
QY 121 IRHGADAVRGSWQVPGHSGAWETSGGHGIFGSGGLGGQGGNPGGLGTPWVHGYPGNS 180
DB 113 IROGVDAVH-----NAGSMGTSGHGAYGSGGAG--VQGNPGPGQGTWASG----- 157
QY 181 AGSGFMNPQAPWGQGGNGGPPNFGTNTQGAVAQPGYGVSRASQNEGGCTNPPPSGS--- 237
DB 158 -GNYGTNSLGGVGGQGGNGGPLYETNAQGAQVAGYGVGTVRGNQNSGCTNPPPSGSHS 216
QY 238 ---GGGSSNSGG--GSGSQSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 286
DB 217 FNSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 274
QY 287 GSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 325
DB 275 GNSNSGNSGNSGSGSGSRDIETSNFDEGYSVSRGTGSRGSGG-----GSGSGSGSGSGSG 329
QY 326 GNGHKGPKGCEKPGNEARGSGESGIGQFRRGQGYSSNMRREISKGNRLGGSGDNYRGQSS 385
DB 330 GGN--KPECNPNPNVDMAGSGSQ-----GSGSGSGSGSGSGSGSGSGSGSGSGSG 357
QY 386 WSGSGGDAVGGVNTVNTSETSPGMFNFTFWKNFKSLGFINWDAINKQDQRSS 437
DB 358 GGNIQKEAVNGLATMNSDASTLFPNIDNFWENLKS KTRFINWDAINKHAPS 409

RESULT 4
Q6P253 PRELIMINARY; PRT; 508 AA.
AC Q6P253;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE 1110014F24Rik protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning.";
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX RIKEN FANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK081753; BAC38319.1;
 DR GGD; MGI:1920962; 1110014P24Rik.
 DR GO; GO:0005615; C:extracellular space; TAS.
 SQ SEQUENCE 407 AA; 42735 MW; 9D243DA7077983F6 CRC64;
 Query Match 23.1%; Score 546.5; DB 2; Length 407;
 Best Local Similarity 45.8%; Pred. No. 1.9e-18;
 Matches 130; Conservative 29; Mismatches 86; Indels 39; Gaps 9;
 QY 175 GYPCNSAGSGFMPPQCAPWCGGNGPPNFTGTTCGAVAPQGYGVRASNQNEGCTNPPPP 234

Db 34 GHPGQEQATMGLTLWALVVRVAMADHSTKMPRELWLSLGYGTVRGNQNSGCTNPPPP 93
 QY 235 SGS-----GGSSNSGG-GSGSQSGSGSGNG-----DNNKSSSGSGSSSGSSGS 280
 Db 94 SGSHSFNSGSGSNDGSRGSGSGSHGSGGSGGSGGSGGSGSS--SSGSNSGN 151
 QY 281 SSGSGSGSGSGSGSGSGSG--GSRG-----DSGSESSGSSSTGSSGNHSGSGGNGHKPG 333
 Db 152 SNSGNSGNSGNSGNSGSGSGSDIETSPDEGYSVSRGTGSGSGSGSGSGG--KEP 209
 QY 334 CEKPGNEARGSGESGICQPRGQGVSNMREISKENRLGLGSGGDNRYRGSGSGSGGDA 393
 Db 210 CNPFGNDVRMAGSGSQE-----SKSSHLLGGSHD-YQHGSGNGNIOKEA 255
 QY 394 VGGVTVNSETSPGMPNPDFTFWNPKSLGFINWDAINKDQRSS 437
 Db 256 VNGLTMTNSDASTLPFNIDNFWENLKSRTFRFINWDAINKGHAPS 299
 RESULT 7
 ID Q6FPR0 PRELIMINARY; PRT; 1553 AA.
 AC Q6FPR0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Similarities with tr|Q08294 Saccharomyces cerevisiae YOL155c.
 GN ORFNames=CAGLQJ017719;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisramé A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrast A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 DR EMBL; CR380956; CAG60731.1;
 SQ SEQUENCE 1553 AA; 145623 MW; A17810AE221D7480 CRC64;
 Query Match 20.6%; Score 486; DB 2; Length 1553;
 Best Local Similarity 33.6%; Pred. No. 3.9e-15;
 Matches 143; Conservative 38; Mismatches 204; Indels 40; Gaps 10;
 QY 17 GSGEAPLQSGES---TGNTIGALGHLGDLSEGVGKALGKAGGAGKVSSEALQ 73
 Db 432 GSGSGSGTSGSGSGSGSGSESGSGSGSGSGSTPGECSGSGSGSGSNAPGSGSGS 491
 QY 74 GTREAVGTGVRQVP---CFGAADALGNRVGSAHALGNTGHEIGRAQEDVIRHGADAVR 129
 Db 492 GSGSGSGSGSGTTPGEGSGSGSGTGTSGSGSGSEGGSGSGSGSGSTPGECSGSGS 551
 QY 130 GSWQGVPHSGAWETSGGHGIGSGSGGLG-----GCGQGNPGCLGTPWHVYPGNSAGSF 184
 Db 552 GSGSGTSGSGSGSGSGSESGSGSGSGSGSTPGECSGSGSGSGSGSTPGECSGSGSG 610
 QY 185 GNPQCAPWCGGNGPPNFTGTTCGAVAPQGYGVRASNQNEGCTNPPPPSGSGGS --- 241


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Db 611 TGSAGSGSGSGSGSGSGSGSGTTPCGSGSGSGSVSGSGSGTTPCGSGSGSGSG 670
Qy 242 ---SNGSGSGSGSGSGSGSGSGTTPCGSGSGSGSVSGSGSGTTPCGSGSGSGSG 291
Db 671 TGSAGSGSGSGSGSGSGSGSGTTPCGSGSGSGSVSGSGSGTTPCGSGSGSGSG 730
Qy 292 GSSGSGSGSGSGSGSGSGSGTTPCGSGSGSGSVSGSGSGTTPCGSGSGSGSG 346
Db 731 SGSGSGSGSGSGSGSGSGTTPCGSGSGSGSVSGSGSGTTPCGSGSGSGSGSG 790
Qy 347 ---SGTCGFCGCGVSSNMREISKEGNRLCGSGDNRGCGSGSGSGSGSGSGSG 402
Db 791 PEGSGSGSGSGSGSGSGSGTTPCGSGSGSGSVSGSGSGTTPCGSGSGSGSGSG 402
Qy 403 ETSFG 407
Db 846 GSNFG 850

RESULT 8
Q6CHN8
ID Q6CHN8 PRELIMINARY; PRT; 1274 AA.
AC Q6CHN8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarity (Fragment).
GN ORFNames=YAL10A06853g;
OS Yarrowia lipolytica CL1B99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1B99;
RG Genolevures;
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blyksten C.,
RA Bolesame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1B99;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382127; CAG3749.1; -.
FT NON TER
SQ SEQUENCE 1274 AA; 116259 MW; 33583C8CE60B3E2 CRC64;

Query Match 19.9%; Score 471; DB 2; Length 1274;
Best Local Similarity 36.2%; Pred. No. 1.7e-14;
Matches 149; Conservative 27; Mismatches 168; Indels 68; Gaps 16;

Qy 17 GSGEAGPLQSGEES-----TGTNIGELGHLGDLALSGVGKAIKGAAGAAAGSKVSE 69
Db 881 GSGSGGDTSGNGSGSGDGTSGNGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 932
Qy 70 ALGGTGTEAVGTGVRVPGFAGADALGNRVGEAAHALNTGHEIGROAEDVIRGADAV 128
Db 933 --GDGTS---GNGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 981
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Qy 129 ---RGSMQGVPHSGAWETSGHGIFGSGQGLG-GQGGNPGGLGTPTWVHYVPGNSAGSF 184
Db 982 GNGSGSGSGDGGSSNGSGSGDGTSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 1036
Qy 185 GMPPOGAPWQGGNGGPPNFTGTQGAAPGCVGSVFASNQNECTNPPPSGSGSGS--- 241
Db 1037 -----SGNGG-----SGSGSGSDSGSGSGSGSGSGSGSGSGSGSGSGSG 1080
Qy 242 SNGSGSGSGSGSGSGSGSGNDNNGSSG---GSSGSGSGSGSGSGSGSGSGSGSGSG 298
Db 1081 SDGSGSGSGSGSGSGSGSGSDSGSGSGSGSGSGSGSGSDSGSGSGSGSGSGSG 1139
Qy 299 GSRGDSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 357
Db 1140 GSDSGSGSGSGSGSGSGSGSDSGSGSGSGSGSGSGSGSDSGSGSGSGSGSGSG 1199
Qy 358 SSNWREISKEGNRLCGSGDNRGCGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 409
Db 1200 DSGSGSGSGSGSDSGSGSGS-----GSGSDSGSGSGSGSGSGSGSGSGSG 1243

RESULT 9
Q7TWC0
ID Q7TWC0 PRELIMINARY; PRT; 1938 AA.
AC Q7TWC0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PE-PGRS FAMILY PROTEIN.
GN Name=PE_PGRS55; OrderedLocusNames=Mb3541;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duchoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
DR EMBL; BX248346; CAD95727.1; -.
DR InterPro; IPR002202; HMG-CoA_red.
DR InterPro; IPR000084; PE_region_N.
DR InterPro; IPR002173; PfKB.
DR Pfam; PF00934; PE; 1.
DR ProDom; PD001223; PE_region_N; 1.
DR PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1.
DR PROSITE; PS00583; PFKE_KINASES_1; UNKNOWN_2.
KW Complete proteome.
SQ SEQUENCE 1938 AA; 152029 MW; 3C73A507FEB0F9C CRC64;

Query Match 19.5%; Score 460.5; DB 2; Length 1938;
Best Local Similarity 31.5%; Pred. No. 7.3e-14;
Matches 146; Conservative 36; Mismatches 173; Indels 109; Gaps 17;

Qy 17 GSGEAGPLQSGEESTGTNIGELGHLGDLALSGVGKAIKGAAGAAAGSKVSEALGG 76
Db 1218 GAGSGP-----NTSPGNGSGQ-----GQGGSGSGAGGAAG--AGGAGGANGTAGNGGQ 1266
Qy 77 EAVGTGVRVPGFAGADALGNRVGEAAHALNTGHEIGROAEDVIRGADAVRGSWGVP 136
Db 1267 GAGGTG-----GAGAAASSATNGSGSGAGGTGGAGTGGG-----GGDVGAGGANG 1313
Qy 137 GH-----SGAWETSGHGIFGSGQGLGQ-----GQGNPGGLGTP 171
Db 1314 GHGSDAGDGGANGANNRSGSGSFLAGGTGGAAGDGGQGGGAGGAGGAGGAGGT 1373
Qy 172 WHGYFGN-----SAGSFCMNPQAGPWQGGNGGPPNFTGTQ--GAVAQPGYGSV 220
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